

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds
(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-1
Perfect score: 44
Sequence: 1 FLYDVIAT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	74	2	Q29311 sus scrofa
2	44	100.0	1304	1	CD45_HUMAN
3	43	97.7	1200	2	Q91054
4	40	90.9	1290	2	O6ED60
5	40	90.9	1303	2	O6ED61
6	40	90.9	1303	2	O6ED62
7	39	88.6	365	2	O6MI02
8	38	86.4	300	2	P94296
9	38	86.4	445	1	ARLY_XYLFA
10	38	86.4	445	1	ARLY_XYLFA
11	38	86.4	1152	1	CD45_MOUSE
12	38	86.4	1291	2	O618T2
13	38	86.4	1343	2	O64730
14	37	84.1	681	1	VGP_MABVM
15	37	84.1	681	1	VGP_MABVM
16	37	84.1	681	2	O36428
17	37	84.1	681	2	O6T6U0
18	37	84.1	681	2	O6U666
19	37	84.1	681	2	O71VM1
20	36	81.8	681	2	O36429
21	36	81.8	1817	2	O8YTS1
22	35	79.5	267	2	O61SF9
23	35	79.5	297	2	O6VIO5
24	35	79.5	297	2	O9YMG2
25	35	79.5	364	1	USGP_EBOIC
26	35	79.5	364	1	USGP_EBOIC
27	35	79.5	364	1	USGP_EBOIC
28	35	79.5	364	1	USGP_EBOIC
29	35	79.5	364	1	USGP_EBOIC
30	35	79.5	364	1	USGP_EBOIC
31	35	79.5	364	2	O771U4

32	35	79.5	365	1	USGP_EBOIC	O66811 ebola virus
33	35	79.5	367	1	USGP_EBOIC	O66800 ebola virus
34	35	79.5	367	1	USGP_EBOIC	O89559 ebola virus
35	35	79.5	367	2	O89559	O89559 ebola virus
36	35	79.5	367	2	O89559	O89559 ebola virus
37	35	79.5	372	1	USGP_EBOIC	O60172 ebola virus
38	35	79.5	372	1	USGP_EBOIC	O60173 ebola virus
39	35	79.5	372	2	O771U4	O771U4 ebola virus
40	35	79.5	676	1	VGP_EBOIC	O66810 ebola virus
41	35	79.5	676	1	VGP_EBOIC	O66810 ebola virus
42	35	79.5	676	1	VGP_EBOIC	O66810 ebola virus
43	35	79.5	676	1	VGP_EBOIC	O66810 ebola virus
44	35	79.5	676	1	VGP_EBOIC	O66810 ebola virus
45	35	79.5	676	1	VGP_EBOIC	O66810 ebola virus

ALIGNMENTS

RESULT 1
ID: Q29311 PRELIMINARY; PRT; 74 AA.
AC: Q29311;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Leukocyte common antigen (CD45) (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine CDNA
RT library."
RL Mamm. Genome 7:509-517 (1996).
DR EMBL; F14696; CAA23198.1; -.
DR HSSP; P18052; 1P15.
FT NON_TER 1 74 1
FT NON_TER 74 74 1
SQ SEQUENCE 74 AA; 8358 MW; 0398586AB935ADAE CRC64;
Query Match 100.0%; Score 44; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIAT 9
Db 27 FLYDVIAT 35
RESULT 2
ID: CD45_HUMAN STANDARD; PRT; 1304 AA.
AC P08575; Q16614; Q9H0Y6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (BC 3.1.3.48) (L-CA) (CD45 antigen)
DE (1200).
GN Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RX MEDLINE=88061067; PubMed=2824653;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;

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DR	GO; GO:0042098; P:T-cell proliferation; IMP.
DR	GO; GO:0046552; P:lymphocyte differentiation; IMP.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR000387; TYR_phosphatase.
DR	InterPro; IPR000242; Tyr_PP.
DR	Pfam; PF00041; fn3; 3.
DR	Pfam; PF00102; Y_phosphatase; 2.
DR	PRINTS; PR00700; PRTPHPTASE.
DR	SMART; SM00060; FN3; 2.
DR	SMART; SM00194; PTFC; 1.
DR	PROSITE; PS00853; FN3; 2.
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW	Hydrolase; Receptor.
FT	NON TER
SO	SEQUENCE 878 AA; 99891 MW; 19E5FCD7909D4CA6 CRC64;
Cy	Query Match 1 ILPYDYNRV 9 100.0%; Score 50; DB 2; Length 878; Best Local Ssimilarity 100.0%; Pred. No. 0.78; Mismatches 0; Gaps 0; Matches 9; Conservative 0; Indels 0;
Db	536 ILPYDYNRV 544
RESULT 4	
O6LDD3	PRELIMINARY; PRT; 962 AA.
ID O6LDD3	
AC O6LDD3	
DT 05-JUL-2004 (TRENBLREL. 27, Created)	
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)	
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)	
BT leukocyte common antigen.	
CN Name-L-CA:	
OS Rattus norvegicus (Rat).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX NCBI_TaxID=10116;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN-Sprague-Dawley;	
RA MEDLINE=85201591; PubMed=3158393; DOI=10.1016/0092-8674(85)90063-7;	
RT Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;	
RT "Evidence from cDNA clones that rat leukocyte-common antigen (T200 M-	
RT spans the lipid bilayer and contains a cytoplasmic domain of 80,000 M-	
RT r";	
RL Cell 41:83-93(1985).	
EMBL; M10072; AAAI513.1; -.	
DR HSSP; PI8031; IASV.	
DR GO; GO:0015787; F:hydrolyase activity; IEA.	
DR GO; GO:0004725; F:protein tyrosine acid dephosphorylation; IEA.	
DR GO; GO:0006470; P:protein amino acid phosphorylation; IEA.	
DR InterPro; IPR003961; FN_III.	
DR InterPro; IPR008957; FN_III-like.	
DR InterPro; IPR003595; PTPC_motif.	
DR InterPro; IPR000387; TYR_phosphatase.	
DR InterPro; IPR000242; Tyr_PP.	
DR Pfam; PF00041; fn3; 2.	
DR Pfam; PF00102; Y_phosphatase; 2.	
DR PRINTS; PR00700; PRTPHPTASE.	
DR SMART; SM00060; FN3; 2.	
DR SMART; SM00194; PTFC; 2.	
DR PROSITE; PS00853; FN3; 2.	
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.	
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.	
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.	
KW Hydroxylase.	
SO SEQUENCE 962 AA; 109934 MW; D2E6B7F23D29CC92 CRC64;	

Query Match	100.0%	Score 50.1	DB 2	Length 962
Best Local Similarity	100.0%	Pred. No. 0.86		
Matches	9	Conservative 0	Mismatches 0	Indels 0
QY	1 ILPDYNRV 9			
DB	344 ILPDYNRV 352			
RESULT	Unigene			
CD45_MOUSE	STANDARD;	PRT;	1152 AA.	
AC	P06800;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	05-JUN-2004 (Rel. 44, Last annotation update)			
DE	Leukocyte common antigen precursor (EC 3.1.3.48)..(L-CN)..(Lymphocyte			
DS	Common antigen Ly-5 (CD45) (1200).			
OS	Name=Peptic; Synonyms=Ly-5;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OK	NCBI_TaxId=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=86313686; PubMed=2944116;			
RA	Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;			
RT	"Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).			
RN	(2)			
RP	REVISIONS.			
RA	Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).			
RN	(3)			
RP	SEQUENCE OF 10-124 FROM N.A.			
RC	TISSUE=T-cell;			
RX	MEDLINE=86042665; PubMed=3864163;			
RA	Shen F.-W., Saga Y., Littman G., Freeman G., Tung J.-S., Cantor H.,			
RA	Boyse E.A.;			
RT	"Cloning of Ly-5 cDNA."			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).			
RN	(4)			
RP	SEQUENCE OF 822-1152 FROM N.A.			
RX	MEDLINE=87092355; PubMed=2948186;			
RA	Raechke W.C.;			
RT	"Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B-			
RL	and T-lymphocyte lineages.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).			
RN	(5)			
RP	INTERACTIONS WITH GANAB AND PRKCSH.			
RA	MEDLINE=91294720; PubMed=9148925; DOI=10.1074/jbc.272.20.13117;			
RA	Arendt C.W., Ostergaard H.L.;			
RT	"Identification of the CD45-associated 116-kDa and 80-kDa proteins as			
RT	the alpha- and beta-subunits of alpha-glucosidase II."			
RL	J. Biol. Chem. 272:13117-13125(1997).			
CC	-1- FUNCTION: Required for T-cell activation through the antigen			
CC	receptor. The first PPRase domain has enzymatic activity, while			
CC	the second one seems to affect the substrate specificity of the			
CC	first one.			
CC	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	-1- SUBUNIT: Binds GANAB and PRKCSH.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named isoforms=1;			
CC	Comment=A number of isoforms are produced.			
CC	Name=1;			
CC	Isoid=P06800-1; Sequence=Displayed;			
CC	-1- DEVELOPMENTAL STAGE: Expression is restricted to the hematopoietic			
CC	compartment of development.			
CC	-1- PTM: Heavily N- and O-glycosylated.			
CC	-1- SIMILARITY: Belongs to the tyrosine phosphatase family.			
CC	Receptor class 1/6 subfamily.			

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CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: M14342; AAA39458.1; -
 DR EMBL: M1934; AAA39461.1; -
 DR EMBL: M15174; AAA40161.1; -
 DR PIR: A23329; A23329.
 DR PIR: A23334; A23334.
 DR HSSP: P18052; 1YFO.
 DR MGD: MG1:97810; PEPIC.
 DR GO: GO:0005515; Cytoplasmic side of plasma membrane; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN III-11ke.
 DR InterPro: IPR000387; Tyr. phosphatase.
 DR InterPro: IPR000242; Tyr. P.
 DR Pfam: PF00041; fn3; 3.
 DR Pfam: PF00102; Y. phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS50383; TYR. PHOSPHATASE 1; 2.
 DR PROSITE: PS50056; TYR. PHOSPHATASE 2; 2.
 DR PROSITE: PS50055; TYR. PHOSPHATASE_PTP; 2.
 DR Alternative splicing; Antigen; Glycoprotein; Hydrolase;
 DR Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 DR Transmembrane.
 KM SIGNL 1 23
 FT CHAIN 24 1152
 FT DOMAIN 24 425
 FT TRANSMEM 426 447
 FT DOMAIN 448 1152
 FT DOMAIN 332 420
 FT DOMAIN 333 420
 FT DOMAIN 520 769
 FT DOMAIN 811 1084
 FT ACT_SITE 701 701
 FT ACT_SITE 1016 1016
 FT ACT_SITE 1016 1016
 FT CARBOHYD 68 68
 FT CARBOHYD 72 72
 FT CARBOHYD 79 79
 FT CARBOHYD 114 114
 FT CARBOHYD 119 119
 FT CARBOHYD 151 151
 FT CARBOHYD 172 172
 FT CARBOHYD 183 183
 FT CARBOHYD 208 208
 FT CARBOHYD 277 277
 FT CARBOHYD 288 288
 FT CARBOHYD 318 318
 FT CARBOHYD 350 350
 FT CARBOHYD 379 379
 FT SEQUENCE 1152 AA; 130421 MW; 130421 MW; BAD956B4E32E812 CRC64;
 Query Match 100.0%; Score 50; DB 1; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q91BD8 PRELIMINARY; PRT; 1216 AA.
 ID Q91BD8
 AC Q91BD8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE CD45
 OS *Cyprinus carpio* (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 NC NCB1_TaxID=7962;
 RX MEDLINE=20531692; PubMed=11081442; DOI=10.1006/esim.2000.0294;
 RA Fujiki K., Shin D.H., Nakao M., Yano T.;
 RT "Molecular cloning of carp (*Cyprinus carpio*) leukocyte cell-derived
 RT chemotaxin 2, a late maturation factor beta, CD45 and lysozyme C by use
 RT of suppression subtractive hybridisation.";
 RL Fish Shellfish Immunol. 10:643-650(2000).
 DR EMBL: AB031424; BA92179.1; -
 DR HSSP: P18052; 1YFO.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR000387; Tyr. phosphatase.
 DR InterPro: IPR000242; Tyr. P.
 DR Pfam: PF00102; Y. phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 2.
 DR PROSITE: PS50853; FN3; 1.
 DR PROSITE: PS50383; TYR. PHOSPHATASE 1; 2.
 DR PROSITE: PS50056; TYR. PHOSPHATASE 2; 2.
 DR PROSITE: PS50055; TYR. PHOSPHATASE_PTP; 2.
 DR Hydrolase. 1216 AA; 138251 MW; 9D2E45F41721D2CF CRC64;
 KM SEQUENCE 1216 AA; 138251 MW; 9D2E45F41721D2CF CRC64;
 Query Match 100.0%; Score 50; DB 2; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDNRV 9
 DB 596 ILPYDNRV 604
 RESULT 7
 Q91BF0 PRELIMINARY; PRT; 1245 AA.
 ID Q91BF0;
 AC Q91BF0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE CD45 (EC 3.1.3.48).
 GN Name=PTPrc;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 NC NCB1_TaxID=31033;
 RX NCB1_TaxID=31033;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A0243430; CAB96212.1; -
 DR HSSP: P18052; 1YFO.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-1

Perfect score: 44

Sequence: 1 FLYDVIAST 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	74	2 Q29311	Q29311 sus scrofa
2	44	100.0	1304	1 CD45 HUMAN	P08575 homo sapien
3	43	97.7	1200	2 Q91054	Q91054 heterodontu
4	40	90.9	1290	2 Q6ED60	Q6ED60 actus vocif
5	40	90.9	1303	2 Q6ED61	Q6ED61 actus nancy
6	40	89.6	1303	2 Q6ED62	Q6ED62 actus nigri
7	39	88.6	365	2 Q8MJQ2	Q8MJQ2 actus vocif
8	38	86.4	300	2 P94296	P94296 bacillus fi
9	38	86.4	445	1 ARLY_XYLFA	Q9PEMS xyliella fas
10	38	86.4	445	1 ARLY_XYLFT	P59621 xyliella fas
11	38	86.4	1152	1 CD45 MOUSE	P06800 mus musculu
12	38	86.4	1291	2 Q61812	Q61812 mus musculu
13	38	86.4	1343	2 Q64730	Q64730 mus musculu
14	37	84.1	681	1 VGP_MABVM	P35253 marburg vir
15	37	84.1	681	1 VGP_MABVP	P35254 marburg vir
16	37	84.1	681	2 Q6T6U0	Q6T6U0 lake victor
17	37	84.1	681	2 Q6T6U0	Q6T6U0 lake victor
18	37	84.1	681	2 Q6T6U0	Q6T6U0 lake victor
19	37	84.1	681	2 Q6T6U0	Q6T6U0 lake victor
20	36	81.8	681	2 Q36429	Q36429 lake victor
21	36	81.8	1817	2 Q81751	Q81751 anabaena sp
22	35	79.5	267	2 Q6LSF9	Q6LSF9 photobacter
23	35	79.5	297	2 Q6VIO5	Q6VIO5 zaire ebola
24	35	79.5	297	2 Q6VIO5	Q6VIO5 zaire ebola
25	35	79.5	364	1 VSGP_EBOEC	P87670 ebola virus
26	35	79.5	364	1 VSGP_EBOEC	P87670 ebola virus
27	35	79.5	364	1 VSGP_EBOEC	P87670 ebola virus
28	35	79.5	364	1 VSGP_EBOEC	P87670 ebola virus
29	35	79.5	364	1 VSGP_EBOEC	P87670 ebola virus
30	35	79.5	364	1 VSGP_EBOEC	P87670 ebola virus
31	35	79.5	364	2 Q77LU4	Q77LU4 zaire ebola

ALIGNMENTS

RESULT 1									
ID	Q29311	PRELIMINARY;	PRT;	74 AA.					
AC	Q29311								
DT	01-NOV-1996 (TREMBLrel. 01, Created)								
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)								
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)								
DE	Leukocyte common antigen (CD45) (Fragment).								
OS	Sus scrofa (Pig).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.								
OX	NCBI_TaxID=9823;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Small intestine;								
RX	MEDLINE=96327607; PubMed=8672129;								
RA	Winerice A.K., Fredholm M., Davies W.;								
RT	"Evaluation and characterization of a porcine small intestine cDNA								
RL	library".								
DR	Mamm. Genome 7:509-517(1996).								
DR	EMBL; F14696; CAA23198.1; -.								
DR	HSSP; P18052; P1P5.								
FT	NON TER	1							
FT	NON TER	1							
SQ	SEQUENCE	74 AA;	8358 MW;	0398586AB935ADAE CRC64;					
Query Match									
Best Local Similarity 100.0%; Score 44; DB 2; Length 74;									
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1 FLYDVIAST 9								
DB	27 FLYDVIAST 35								
RESULT 2									
ID	CD45_HUMAN	STANDARD;	PRT;	1304 AA.					
AC	P08575; Q16614; Q9H0Y6;								
DT	01-AUG-1988 (Rel. 08, Created)								
DT	10-OCT-2003 (Rel. 42, Last sequence update)								
DT	05-JUL-2004 (Rel. 44, Last annotation update)								
DE	Leukocyte common antigen precursor (EC 3.1.1.3.48) (L-CAN) (CD45 antigen)								
DE	(T200).								
GN	Name=PTPRC; Synonyms=CD45;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.								
RC	TISSUE=Lymphocytes;								
RX	MEDLINE=88061067; PubMed=2824653;								
RA	Struelli M., Hall L.R., Saga Y., Schlossman S.F., Salto H.;								

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RT "differential usage of three exons generates at least five different
RT mRNAs encoding human leukocyte common antigens."
RT J. Exp. Med. 166:1548-1566 (1987).
RT [2]
RX SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RX MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common
RT antigen).";
RT EMBO J. 6:1251-1257 (1987).
RT [3]
RP SEQUENCE OF 191-1304 FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=89009812; PubMed=2971730;
RX Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
RT antigen (CD45) gene."
RT J. Immunol. 141:2781-2787 (1988).
RT [4]
RN FUNCTION
RX MEDLINE=89017162; PubMed=2845400;
RA Chatomneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
RT protein tyrosine phosphatase."
RT Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186 (1988).
RT [5]
RN MOTAGENESIS
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
RT domains of the receptor-linked protein tyrosine phosphatases LCA and
RT LAR."
RT EMBO J. 9:2399-2407 (1990).
CC -1- FUNCTION: Required for T-cell activation through the antigen
CC receptor. The first PTase domain has enzymatic activity, while
CC the second one seems to affect the substrate specificity of the
CC first one.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBUNIT: Binds GANAB and PRKCSH (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=At least 8 isoforms are produced;
CC Name=1;
CC IsoId=P08575-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P08575-2; Sequence=VSP_007780;
CC -1- PTM: Heavily N- and O-glycosylated.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 1/6 subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD45 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
CC
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CC
CC EMBL; Y00638; CAA68669.1; -
CC EMBL; Y00662; CAA68269.1; -
CC EMBL; M23492; AAD15273.2; -
CC EMBL; M23496; AAD15273.2; JOINED.
CC EMBL; M23466; AAD15273.2; JOINED.
CC EMBL; M23467; AAD15273.2; JOINED.
CC EMBL; M23468; AAD15273.2; JOINED.
CC EMBL; M23469; AAD15273.2; JOINED.
CC EMBL; M23470; AAD15273.2; JOINED.

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DR EMBL; M23471; AAD15273.2; JOINED.
DR EMBL; M23472; AAD15273.2; JOINED.
DR EMBL; M23473; AAD15273.2; JOINED.
DR EMBL; M23474; AAD15273.2; JOINED.
DR EMBL; M23475; AAD15273.2; JOINED.
DR EMBL; M23476; AAD15273.2; JOINED.
DR EMBL; M23477; AAD15273.2; JOINED.
DR EMBL; M23478; AAD15273.2; JOINED.
DR EMBL; M23479; AAD15273.2; JOINED.
DR EMBL; M23480; AAD15273.2; JOINED.
DR EMBL; M23481; AAD15273.2; JOINED.
DR EMBL; M23482; AAD15273.2; JOINED.
DR EMBL; M23483; AAD15273.2; JOINED.
DR EMBL; M23484; AAD15273.2; JOINED.
DR EMBL; M23485; AAD15273.2; JOINED.
DR EMBL; M23486; AAD15273.2; JOINED.
DR EMBL; M23487; AAD15273.2; JOINED.
DR EMBL; M23488; AAD15273.2; JOINED.
DR EMBL; M23489; AAD15273.2; JOINED.
DR EMBL; M23490; AAD15273.2; JOINED.
DR EMBL; M23491; AAD15273.2; JOINED.
DR PIR; A46546; A46546.
DR HSSP; P18031; 1C88.
DR Inact; P08575; -.
DR GlycoSiteDB; P08575; -.
DR Genew; HGNC:9666; PTPRC.
DR MIM; 151460; -.
DR GO; GO:0005887; C:integral to plasma membrane; TMS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TMS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TMS.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR00242; Tyr_pe.
DR Pfam; PF00102; Y_phosphatase.
DR PRINTS; PR00700; TRYPPHPTASE.
DR PROSITE; PS50853; RN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1304
FT DOMAIN 24 575
FT TRASMEM 576 597
FT DOMAIN 598 1304
FT DOMAIN 390 478
FT DOMAIN 482 570
FT DOMAIN 670 919
FT DOMAIN 961 1235
FT ACT_SITE 851 851
FT ACT_SITE 1167 1167
FT CARBOHD 78 78
FT CARBOHD 90 90
FT CARBOHD 95 95
FT CARBOHD 184 184
FT CARBOHD 184 184
FT CARBOHD 190 190
FT CARBOHD 197 197
FT CARBOHD 232 232
FT CARBOHD 260 260
FT CARBOHD 270 270
FT CARBOHD 276 276
FT CARBOHD 335 335
FT CARBOHD 378 378
FT CARBOHD 419 419
FT CARBOHD 468 468
FT CARBOHD 488 488
FT CARBOHD 529 529
FT VARSPIC 32 192

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FT MTAGEN 851 851 /Frid=VSP 007780.
RT CONFLICT 650 650 C->S: loss of activity.
FT CONFLICT 1207 1207 L -> P (in Ref. 1).
SQ SEQUENCE 1304 AA; 147253 MW; A08FC2D6069BAF7 CRC64;

Query Match 100.0%; Score 44; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
Db 1218 FLYDVIAST 1226

RESULT 3
ID Q91054 PRELIMINARY; PRT; 1200 AA.
AC Q91054;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CD45 homolog.
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_TaxID=7792;
RN [1]
RP SEQUENCE FROM N.A.
RA Okumura M., Matthews R.J., Robb B., Bork P., Thomas M.L.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34750; AAB01087.1; -.
DR FJR; T43148; T43148.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolyase.
SQ SEQUENCE 1200 AA; 135372 MW; EFC6B62B4DC02BC2 CRC64;

Query Match 97.7%; Score 43; DB 2; Length 1200;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
Db 1114 FLYDVIAST 1122

RESULT 4
ID Q6ED60 PRELIMINARY; PRT; 1290 AA.
AC Q6ED60;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD45.
OS Actus vociferans (Spix's owl monkey).
OC Mammalia; Metazoa; Chordata; Cranialia; Vertebrata; Euleleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RM PubMed=15245371;

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RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL; AY445817; AAS06902.1; -.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC_motif; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolyase.
SQ SEQUENCE 1290 AA; 145616 MW; 99E810C75D932824 CRC64;

Query Match 90.9%; Score 40; DB 2; Length 1290;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
Db 1204 FLYDVIAST 1212

RESULT 5
ID Q6ED61 PRELIMINARY; PRT; 1303 AA.
AC Q6ED61;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD45.
OS Actus nancyanae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euleleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RM PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL; AY445817; AAS06902.1; -.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC_motif; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolyase.
SQ SEQUENCE 1303 AA; 146929 MW; D0EB0C640D1D17B8 CRC64;

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Query Match 90.9%; Score 40; DB 2; Length 1303;
 Best Local Similarity 88.9%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIASST 9
 DB 1217 FLYDVIASST 1225

RESULT 6

ID 06ED62 PRELIMINARY; PRT; 1303 AA.
 AC 06ED62;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE CD45.
 OS *Actus nigricaps* (Black-headed owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patarro M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human";
 RT Tissue Antigens 64:165-172(2004).
 RL EMBL; AY45816; AAS06901.1; -;
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III-like.
 DR InterPro; IPR003595; PTPC motif.
 DR InterPro; IPR00387; TYR_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPPHTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC motif; 2.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrobase.
 SQ SEQUENCE 1303 AA; 146586 MW; 98B023B8F4BC165 CRC64;

Query Match 90.9%; Score 40; DB 2; Length 1303;
 Best Local Similarity 88.9%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIASST 9
 DB 1217 FLYDVIASST 1225

RESULT 7

ID 08MJ02 PRELIMINARY; PRT; 365 AA.
 AC 08MJ02;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE CD45 phosphatase (Fragment).
 OS *Actus vociferans* (Spix's owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 NCBI_TaxID=57176;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Montoya G.E., Vernot J.P., Patarro M.E.;
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF364096; AAM48512.1; -;
 DR HSBP; F18052; 1P15.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR00387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPPHTASE.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.
 DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
 FT NON_TER 1 365
 FT NON_TER 1 365
 SQ SEQUENCE 365 AA; 41720 MW; BA950C4E56E27902 CRC64;

Query Match 88.6%; Score 39; DB 2; Length 365;
 Best Local Similarity 88.9%; Pred. No. 8.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIASST 9
 DB 290 FLYDVIASST 298

RESULT 8

ID P94296 PRELIMINARY; PRT; 300 AA.
 AC P94296;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE CapB (Fragment).
 RN Name=capB;
 OS *Bacillus firmus*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1399;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OF4;
 RA Ito M., Kuriuchi T.A.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U60883; AAB41841.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0045227; P:capsule polysaccharide biosynthesis; IEA.
 DR InterPro; IPR008337; CapB.
 DR PRINTS; PR01758; CAPSULEPROTB.
 FT NON_TER 1 300
 FT NON_TER 1 300
 SQ SEQUENCE 300 AA; 33317 MW; 602BHC2501756AB CRC64;

Query Match 86.4%; Score 38; DB 2; Length 300;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIASST 9
 DB 263 FLYDVIASST 271

RESULT 9

ID ARLY_XYLFA STANDARD; PRT; 445 AA.
 AC Q9PEM5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Argininosuccinate lyase (EC 4.3.2.1) (Argininosuccinase) (ASAL).
 GN Name=argH; Ordered locus names=Xf1003;
 OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.

01-JAN-1988 (Rel. 06, Created)
 01-JAN-1988 (Rel. 06, Last sequence update)
 05-JUL-2004 (Rel. 44, Last annotation update)
 Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (Lymphocyte
 DE common antigen Ly-5) (CD45) (T200).
 GN Name=Ppirc; Synonyms=Ly-5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8631366; PubMed=2944116;
 RA Suga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RT "Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
 RP REVISIONS.
 RA Suga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
 RN [3]
 RP SEQUENCE OF 10-124 FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=8604266; PubMed=3864163;
 RA Shen F.-W., Suga Y., Litman G., Freeman G., Tung J.-S., Cantor H.,
 RT Boyse E.A.;
 RL "Cloning of Ly-5 cDNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
 RP [4]
 RP SEQUENCE OF 822-1152 FROM N.A.
 RX MEDLINE=8709235; PubMed=2948186;
 RA Raschke W.C.;
 RT "Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B-
 and T-lymphocyte lineages."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
 RN [5]
 RP INTERACTIONS WITH GANAB AND PRKCSH.
 RX MEDLINE=97294720; PubMed=914925; DOI=10.1074/jbc.272.20.13117;
 RA Arendt C.W., Ostergaard H.L.;
 RT "Identification of the CD45-associated 116-kDa and 80-kDa proteins as
 the alpha- and beta-subunits of alpha-glucosidase II."
 RL J. Biol. Chem. 272:13117-13125(1997).
 CC -1- FUNCTION: Required for T-cell activation through the antigen
 receptor. The first p135 domain has enzymatic activity, while
 the second one seems to affect the substrate specificity of the
 first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 tyrosine + phosphate.
 CC -1- SUBUNIT: Binds GANAB and PRKCSH.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;
 CC IsoId=P06800-1; Sequence=displayed;
 CC -1- DEVELOPMENTAL STAGE: Expression is restricted to the hematopoietic
 compartment of development.
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 1/6 subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
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 CC -----
 DR EMBL: M14342; AAA39456.1; -;
 DR EMBL: M1934; AAA39461.1; -;
 DR

DR EMBL: M15174; AAA40161.1; -;
 DR PIR: A23329; A23329.
 DR PIR: A28334; A28334.
 DR HSSP: P18052; 1YFO.
 DR MGD: MG1:97810; Ppirc.
 DR GO: GO:0009897; C:external side of plasma membrane; IDA.
 DR GO: GO:000515; F:protein binding; IPI.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; ERTYHPHTASE.
 DR PROSITE: PS00853; FN3; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 2.
 DR Alternative splicing; Antigen; Glycoprotein; Hydrolyase;
 KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 KW Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 1152
 FT DOMAIN 24 425
 FT TRANSMEM 426 447
 FT DOMAIN 448 1152
 FT DOMAIN 232 328
 FT DOMAIN 333 420
 FT DOMAIN 520 769
 FT DOMAIN 811 1084
 FT ACT_SITE 701 701
 FT ACT_SITE 1016 1016
 FT ACT_SITE 1016 1016
 FT CARBOHYD 68 68
 FT CARBOHYD 72 72
 FT CARBOHYD 79 79
 FT CARBOHYD 114 114
 FT CARBOHYD 119 119
 FT CARBOHYD 151 151
 FT CARBOHYD 172 172
 FT CARBOHYD 183 183
 FT CARBOHYD 208 208
 FT CARBOHYD 277 277
 FT CARBOHYD 288 288
 FT CARBOHYD 318 318
 FT CARBOHYD 350 350
 FT CARBOHYD 379 379
 SQ SEQUENCE 1152 AA; 130421 MW; B4D956B4E32EA812 CRC64;
 Query Match 86.4%; Score 38; DB 1; Length 1152;
 Best Local Similarity 87.5%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLYDVIAS 8
 DB 1067 FLYDVIAS 1074
 ID 061812 PRELIMINARY; PRT; 1291 AA.
 AC 061812
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lymphocyte common antigen precursor.
 GN Name=Ppirc; Synonyms=Ly5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=92361152; PubMed=1822988;
RA Zebadee S.L., Barritt D.S., Raschke W.C.;
RT "Comparison of mouse Ly5 A and Ly5 B leukocyte common antigen alleles."
RL Dev. Immunol. 1:243-254(1991).
DR EMBL; M92933; AAA39459.1; -.
DR HSSP; P18052; 1YFO.
DR MED; MGT197810; PTPRC.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; TMS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030183; P:B-cell differentiation; IMP.
DR GO; GO:0030217; P:T-cell differentiation; IMP.
DR GO; GO:0042098; P:T-cell proliferation; IMP.
DR GO; GO:0046652; P:T-cell proliferation; IMP.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; FN3; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PSS0853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrobase; Signal.
FT SIGNAL 1
SQ SEQUENCE 1291 AA; 14559 MW; 253C6B1AF4350CE CRC64;
Potential.
Query Match 86.4%; Score 38; DB 2; Length 1291;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVITAS 8
Db 1206 FLYDVITAS 1213

RESULT 13
O64730
ID O64730 PRELIMINARY; PRT; 1343 AA.
AC O64730;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leucocyte common antigen (L-Ca) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260986; PubMed=2955416;
RA Thomas M.L., Reynolds P.J., Chain A., Ben-Neriah Y., Trowbridge I.S.;
RT "B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA
RT splicing."
RL Proc. Natl. Acad. Sci. U.S.A. 84:5360-5363(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89197920; PubMed=2522930;
RA Johnson N.A., Meyer C.M., Pingel J.T., Thomas M.L.;
RT "Sequence conservation in potential regulatory regions of the mouse
RT and human leukocyte-common antigen gene."
RL J. Biol. Chem. 264:6220-6229(1989).
DR EMBL; M23148; AAA39418.1; JOINED.
DR EMBL; M23149; AAA39418.1; JOINED.
DR EMBL; M23150; AAA39418.1; JOINED.
DR EMBL; M23151; AAA39418.1; JOINED.

DR EMBL; M23153; AAA39418.1; JOINED.
DR EMBL; M23155; AAA39418.1; JOINED.
DR EMBL; M23157; AAA39418.1; JOINED.
DR EMBL; M23156; AAA39418.1; JOINED.
DR EMBL; M23154; AAA39418.1; JOINED.
DR EMBL; M23135; AAA39418.1; JOINED.
DR EMBL; M23134; AAA39418.1; JOINED.
DR EMBL; M23133; AAA39418.1; JOINED.
DR EMBL; M23132; AAA39418.1; JOINED.
DR EMBL; M23131; AAA39418.1; JOINED.
DR EMBL; M23130; AAA39418.1; JOINED.
DR EMBL; M23129; AAA39418.1; JOINED.
DR EMBL; M23128; AAA39418.1; JOINED.
DR EMBL; M23127; AAA39418.1; JOINED.
DR EMBL; M23144; AAA39418.1; JOINED.
DR EMBL; M23143; AAA39418.1; JOINED.
DR EMBL; M23142; AAA39418.1; JOINED.
DR EMBL; M23141; AAA39418.1; JOINED.
DR EMBL; M23140; AAA39418.1; JOINED.
DR EMBL; M23139; AAA39418.1; JOINED.
DR EMBL; M23138; AAA39418.1; JOINED.
DR EMBL; M23137; AAA39418.1; JOINED.
DR EMBL; M23136; AAA39418.1; JOINED.
DR EMBL; M23147; AAA39418.1; JOINED.
DR EMBL; M23146; AAA39418.1; JOINED.
DR EMBL; M23145; AAA39418.1; JOINED.
DR EMBL; M23158; AAA39418.1; JOINED.
DR EMBL; M23152; AAA39418.1; JOINED.
DR HSSP; P18052; 1YFO.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; FN3; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PSS0853; FN3; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR NON TER 1
FT NON TER 1
SQ SEQUENCE 1343 AA; 150679 MW; 0DEBDEC97FC4C6A9 CRC64;
Query Match 86.4%; Score 38; DB 2; Length 1343;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVITAS 8
Db 1258 FLYDVITAS 1265

RESULT 14
VGP_MABVM
ID VGP_MABVM STANDARD; PRT; 681 AA.
AC P35253;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Structural glycoprotein precursor (Varian spike glycoprotein).
GN Name=GP;
OS Marburg virus (strain Musoke).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Marburg-like viruses.
OX NCBI_Taxid=33727;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-37.
RX MEDLINE=93172334; PubMed=8437211;
RA Will C., Muehberger E., Linder D., Slenczka W., Klenk H.-D.,
RA Feldmann H.;
RT "Marburg virus gene 4 encodes the virion membrane protein, a type I

RT transmembrane glycoprotein.";
RL J. Virol. 67:1203-1210(1993).
CC -1- FUNCTION: Structural protein that forms the virion spike and which
CC is responsible for binding to target cells and subsequent fusion
CC of the viral and host-cell membranes.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: O-glycosylated (Probable).
CC -1- SIMILARITY: Belongs to the filoviruses glycoprotein family.

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CC EMBL; Z11213; CAA78117.1; -.
CC PIR; A45705; A45705.
CC HSSP; Q05320; 2EBO.
CC DR GlycosultedB; P35253; -.
CC DR InterPro; IPR002561; Filo_glycop.
CC DR Pfam; PF01611; Filo_glycop; 1.
CC DR Direct protein sequencing; Envelope protein; Glycoprotein; Signal;
CC Transmembrane.
KM SIGNAL 1 18
FT CHAIN 19 681 Structural glycoprotein.
FT DOMAIN 19 648 Extracellular (Potential).
FT TRANSMEM 649 673 Potential.
FT DOMAIN 674 681 Cytoplasmic (Potential).
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 207 207 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 219 219 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 225 225 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 325 325 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 326 326 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 337 337 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 344 344 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 345 345 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 350 350 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 360 360 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 408 408 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 487 487 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 564 564 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 619 619 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 681 AA; 74376 MW; CC89305C64D3480B CRC64;

Query Match 84.1%; Score 37; DB 1; Length 681;
Best Local Similarity 88.9%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIAT 9
Db 144 FLYDRIAT 152

RESULT 15
VGP_MABVP STANDARD; PRT; 681 AA.
AC P35254;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Structural glycoprotein precursor (Virion spike glycoprotein).
GN Name=GP;
OS Marburg virus (strain Popp).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC Marburg-like viruses.
OC NCBI_taxonomy33728;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93265932; PubMed=8495737; DOI=10.1016/0014-5793(93)81476-G;
RA Bukreyev A.A., Volchok V.E., Blinov V.M., Neresov S.V.;
RT "The GP-protein of Marburg virus contains the region similar to the
RT 'Immunosuppressive domain' of oncogenic retrovirus P15E proteins.";
RN FEBS Lett. 323:183-187(1993).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96028047; PubMed=7487490;
RA Bukreyev A.A., Volchok V.E., Blinov V.M., Dryga S.A., Neresov S.V.;
RT "The complete nucleotide sequence of the Popp (1967) strain of Marburg
RT virus: a comparison with the Musoke (1980) strain.";
RL Arch. Virol. 140:1589-1600(1995).
CC -1- FUNCTION: Structural protein that forms the virion spike and which
CC is responsible for binding to target cells and subsequent fusion
CC of the viral and host-cell membranes.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: O-glycosylated (Probable).
CC -1- SIMILARITY: Belongs to the filoviruses glycoprotein family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; X68493; CAA48507.1; -.
CC EMBL; Z29337; CAA82539.1; -.
CC PIR; S3316; S3316.
CC HSSP; Q05320; 2EBO.
CC DR InterPro; IPR002561; Filo_glycop.
CC DR Pfam; PF01611; Filo_glycop; 1.
CC DR Envelope protein; Glycoprotein; Signal; Transmembrane.
KM SIGNAL 1 18
FT CHAIN 19 681 Structural glycoprotein.
FT DOMAIN 19 648 Extracellular (Potential).
FT TRANSMEM 649 673 Potential.
FT DOMAIN 674 681 Cytoplasmic (Potential).
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 207 207 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 219 219 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 225 225 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 325 325 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 326 326 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 337 337 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 344 344 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 345 345 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 350 350 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 360 360 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 389 389 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 397 397 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 408 408 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 487 487 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 564 564 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 619 619 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 681 AA; 74485 MW; D574E16FCD8C8EE CRC64;

Query Match 84.1%; Score 37; DB 1; Length 681;
Best Local Similarity 88.9%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	FLYDVIAST	9
Db	144	FLYDRIAST	152

Search completed: May 3, 2005, 05:58:21
Job time : 47.1351 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds
(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-12

Perfect score: 50

Sequence: 1 ILPYDYNRV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	433	2	Q8MUQ3
2	50	100.0	756	2	Q6PUK7
3	50	100.0	878	2	Q8C6Q7
4	50	100.0	962	2	Q6LDD3
5	50	100.0	1152	1	CD45_MOUSE
6	50	100.0	1216	2	Q9IBD8
7	50	100.0	1245	2	Q9IBF0
8	50	100.0	1246	2	Q9IBF1
9	50	100.0	1255	1	CD45_RAT
10	50	100.0	1285	2	Q6UNF4
11	50	100.0	1290	2	Q6ED60
12	50	100.0	1291	2	Q61812
13	50	100.0	1303	2	Q6ED61
14	50	100.0	1304	1	CD45_HUMAN
15	50	100.0	1343	2	Q64730
16	47	94.0	306	2	Q42243
17	46	92.0	696	2	Q21527
18	46	92.0	753	2	Q6EBU3
19	46	92.0	1303	2	Q6ED62
20	45	90.0	179	2	Q8WML
21	45	90.0	752	2	Q6IPX8
22	45	90.0	799	2	Q9P0U2
23	45	90.0	807	1	PTNM_HUMAN
24	45	90.0	1056	2	Q8AVJ3
25	45	90.0	1200	2	Q91054
26	45	90.0	1237	2	Q91976
27	44	88.0	419	2	Q8J1Q4
28	44	88.0	471	2	Q91BA3
29	44	88.0	473	2	Q9N105
30	44	88.0	515	2	Q8SMR7
31	44	88.0	642	2	Q60986

32	44	88.0	659	2	Q63477	Q63477	rattus norv
33	44	88.0	667	2	Q703W8	Q703W8	anopheles g
34	44	88.0	680	2	Q76K54	Q76K54	oryzias lat
35	44	88.0	680	2	Q76K57	Q76K57	oryzias lat
36	44	88.0	682	2	Q9VJ95	Q9VJ95	drosophila
37	44	88.0	699	1	PTPE_MOUSE	P49446	mus musc
38	44	88.0	699	2	Q61042	Q61042	mus musc
39	44	88.0	700	1	PTPE_HUMAN	P23469	homo sapien
40	43	86.0	365	2	Q8MUQ2	Q8MUQ2	actus vocif
41	41	82.0	206	2	Q801L3	Q801L3	petromyzon
42	41	82.0	377	2	Q9UBT5	Q9UBT5	homo sapien
43	41	82.0	405	2	Q9UBF0	Q9UBF0	homo sapien
44	41	82.0	405	2	Q29500	Q29500	oryctolagus
45	41	82.0	405	2	Q60998	Q60998	mus musc

ALIGNMENTS

RESULT 1									
Q8MUQ3	ID	Q8MUQ3	PRELIMINARY	PRT	433	AA.			
DT	01-OCT-2002	(Tremblrel. 22, Created)							
DT	01-OCT-2002	(Tremblrel. 22, Last sequence update)							
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)							
DE	CD45 phosphatase (Fragment)								
OS	Actus vociferans (Spix's owl monkey)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotidae; Aotus.								
OX	NCBI_TaxId=57176;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Montoya G.E., Vernot J.P., Patarroyo M.E.								
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AF364095; AAM48511.1; -								
DR	HSSP; P18052; 1YFO.								
DR	GO; GO:0016787; F-hydrolase activity; IEA.								
DR	GO; GO:0004725; F-protein tyrosine phosphatase activity; IEA.								
DR	GO; GO:0006470; P-protein amino acid dephosphorylation; IEA.								
DR	InterPro; IPR003961; FN III-like.								
DR	InterPro; IPR008957; FN III-like.								
DR	InterPro; IPR000387; Tyr phosphatase.								
DR	InterPro; IPR000242; Tyr_PP.								
DR	Pfam; PF00041; fn3.1.								
DR	Pfam; PF00102; Y_phosphatase.1.								
DR	PRINTS; PR00700; PRTYPHTASE.								
DR	SMART; SM00060; FN3.1.								
DR	SMART; SM00194; PTPC.1.								
DR	PROSITE; PSS0853; FN3.1.								
DR	PROSITE; PSS00383; TYR_PHOSPHATASE_1.1.								
DR	PROSITE; PSS0056; TYR_PHOSPHATASE_2.1.								
DR	PROSITE; PSS0055; TYR_PHOSPHATASE_PTP.1.								
KW	Hydrolase.								
FT	NON_TER								
FT	NON_TER								
SQ	SEQUENCE	433	433	1					
		AA;	50151	MM;	BBAB00C4F008EB80D	CRC64;			
Query Match									
Best Local Similarity 100.0%; Score 50; DB 2; Length 433;									
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ILPYDYNRV	9						
DB	222	ILPYDYNRV	230						
RESULT 2									
ID	Q6PUK7	PRELIMINARY;	PRT;	756	AA.				
DT	05-JUL-2004	(Tremblrel. 27, Created)							
DT	05-JUL-2004	(Tremblrel. 27, Last sequence update)							

DT 05-JUN-2004 (Tremblrel. 27, Last annotation update)
 DE PTPRC protein (Fragment).
 GN Name=PTPRC;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Murray D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Green E.D., Dickson M.C.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014239; AAI4239.1; -.
 DR HSP: F18031; IAX.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR000242; TYF_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00102; Y-phosphatase; 1.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 DR NCBI TER 756 756
 SQ SEQUENCE 756 AA; 85430 MW; 8A9A863827BD69B6 CRC64;
 Query Match 100.0%; Score 50; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPDYKRV 9
 DB 636 ILPDYKRV 644
 RESULT 3
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RA The FANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.152600;
 RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtration of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Maruoka S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagata T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Ito S., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Koyama S.,
 RA Kurihara C., Matsuyama T., Miyazaki R., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK054056; BAC35638.1; -.
 DR HSP: P18052; IYFO.
 DR MGP: MGI:97810; PEPIC.
 DR GO: GO:0009897; C:external side of plasma membrane; IDA.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0030183; P:B-cell differentiation; IMP.
 DR GO: GO:0042100; P:B-cell proliferation; IMP.
 DR GO: GO:0030217; P:T-cell differentiation; IMP.

DR GO; GO:0042098; P:T-cell proliferation; IMP.
 DR GO; GO:004652; P:thymocyte differentiation; IMP.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR00387; TYR_phosphatase.
 DR Pfam; PF00041; FN3_3.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS50853; FN3_2.
 DR PROSITE; PS50383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase; Receptor.
 FT NON TER 878 878
 SQ SEQUENCE 878 AA; 99891 MW; 19E5FCD7909D4CA6 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 878;
 Best Local Similarity 100.0%; Pred. No. 0.78; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPDYNNRV 9
 DB 536 ILPDYNNRV 544

RESULT 4
 Q6LD23 PRELIMINARY; PRT; 962 AA.
 ID Q6LD23;
 AC Q6LD23;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Leukocyte common antigen.
 GN Name=L-CA;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=85201691; PubMed=3158393; DOI=10.1016/0092-8674(85)90063-7;
 RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;
 RT Evidence from cDNA clones that rat leukocyte-common antigen (T200)
 RT spans the lipid bilayer and contains a cytoplasmic domain of 80,000 M-
 RT r.";

RL Cell 41.83-93(1985).
 DR EMBL; M10072; AAA41513.1; -.
 DR HSP; P18031; IASY.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003595; PTPC_motif.
 DR InterPro; IPR00387; TYR_phosphatase.
 DR InterPro; IPR00242; TYR_PP.
 DR Pfam; PF00041; FN3_2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC_motif; 2.
 DR PROSITE; PS50853; FN3_2.
 DR PROSITE; PS50383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase.
 FT NON TER 962 AA; 109934 MW; D2E6B7F23D29CC92 CRC64;
 SQ SEQUENCE 962 AA; 109934 MW; D2E6B7F23D29CC92 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 962;
 Best Local Similarity 100.0%; Pred. No. 0.86; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPDYNNRV 9
 DB 344 ILPDYNNRV 352

RESULT 5
 CD45_MOUSE STANDARD; PRT; 1152 AA.
 ID CD45_MOUSE
 AC P06800;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (lymphocyte
 DE common antigen Ly-5) (CD45) (T200).
 GN Name=Ptpcr; Synonyms=Ly-5;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=86313686; PubMed=2944116;
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RT "Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
 RN [2]
 RP REVISIONS.
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
 RN [3]
 RC SEQUENCE OF 10-124 FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=86042665; PubMed=3864163;
 RA Shen F.-W., Saga Y., Litman G., Freeman G., Tung J.-S., Cantor H.,
 RA Boyse E.A.;
 RT "Cloning of Ly-5 cDNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
 RN [4]
 RP SEQUENCE OF 822-1152 FROM N.A.
 RX MEDLINE=87092355; PubMed=2948186;
 RA Raschke W.C.;
 RT "Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B-
 RT and T-lymphocyte lineages."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
 RN [5]
 RP INTERACTIONS WITH GAMMA AND PRKCSH.
 RX MEDLINE=97294720; PubMed=9148925; DOI=10.1074/jbc.272.20.13117;
 RA Arendt C.W., Ostergaard H.L.;
 RT "Identification of the CD45-associated 116-kDa and 80-kDa proteins as
 RT the alpha- and beta-subunits of alpha-glucosidase."
 RL J. Biol. Chem. 272:13117-13125(1997).
 CC -1- FUNCTION: Required for T-cell activation through the antigen
 CC receptor. The first PTPase domain has enzymatic activity, while
 CC the second one seems to affect the substrate specificity of the
 CC first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBUNIT: Binds GAMMA and PRKCSH.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;
 CC -1- IsoId=P06800-1; Sequence=Displayed;
 CC -1- DEVELOPMENTAL STAGE: Expression is restricted to the hematopoietic
 CC compartment of development.
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 1/6 subfamily.

CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M14342; AAA39458.1; -
 CC EMBL; M1934; AAA39461.1; -
 CC EMBL; M5174; AAA40161.1; -
 CC PIR; A23329; A23329.
 CC PIR; A28334; A28334.
 CC HSSP; P18052; 1YFO.
 CC MD; MGI:97810; PcpPC.
 CC GO; GO:0009897; C:external side of plasma membrane; IDA.
 CC GO; GO:000515; F:protein binding; IPI.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR000387; TYR_phosphatase.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00041; fn3; 3.
 CC Pfam; PF00102; Y_phosphatase; 2.
 CC PRINTS; PR00700; PRTYPHTASE.
 CC PROSITE; PS50853; FN3; 2.
 CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 CC Alternative splicing; Antigen; Glycoprotein; Hydrolase;
 CC Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 CC Transmembrane.
 CC STGNL 1 23
 CC CHAIN 24 1152
 CC DOMAIN 24 425
 CC TRANSMEM 426 447
 CC DOMAIN 448 1152
 CC DOMAIN 232 328
 CC DOMAIN 333 420
 CC DOMAIN 520 769
 CC DOMAIN 811 1084
 CC ACT_SITE 701 701
 CC ACT_SITE 1016 1016
 CC ACT_SITE 1016 1016
 CC CARBOHYD 68 68
 CC CARBOHYD 72 72
 CC CARBOHYD 79 79
 CC CARBOHYD 114 114
 CC CARBOHYD 119 119
 CC CARBOHYD 151 151
 CC CARBOHYD 172 172
 CC CARBOHYD 183 183
 CC CARBOHYD 208 208
 CC CARBOHYD 277 277
 CC CARBOHYD 288 288
 CC CARBOHYD 318 318
 CC CARBOHYD 350 350
 CC CARBOHYD 379 379
 CC SEQUENCE 1152 AA; 130421 MW; BAD956B4E32EA812 CRC64;
 Query Match 100.0%; Score 50; DB 1; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

091B08
 ID 091B08 PRELIMINARY; PRT; 1216 AA.
 AC 091B08;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CD45.
 OS *Cyprinus carpio* (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 CC NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20531692; PubMed=11081442; DOI=10.1006/fsim.2000.0294;
 RA Fujiki K., Shin D.H., Nakao M., Yano T.;
 RT "Molecular cloning of carp (*Cyprinus carpio*) leucocyte cell-derived
 RT chemotaxin 2, glia maturation factor beta, CD45 and lysozyme C by use
 RT of suppression subtractive hybridisation."
 RL Fish Shellfish Immunol. 10:643-650 (2000).
 DR EMBL; AB031424; BAA92179.1; -.
 DR HSSP; P18052; 1YFO.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHTASE.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS50853; FN3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrolase.
 SQ SEQUENCE 1216 AA; 138251 MW; 9D2E45F41721D2CF CRC64;

Query Match 100.0%; Score 50; DB 2; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDNRV 9
 DB 596 ILPYDNRV 604
 RESULT 7
 ID 091B08 PRELIMINARY; PRT; 1245 AA.
 AC 091B08;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CD45 (EC 3.1.3.48).
 GN Name=PTPRC.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 CC NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Diaz del Pozo E.M., Beverley P.C., Timon M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ24430; CAB96212.1; -.
 DR HSSP; P18052; 1YFO.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

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DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; FN3; 1.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00853; FN3; 1.
DR PROSITE: PS00383; Tyr_PHOSPHATASE_1; 2.
DR PROSITE: PS00056; Tyr_PHOSPHATASE_2; 2.
DR PROSITE: PS00055; Tyr_PHOSPHATASE_PTP; 2.
KM Hydrolyase.
SQ SEQUENCE 1245 AA; 141324 MW; 6CB711EF5797555 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 1245;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPDYRV 9
Db 651 ILPDYRV 659

RESULT 8
Q918F1 PRELIMINARY; PRT; 1246 AA.
ID Q918F1
AC Q918F1;
DT 01-OCT-2000 (TRENBLUREL. 15, Created)
DT 01-OCT-2000 (TRENBLUREL. 15, Last sequence update)
DT 01-MAR-2004 (TRENBLUREL. 26, Last annotation update)
DE CD45 precursor (EC 3.1.3.48).
OS Name=PTPC;
GN Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorph; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spine;
RA Diaz del Pozo E.M., Beverley P.C., Timon M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ243429; CAB96211.1; -.
DR HSSP: P18052; 1YFO.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; FN3; 1.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00853; FN3; 1.
DR PROSITE: PS00383; Tyr_PHOSPHATASE_1; 2.
DR PROSITE: PS00056; Tyr_PHOSPHATASE_2; 2.
DR PROSITE: PS00055; Tyr_PHOSPHATASE_PTP; 2.
KM Hydrolyase; Signal.
FT SIGNAL 19 Potential.
FT CHAIN 20 1246 CD45.
SQ SEQUENCE 1246 AA; 141363 MW; 4643259F5CA40E8E CRC64;

Query Match 100.0%; Score 50; DB 2; Length 1246;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPDYRV 9

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Db 652 ILPDYRV 660

RESULT 9
CD45_RAT STANDARD; PRT; 1255 AA.
ID CD45_RAT
AC P04157;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen variant 4 precursor (EC 3.1.3.48) (L-CA)
DE (CD45) (T200) (Fragment).
GN Name=PTPC;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;
RL Submitted (MAY-1987) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 190-1255 FROM N.A.
RX MEDLINE=85201691; PubMed=3158393; DOI=10.1016/0092-8674(85)90063-7;
RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;
RT "Evidence from cDNA clones that the rat leukocyte-common antigen
RT (T200) spans the lipid bilayer and contains a cytoplasmic domain of
RT 80,000 Mr."
RL Cell 41:83-93 (1985).
RN [3]
RP ALTERNATIVE SPLICING.
RX MEDLINE=87275817; PubMed=2440674;
RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;
RT "Lymphocyte specific heterogeneity in the rat leukocyte common antigen
RT (T200) is due to differences in polypeptide sequences near the NH2-
RT terminus."
RL EMBO J. 6:1259-1264 (1987).
CC -1- FUNCTION: Required for T-cell activation through the antigen
CC receptor. The first PTPase domain has enzymatic activity, while
CC the second one seems to affect the substrate specificity of the
CC first one.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBUNIT: Binds GANAB and PRKCSH (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P04157-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P04157-2; Sequence=VSP_005167;
CC Name=3;
CC IsoId=P04157-3; Sequence=VSP_005166;
CC Name=4;
CC IsoId=P04157-4; Sequence=VSP_005165, VSP_005168;
CC -1- TISSUE SPECIFICITY: Variants 4 and 3 are found in the lymph node,
CC variants 1 and 2 are found in thymocyte and lymph node.
CC -1- PTM: Heavily N- and O-glycosylated.
CC -1- PTM: The cytoplasmic domain contains potential phosphorylation
CC sites.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 1/6 subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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```

[illegible]

Db	637	ILPYDYNRV	645
RESULT 10			
ID	Q6UNF4	PRELIMINARY;	PRT; 1285 AA.
AC	Q6UNF4;		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	C945.		
OS	Ictalurus punctatus (Channel catfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;		
OC	Ictaluridae; Ictalurus.		
OX	NCBI_TaxId=7998;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kountikov E.I., Wilson M., Miller N., Clem W., Bengten E.;		
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY366233; AAQ72837.1; -.		
DR	HSSP; P18031; IKAV.		
DR	GO: GO:0016787; F:hydrolase activity; IEA.		
DR	GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.		
DR	GO: GO:0006470; F:protein amino acid dephosphorylation; IEA.		
DR	InterPro; IPR003595; PTPC_motif.		
DR	InterPro; IPR002424; TYR_PP.		
DR	Pfam; PF00102; Y_phosphatase; 2.		
DR	PRINTS; PR00700; PRTYPHPTASE.		
DR	SMART; SM00394; PTPC; 2.		
DR	SMART; SM00404; PTPC_motif; 2.		
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.		
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.		
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.		
KM	Hydrolase.		
SEQ	SEQUENCE 1285 AA; 144218 MW; BAC75A2A47452330 CRC64;		
Query Match 100.0%; Score 50; DB 2; Length 1285;			
Best Local Similarity 100.0%; Pctd. No. 1.2;			
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ILPYDYNRV 9		
Db	657 ILPYDYNRV 665		
RESULT 11			
Q6ED60	PRELIMINARY;	PRT; 1290 AA.	
ID	Q6ED60;		
AC	Q6ED60;		
DT	25-OCT-2004 (TREMBLrel. 28, Created)		
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
DE	CD45.		
OS	Actus vociferans (Spix's owl monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.		
OX	NCBI_TaxId=57176;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RA	PubMed;15245317;		
RA	Montoya G.E., Vernot J.P., Patarrayo M.E.;		
RT	"Comparative analysis of CD45 protein in primate context: owl monkeys		
RT	vs. human."		
RL	Tissue Antigens 64:165-172(2004).		
EMBL	EMBL; AY445818; AAS06903.1; -.		
GO	GO:0004725; F:protein tyrosine phosphatase activity; IEA.		
GO	GO:0006470; P:protein amino acid dephosphorylation; IEA.		
InterPro	IPR003961; FN_III.		
InterPro	IPR008957; FN_III-1ike.		
InterPro	IPR003595; PTPC_motif.		
InterPro	IPR00387; TYR_phosphatase.		

DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; fn3; 2.
DR PRINTS: PR00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00853; Tyr_PHOSPHATASE_1; 2.
DR PROSITE; PS00853; Tyr_PHOSPHATASE_2; 2.
DR PROSITE; PS50056; Tyr_PHOSPHATASE_PTP; 2.
DR PROSITE; PS50055; Tyr_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1290 AA; 145616 MW; 998B10C75D932824 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 1290;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ILPYDYNRV 9
Db 670 ILPYDYNRV 678

RESULT 12
ID 061812 PRELIMINARY; PRT; 1291 AA.
AC 061812.
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Lymphocyte common antigen precursor.
GN Name: Ptpc; Synonyms: Lys5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C.
RX MEDLINE=92361152; PubMed=1822989;
RA Zedede S.L., Barritt D.S., Raechke W.C.;
RT "Comparison of mouse Lys 5 A and Lys 5 B leukocyte common antigen alleles."
RL Dev. Immunol. 1:243-254 (1991).
DR EMBL; M92833; AAA39459.1; -.
DR HSBP; P18052; IYFO.
DR MGD; MGI:97810; PTPC.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030183; F:B-cell differentiation; IMP.
DR GO; GO:0042100; F:B-cell proliferation; IMP.
DR GO; GO:0030217; P:T-cell differentiation; IMP.
DR GO; GO:0042098; P:T-cell proliferation; IMP.
DR GO; GO:0046652; P:B-lymphocyte differentiation; IMP.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00853; Tyr_PHOSPHATASE_1; 2.
DR PROSITE; PS00853; Tyr_PHOSPHATASE_2; 2.
DR PROSITE; PS50056; Tyr_PHOSPHATASE_PTP; 2.
KW Hydrolase; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 1291 AA; 144559 MW; 25C3CB61AF4350CE CRC64;

Query Match 100.0%; Score 50; DB 2; Length 1291;
Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ILPYDYNRV 9
Db 673 ILPYDYNRV 681

RESULT 13
ID 06ED61 PRELIMINARY; PRT; 1303 AA.
AC 06ED61.
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE CD45.
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarro M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys vs. human."
RL Tissue Antigens 64:165-172 (2004).
DR EMBL; AY45817; AAS06902.1; -.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN III-like.
DR InterPro: IPR003595; PTPC motif.
DR InterPro: IPR00387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00853; Tyr_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; Tyr_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; Tyr_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1303 AA; 146929 MW; DOEB0C640D1D17E8 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ILPYDYNRV 9
Db 683 ILPYDYNRV 691

RESULT 14
ID CD45 HUMAN STANDARD; PRT; 1304 AA.
AC P08575; O16614; Q9H0V6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen) (7200).
GN Name=PTPC; Synonyms=CD45;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;

FT CARBOHYD 529 529 N-linked (GlcNAc...) (Potential).
 FT VARSPIC 32 192 Missing (in isoform 2).
 FT MTAGN 851 851 /FTD_VSP_007880.
 FT CONFLICT 650 650 C-2S: loss of activity.
 FT CONFLICT 1207 1207 L -> P (in Ref. 1).
 FT CONFLICT 1207 1207 P -> L (in Ref. 1).
 SQ SEQUENCE 1304 AA; 147253 MW; A08FC22D6069BAF7 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILPYDYNRV 9
 Db 684 ILPYDYNRV 692

RESULT 15

064730 PRELIMINARY; PRT; 1343 AA.
 AC 064730;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Leucocyte common antigen (L-CA) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8726096; PubMed=2955416;
 RA Thomas M.L., Reynolds P.J., Chain A., Ben-Neriah Y., Trowbridge I.S.;
 RT "B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA
 RT splicing.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5360-5363(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89197920; PubMed=2522930;
 RA Johnson N.A., Meyer C.M., Pingel J.T., Thomas M.L.;
 RT "Sequence conservation in potential regulatory regions of the mouse
 RT and human leukocyte-common antigen gene.";
 RL J. Biol. Chem. 264:6220-6229(1989).
 DR EMBL; M23148; AAA39418.1; JOINED.
 DR EMBL; M23148; AAA39418.1; JOINED.
 DR EMBL; M23150; AAA39418.1; JOINED.
 DR EMBL; M23150; AAA39418.1; JOINED.
 DR EMBL; M23151; AAA39418.1; JOINED.
 DR EMBL; M23153; AAA39418.1; JOINED.
 DR EMBL; M23155; AAA39418.1; JOINED.
 DR EMBL; M23157; AAA39418.1; JOINED.
 DR EMBL; M23155; AAA39418.1; JOINED.
 DR EMBL; M23154; AAA39418.1; JOINED.
 DR EMBL; M23154; AAA39418.1; JOINED.
 DR EMBL; M23135; AAA39418.1; JOINED.
 DR EMBL; M23135; AAA39418.1; JOINED.
 DR EMBL; M23133; AAA39418.1; JOINED.
 DR EMBL; M23133; AAA39418.1; JOINED.
 DR EMBL; M23132; AAA39418.1; JOINED.
 DR EMBL; M23131; AAA39418.1; JOINED.
 DR EMBL; M23130; AAA39418.1; JOINED.
 DR EMBL; M23129; AAA39418.1; JOINED.
 DR EMBL; M23128; AAA39418.1; JOINED.
 DR EMBL; M23127; AAA39418.1; JOINED.
 DR EMBL; M23144; AAA39418.1; JOINED.
 DR EMBL; M23144; AAA39418.1; JOINED.
 DR EMBL; M23142; AAA39418.1; JOINED.
 DR EMBL; M23142; AAA39418.1; JOINED.
 DR EMBL; M23141; AAA39418.1; JOINED.
 DR EMBL; M23140; AAA39418.1; JOINED.
 DR EMBL; M23139; AAA39418.1; JOINED.
 DR EMBL; M23138; AAA39418.1; JOINED.
 DR EMBL; M23137; AAA39418.1; JOINED.
 DR EMBL; M23136; AAA39418.1; JOINED.
 DR EMBL; M23147; AAA39418.1; JOINED.
 DR EMBL; M23146; AAA39418.1; JOINED.
 DR EMBL; M23145; AAA39418.1; JOINED.

DR EMBL; M23158; AAA39418.1; -.
 DR EMBL; M23152; AAA39418.1; JOINED.
 DR HSSP; P18052; TYRO. Protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_Pp.
 DR Pfam; PF00061; fn3_3.
 DR DR PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTPHPTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTpc; 2.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 FT NON_TER 1
 SQ SEQUENCE 1343 AA; 150679 MW; 0DEBDEC97FC4C6A9 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 1343;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILPYDYNRV 9
 Db 673 ILPYDYNRV 681

Search completed: May 3, 2005, 06:01:18
 Job time : 41.1351 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds
(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-2

Perfect score: 40

Sequence: 1 ALIAFLAFL 9

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	1304	1 A46546	leukocyte common a
2	35	90.0	1444	2 H89792	conserved hypochet
3	35	87.5	1291	2 T22382	hypothetical prote
4	34	85.0	114	2 S09222	capsid protein - d
5	34	85.0	114	2 S09220	protein - d
6	34	85.0	179	2 S04858	insulin-like growt
7	34	85.0	257	2 A88618	protein ZKS20.2 [i
8	34	85.0	332	2 T21399	hypothetical prote
9	34	85.0	333	2 T27883	hypothetical prote
10	34	85.0	773	2 G83816	late competence op
11	34	85.0	3388	1 GNMVDP	genome polypotein
12	34	85.0	3391	1 GNMV16	genome polypotein
13	34	85.0	3391	1 GNMV26	genome polypotein
14	34	85.0	3391	1 GNMV26	genome polypotein
15	34	85.0	3391	1 GNMV26	genome polypotein
16	34	85.0	3391	1 GNMV26	genome polypotein
17	34	85.0	3391	1 GNMV26	genome polypotein
18	34	85.0	3391	1 GNMV26	genome polypotein
19	34	85.0	3391	1 GNMV26	genome polypotein
20	34	85.0	3391	1 GNMV26	genome polypotein
21	34	85.0	3391	1 GNMV26	genome polypotein
22	34	85.0	3391	1 GNMV26	genome polypotein
23	34	85.0	3391	1 GNMV26	genome polypotein
24	34	85.0	3391	1 GNMV26	genome polypotein
25	34	85.0	3391	1 GNMV26	genome polypotein
26	34	85.0	3391	1 GNMV26	genome polypotein
27	34	85.0	3391	1 GNMV26	genome polypotein
28	34	85.0	3391	1 GNMV26	genome polypotein
29	34	85.0	3391	1 GNMV26	genome polypotein
30	34	85.0	3391	1 GNMV26	genome polypotein

30	32	80.0	353	2 F75581	hypothetical prote
31	32	80.0	393	2 D97979	hypothetical prote
32	32	80.0	394	2 P95110	hypothetical prote
33	32	80.0	474	2 AB2161	hypothetical prote
34	32	80.0	478	2 G69354	TRK potassium upa
35	32	80.0	495	2 I44329	protein-tyrosine k
36	32	80.0	516	2 A84081	hypothetical prote
37	32	80.0	522	2 T02607	probable cytochrom
38	32	80.0	579	2 A86851	amino acid permeas
39	32	80.0	858	2 UC7683	taate receptor TIR
40	32	80.0	913	2 T15474	hypothetical prote
41	32	80.0	1200	2 T43148	probable protein-t
42	32	80.0	1200	2 T42573	DNA-directed DNA p
43	31	77.5	65	2 S19981	hypothetical prote
44	31	77.5	65	2 S19988	hypothetical prote
45	31	77.5	67	2 AC2186	CAB/ELIP/HLIP rela

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type C; T200 glycoprote
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C:Accession: A46546; B46546; A29449; B29449; I57658
R:Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
J. Title: Differential usage of three exons generates at least five different mRNAs enco
A:Reference number: A46546; MUID:88061067; PMID:2824653
A:Accession: A46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1304 <STR>
A:Cross-references: UNIPROT:P08575; GB:Y00638
A:Experimental source: UNIPROT:P08575; GB:Y00638
A:Accession: B46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-32,99-264 <ST2>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.111 and clone LCA.260
A:Accession: C46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-31,193-264 <ST3>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.1
R:Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
J. Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A:Reference number: A91066; MUID:87275816; PMID:2955090
A:Accession: A29449
A:Molecule type: mRNA
A:Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
A:Cross-references: GB:Y00662; NID:G34275; PTDN:CA68269.1; PID:G34276
A:Experimental source: clones pHLC-1 and lambdaHLG1
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 32-192 <RA2>
A:Experimental source: clone HLC-2
R:Tsal, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
J. Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative ;
A:Reference number: I57658; MUID:90064668; PMID:2531281
A:Accession: I57658
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 146-192 <RES>

A/Cross-references: GB:M29253; NID:g187020; PIDN:AAAS9497.1; PID:g553521
C/Genetics:
A/Gene: GDB:PTPRC; CD45
A/Cross-references: GDB:119768; OMIM:151460
A/Map position: 1q31-1q32
C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F/594-1235/Domain: leukocyte common antigen cytosolic domain homology <PTP>
F/675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
F/851/Active site: Cys (phosphotyrosine intermediate) #status predicted
F/857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 40; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 576 ALIAFLAFL 584

RESULT 2
H89792
conserved hypothetical protein SA0275 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H89792
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: H89792
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-444 <KIR>
A/Cross-references: UNIPROT:Q99WU0; GB:BA000018; PID:g13700201; PIDN:BA01499.1; GSPDB:C
A/Experimental source: strain N315
C/Genetics:
A/Gene: SA0275

Query Match 90.0%; Score 36; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LIAFLAFL 9
|||
DB 241 LIAFLAFL 248

RESULT 3
T22382
hypothetical protein F48F5.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22382
R/Lloyd, C.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19558
A/Accession: T22382
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1291 <MIL>
A/Cross-references: UNIPROT:Q9XV10; EMBL:Z81541; PIDN:CAB04411.1; GSPDB:GN00023; CSDP:F4
A/Experimental source: clone F48F5
C/Genetics:
A/Gene: CSDP:F48F5.1
A/Map position: 5
A/Introns: 753/2; 814/3; 987/2; 1030/3; 1114/2; 1153/3; 1222/3
Query Match 87.5%; Score 35; DB 2; Length 1291;
Best Local Similarity 88.9%; Pred. No. 81;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 767 ALIAFLAFL 775

RESULT 4
S09222
capsid protein - dengue virus type 2 (strain M3) (fragment)
C/Species: dengue virus type 2
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C/Accession: S09222
R/Sammel, S.; Koh, C.L.; Pang, T.; Lam, S.K.
Nucleic Acids Res. 18, 1904, 1990
A/Title: Nucleotide and encoded amino acid sequences of the capsid protein gene of three
engue fever.
A/Reference number: S09220; PMID:90245598; PMID:2336373
A/Accession: S09222
A/Molecule type: genomic RNA
A/Residues: 1-114 <SAM>
A/Cross-references: UNIPROT:Q67420; EMBL:X51710; NID:g59301; PIDN:CAA36006.1; PID:g59302
C/Superfamily: yellow fever virus genome polyprotein

Query Match 85.0%; Score 34; DB 2; Length 114;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 49 ALIAFLAFL 57

RESULT 5
S09220
capsid protein - dengue virus type 2 (fragment)
C/Species: dengue virus type 2
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C/Accession: S09220; S09221
R/Sammel, S.; Koh, C.L.; Pang, T.; Lam, S.K.
Nucleic Acids Res. 18, 1904, 1990
A/Title: Nucleotide and encoded amino acid sequences of the capsid protein gene of three
engue fever.
A/Reference number: S09220; PMID:90245598; PMID:2336373
A/Accession: S09220
A/Molecule type: genomic RNA
A/Residues: 1-114 <SAM>
A/Cross-references: UNIPROT:Q89715; EMBL:X51708; NID:g59297; PIDN:CAA36004.1; PID:g59298
A/Experimental source: strain M1
A/Accession: S09221
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-114 <SA2>
A/Cross-references: EMBL:X51709; NID:g59299; PIDN:CAA36005.1; PID:g59300
C/Superfamily: yellow fever virus genome polyprotein

Query Match 85.0%; Score 34; DB 2; Length 114;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 49 ALIAFLAFL 57

RESULT 6
S04858
insulin-like growth factor II precursor - sheep
C/Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C/Accession: S04858; S10984; S20731; S04972; S32557; S32558; A61008; S08567
R/O'Mahoney, J.V.; Adams, T.E.

Nucleic Acids Res. 17, 5392, 1989
 A>Title: Nucleotide sequence of an ovine insulin-like growth factor-II cDNA.
 A/Reference number: S04858; MUID:89345107; PMID:2762134
 A/Accession: S04858
 A/Molecule type: mRNA
 A/Residues: 1-179 <OMA>
 A/Cross-references: UNIPROT:P10764; EMBL:X15248; NID:91802; PIDN:CAA33324.1; PID:91803
 R/Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
 Nucleic Acids Res. 18, 4614, 1990
 A>Title: The nucleotide and deduced amino acid sequences of insulin-like growth factor I
 A/Reference number: S10983; MUID:90356421; PMID:2388846
 A/Accession: S10983
 A/Molecule type: mRNA
 A/Residues: 1-179 <BRO>
 A/Cross-references: EMBL:X53554; NID:91262; PIDN:CAA37621.1; PID:91263
 R/Ohlsen, S.M.; Wong, E.A.
 submitted to the EMBL Data Library, September 1990
 A/Reference number: S20731
 A/Accession: S20731
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-179 <OHL>
 A/Cross-references: EMBL:X56638; NID:91266; PIDN:CAA39163.1; PID:91267
 R/Hey, A.W.; Browne, C.A.; Simpson, R.J.; Thorburn, G.D.
 Biochim. Biophys. Acta 997, 27-35, 1989
 A>Title: Simultaneous isolation of insulin-like growth factors I and II from adult sheep
 A/Reference number: S04972; MUID:89323215; PMID:2752053
 A/Accession: S04972
 A/Molecule type: protein
 A/Residues: 25-58 <HEX>
 R/Demmer, J.; Hill, D.F.; Petersen, G.B.
 Biochim. Biophys. Acta 1173, 79-80, 1993
 A>Title: Characterization of two sheep insulin-like growth factor II cDNAs with different
 A/Reference number: S32557; MUID:93250051; PMID:8485157
 A/Accession: S32557
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-179 <DEM>
 A/Cross-references: EMBL:M89788; NID:9165940; PIDN:AAA31548.1; PID:9165941
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992
 A/Accession: S32558
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-120 <DE2>
 A/Cross-references: EMBL:M89789; NID:9165942; PIDN:AAA31549.1; PID:9552424
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992
 R/Stracke, J.; Heulin, M.H.; Chenuet, A.M.; Belleville, F.; Nabec, P.; Denotroy, L.; Bare
 J. Chromatogr. 533, 35-46, 1990
 A>Title: Application of preparative high-performance liquid chromatography to the purifi
 cation of
 A/Reference number: A61008; MUID:91185520; PMID:2081780
 A/Accession: A61008
 A/Molecule type: protein
 A/Residues: 25-32, 'X', 34-44, 'X', 46-55, 'X', 57, 'X', 59-60 <STR>
 A/Experimental source: fetal serum
 R/Franais, G.U.; McNeill, K.A.; Wallace, J.C.; Ballard, F.J.; Owens, P.C.
 Endocrinology 124, 1173-1183, 1989
 A>Title: Sheep insulin-like growth factors I and II: sequences, activities and assays.
 A/Reference number: S07198; MUID:89136887; PMID:2537174
 A/Accession: S08567
 A/Molecule type: protein
 A/Residues: 25-45, 'DG', 48-91 <FRA>
 A/Experimental source: fetal serum
 C/Superfamily: insulin
 C/Keywords: growth factor; plasma
 F/1-24/Domain: signal sequence #status predicted <ST>
 F/25-91/Product: insulin-like growth factor II #status experimental <MAT>
 F/25-52/Domain: insulin chain B-like #status predicted <DOB>
 F/53-64/Domain: insulin connecting peptide-like #status predicted <CHC>
 F/65-85/Domain: insulin chain A-like #status predicted <DOA>
 F/86-91/Domain: D peptide #status predicted <CHD>
 F/92-179/Domain: carboxyl-terminal propeptide (E peptide) #status predicted <CPR>
 F/33-71, 45-84, 70-75/Diulfide bonds: #status predicted

Query Match 85.0%; Score 34; DB 2; Length 179;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 ALIAFLAF 8
 11 ALIAFLAF 18
 Db 11 ALIAFLAF 18
 RESULT 7
 A88618
 protein ZK520.2 (imported) - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: A88618
 R/anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
 A/Reference number: A75000; MUID:99069613; PMID:9851916
 A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_el
 A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
 A/Accession: A88618
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-257 <STO>
 A/Cross-references: UNIPROT:O46019; GB:chr_III; PIDN:CAB07300.1; PID:93881752; GSPDB:GN
 C/genetic8
 A/Gene: ZK520.2
 A/Map position: 3
 C/Superfamily: Caenorhabditis elegans hypothetical protein ZK520.2
 Query Match 85.0%; Score 34; DB 2; Length 257;
 Best Local Similarity 88.9%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 ALIAFLAF 9
 166 ALIAFLAF 174
 Db 166 ALIAFLAF 174
 RESULT 8
 T21399
 hypothetical protein F26D2.4 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T21399
 R/McMurray, A.
 submitted to the EMBL Data Library, November 1996
 A/Reference number: Z19418
 A/Accession: T21399
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-332 <WIL>
 A/Cross-references: UNIPROT:O45403; EMBL:Z81513; PIDN:CAB04175.1; GSPDB:GN00023; CESP:F2
 C/genetic8
 A/Gene: CESP:F26D2.4
 A/Map position: 5
 A/Introns: 59/2; 108/1
 C/Superfamily: Caenorhabditis hypothetical protein C49G7.2
 Query Match 85.0%; Score 34; DB 2; Length 332;
 Best Local Similarity 87.5%; Pred. No. 39;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 2 LIAFLAF 9
 147 LIAFLAF 154
 Db 147 LIAFLAF 154
 RESULT 9
 T27883

hypothetical protein ZK520.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27883
 R:Steward, C.
 Submitted to the EMBL Data Library, March 1997
 A:Reference number: Z20434
 A:Accession: T27883
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1333 <WIL>
 A:Cross-references: UNIPROT:Q66019; EMBL:Z29822; PIDD:CA807300.2; GSPDB:GN000021; CESP:ZK520.2
 A:Experimental source: Clone ZK520
 C:Genetics:
 A:Gene: CESP:ZK520.2
 A:Map position: 3
 A:Insertions: 49/3, 170/3, 185/3, 261/1, 311/3
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZK520.2

Query Match 85.0%; Score 34; DB 2; Length 333;
 Best Local Similarity 88.9%; Pred. No. 39;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALIAFLAFL 9
 ||| ||| |||
 Db 223 ALIAFLAFL 231

RESULT 10
 G83816
 Late competence operon required for DNA binding and uptake comEC [imported] - *Bacillus h*
 C:Species: *Bacillus halodurans*
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: G83816
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: G83816
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-773 <STO>
 A:Cross-references: UNIPROT:Q9KD82; GB:A8001511; GB:BA000004; NID:G10173727; PIDD:BA050
 A:Experimental source: Strain C-125
 C:Genetics:
 A:Gene: comEC
 C:Superfamily: competence protein ComEC

Query Match 85.0%; Score 34; DB 2; Length 773;
 Best Local Similarity 77.8%; Pred. No. 81;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALIAFLAFL 9
 ||| ||| |||
 Db 26 ALIAFLAFL 34

RESULT 11
 GNMVDP
 genome polyprotein - dengue virus type 2 (strain PR159/S1)
 N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
 a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: dengue virus type 2
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 19-Jan-2001
 C:Accession: A29972
 R:Hahn, Y.S.; Gallier, R.; Hunkapiller, T.; Dalrymple, J.M.; Strauss, J.H.; Strauss, E.G.
 Virology 162, 167-180, 1988
 A:Title: Nucleotide sequence of dengue 2 RNA and comparison of the encoded proteins with
 A:Reference number: A29972; MUID:86101365; PMID:2827375
 A:Accession: A29972
 A:Molecule type: genomic RNA
 A:Residues: 1-338 <HHH>
 A:Cross-references: GB:M19197; NID:G323654; PIDD:AAA2962.1; PID:G323655

C:Superfamily: yellow fever virus genome polyprotein
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; membrane protein; nonst
 F:2-114/Product: capsid protein #status predicted <Cb>
 F:115-280/Product: membrane protein precursor #status predicted <MP>
 F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>
 F:206-280/Product: membrane protein #status predicted <MP>
 F:281-775/Product: envelope protein #status predicted <ENP>
 F:776-1188/Product: nonstructural protein NS1 #status predicted <NS1>
 F:1189-1345/Product: nonstructural protein NS2a #status predicted <NS2a>
 F:1346-1475/Product: nonstructural protein NS2b #status predicted <NS2b>
 F:1476-2090/Product: nonstructural protein NS3 #status predicted <NS3>
 F:1668-1675/Region: nucleotide-binding motif A (P-loop)
 F:1755-1760/Region: nucleotide-binding motif B
 F:1759-1762/Region: DBA motif
 F:2091-2376/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:2377-2488/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2489-3388/Product: nonstructural protein NS5 #status predicted <NS5>
 F:189,347,433,905,982,1134,1174,1329,1369,2298,2302,2384,2454,2482,2641,2662,2701,2711/B

Query Match 85.0%; Score 34; DB 1; Length 338;
 Best Local Similarity 77.8%; Pred. No. 2.8e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALIAFLAFL 9
 ||| ||| |||
 Db 49 ALIAFLAFL 57

RESULT 12
 GNMV16
 genome polyprotein - dengue virus type 2 (strain 16681)
 N:Contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstru
 tural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: dengue virus type 2
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A42451; A43496; A43763
 R:Block, J.; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Wellner, G.; Herring, B.L.; Hems
 Virology 187, 573-590, 1992
 A:Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence r
 A:Reference number: A42451; MUID:92188532; PMID:1312269
 A:Accession: A42451
 A:Molecule type: genomic RNA
 A:Residues: 1-3391 <UNO>
 A:Cross-references: UNIPROT:P29990; GB:M84727; GB:M85259; NID:G323472; PIDD:AAA73185.1;
 C:Superfamily: yellow fever virus genome polyprotein
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
 F:1-114/Product: capsid protein C #status predicted <CBC>
 F:115-280/Product: membrane-associated protein M precursor #status predicted <SIG>
 F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>
 F:206-280/Product: membrane-associated protein M #status predicted <MP>
 F:268-284/Domain: transmembrane #status predicted <TM1>
 F:281-775/Product: envelope protein E #status predicted <RPE>
 F:727-743/Domain: transmembrane #status predicted <TM2>
 F:757-773/Domain: transmembrane #status predicted <TM3>
 F:776-1127/Product: nonstructural protein NS1 #status predicted <NS1>
 F:1128-1345/Product: nonstructural protein NS2a #status predicted <NS2a>
 F:1346-1474/Product: nonstructural protein NS2b #status predicted <NS2b>
 F:1475-2093/Product: nonstructural protein NS3 #status predicted <NS3>
 F:1476-2093/Product: nonstructural protein NS3 #status predicted <NS3>
 F:1668-1675/Region: nucleotide-binding motif A (P-loop)
 F:1755-1760/Region: nucleotide-binding motif B
 F:1759-1762/Region: DBA motif
 F:2094-2243/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:2244-2491/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
 F:183,347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.0%; Score 34; DB 1; Length 3391;
 Best Local Similarity 77.8%; Pred. No. 2.8e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALIAFLAFL 9
 ||| ||| |||
 Db 49 ALIAFLAFL 57

RESULT 13

GNMV26
genome polyprotein - dengue virus type 2 (strain 16681-PDX53)
N:Contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: dengue virus type 2
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: B42451
R:Block: J.; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Wellner, G.; Herring, B.L.; Hemmingsley, P.; Smith, R.A.; Smith, T.F.; Smith, D.R.; Smith, J.E.; Smith, J.P.; Smith, J.S.; Smith, J.T.; Smith, J.W.; Smith, J.Z.; Smith, L.A.; Smith, L.B.; Smith, L.C.; Smith, L.D.; Smith, L.E.; Smith, L.F.; Smith, L.G.; Smith, L.H.; Smith, L.I.; Smith, L.J.; Smith, L.K.; Smith, L.L.; Smith, L.M.; Smith, L.N.; Smith, L.O.; Smith, L.P.; Smith, L.Q.; Smith, L.R.; Smith, L.S.; Smith, L.T.; Smith, L.U.; Smith, L.V.; Smith, L.W.; Smith, L.X.; Smith, L.Y.; Smith, L.Z.; Smith, M.A.; Smith, M.B.; Smith, M.C.; Smith, M.D.; Smith, M.E.; Smith, M.F.; Smith, M.G.; Smith, M.H.; Smith, M.I.; Smith, M.J.; Smith, M.K.; Smith, M.L.; Smith, M.M.; Smith, M.N.; Smith, M.O.; Smith, M.P.; Smith, M.Q.; Smith, M.R.; Smith, M.S.; Smith, M.T.; Smith, M.U.; Smith, M.V.; Smith, M.W.; Smith, M.X.; Smith, M.Y.; Smith, M.Z.; Smith, N.A.; Smith, N.B.; Smith, N.C.; Smith, N.D.; Smith, N.E.; Smith, N.F.; Smith, N.G.; Smith, N.H.; Smith, N.I.; Smith, N.J.; Smith, N.K.; Smith, N.L.; Smith, N.M.; Smith, N.N.; Smith, N.O.; Smith, N.P.; Smith, N.Q.; Smith, N.R.; Smith, N.S.; Smith, N.T.; Smith, N.U.; Smith, N.V.; Smith, N.W.; Smith, N.X.; Smith, N.Y.; Smith, N.Z.; Smith, O.A.; Smith, O.B.; Smith, O.C.; Smith, O.D.; Smith, O.E.; Smith, O.F.; Smith, O.G.; Smith, O.H.; Smith, O.I.; Smith, O.J.; Smith, O.K.; Smith, O.L.; Smith, O.M.; Smith, O.N.; Smith, O.O.; Smith, O.P.; Smith, O.Q;

A:Residues: 1-3391 <BLO>
A:Cross-references: UNIPROT:P29991; GB:M85259
C:Superfamily: yellow fever virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; F1-114/Product; capsid protein C #status predicted <CPC>
F:50-66/Domain: transmembrane #status predicted <TM1>
F:102-118/Domain: transmembrane #status predicted <TM2>
F:115-280/Product: membrane-associated protein M precursor #status predicted <MP>
F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>
F:206-280/Product: membrane-associated protein M #status predicted <MPM>
F:268-284/Domain: transmembrane #status predicted <TM3>
F:281-775/Product: envelope protein E #status predicted <EPE>
F:727-743/Domain: transmembrane #status predicted <TM4>
F:757-773/Domain: transmembrane #status predicted <TM5>
F:776-1127/Product: nonstructural protein NS1 #status predicted <NS1>
F:1128-1345/Product: nonstructural protein NS2a #status predicted <NS2a>
F:1158-1174/Domain: transmembrane #status predicted <TM6>
F:1272-1288/Domain: transmembrane #status predicted <TM7>
F:1294-1310/Domain: transmembrane #status predicted <TM8>
F:1346-1474/Product: nonstructural protein NS2b #status predicted <NS2b>
F:1351-1367/Domain: transmembrane #status predicted <TM9>
F:1373-1389/Domain: transmembrane #status predicted <TMA>
F:1448-1464/Domain: transmembrane #status predicted <TMB>
F:1475-2093/Product: nonstructural protein NS3 #status predicted <NS3>
F:1668-1675/Region: nucleotide-binding motif A (P-loop)
F:1755-1760/Region: nucleotide-binding motif B
F:1759-1762/Region: DEAD motif
F:2094-2243/Product: nonstructural protein NS4a #status predicted <NS4a>
F:2148-2164/Domain: transmembrane #status predicted <TMC>
F:2148-2190/Domain: transmembrane #status predicted <TMD>
F:2197-2213/Domain: transmembrane #status predicted <TME>
F:2227-2243/Domain: transmembrane #status predicted <TFW>
F:2244-2491/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2352-2368/Domain: transmembrane #status predicted <TMG>
F:2411-2427/Domain: transmembrane #status predicted <TMH>
F:2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
F:183,347,433,905,982,1134,1174,11359,2301,2305,2346,2387,2457,2485,2644,2665,2704,2714/B

Query Match 85.0%; Score 34; DB 1; Length 3391;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALIAFL 9
Db 49 ALVAFRL 57

RESULT 14

GNMV26
genome polyprotein - dengue virus type 2 (strain Ujamaica)
N:Contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: dengue virus type 2
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A94346; A94378; A25613; A29199
R:Deubel, V.; Kimey, R.W.; Trent, D.W.
Virology 155, 365-377, 1986

A>Title: Nucleotide sequence and deduced amino acid sequence of the structural proteins
A.Reference number: A94346; MUID:8707165e; PMID:3024394

A.Accession: A94346

A:Molecule type: genomic RNA

A.Residues: 1-791 <DE1>

A.Cross-references: UNIPROT:P07564; GB:M15975

R.Denbel, V.; Kinney, R.M.; Trent, D.W.

Virology 165, 234-244, 1988

A>Title: Nucleotide sequence and deduced amino acid sequence of the nonstructural prote
A.Reference number: A94378; MUID:8826586d; PMID:3388770

A.Accession: A94378

A:Molecule type: genomic RNA

A.Residues: 792-3391 <DE2>

A.Cross-references: GB:M20558

C.Superfamily: yellow fever virus genome polypeptide

C.Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F.2-114/Product: capsid protein C #status predicted <CPC>
F.43-59/Domain: transmembrane #status predicted <TM1>
F.101-117/Domain: transmembrane #status predicted <TM2>
F.115-280/Product: membrane-associated protein M precursor #status predicted <MPP>
F.115-205/Domain: nonterminal signal sequence #status predicted <SIG>
F.206-280/Product: membrane-associated protein M #status predicted <MPM>
F.268-284/Domain: transmembrane #status predicted <TM3>
F.281-775/Product: envelope protein E #status predicted <EPB>
F.727-743/Domain: transmembrane #status predicted <TM4>
F.775-773/Domain: transmembrane #status predicted <TM5>
F.776-1127/Product: nonstructural protein NS1 #status predicted <NS1>
F.1128-1345/Product: nonstructural protein NS2a #status predicted <N2A>
F.1346-1474/Product: nonstructural protein NS2b #status predicted <N2B>
F.1475-2093/Product: nonstructural protein NS3 #status predicted <NS3>
F.1668-1675/Region: nucleotide-binding motif A (P-loop)
F.1755-1760/Region: nucleotide-binding motif B
F.1759-1762/Region: DEAH motif
F.2094-2243/Product: nonstructural protein NS4a #status predicted <N4A>
F.2244-2491/Product: nonstructural protein NS4b #status predicted <N4B>
F.2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
F.183,347,433/Binding site: cardiolipate (Asn) (covalent) #status predicted

Query Match 85.0% Score 34; DB 1; Length 3391;
Best Local Similarity 77.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Gy 1 ALINFAFL 9
D_b 49 ALTVAFLRL 57

RESULT 15

J50219

Polyprotein - dengue virus type 2 (strain New Guinea-C)

N.Contains: capsid protein; envelope protein; membrane glycoprotein; nonstructural prot
N.NS4a; nonstructural protein NS4B; nonstructural protein NS5

C.Species: dengue virus type 2

C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C.Accession: J50219; A28646

R.Irte, K.; Mohan, P.M.; Sasaguri, Y.; Putnak, R.; Padmanabhan, R.
Gene 75, 197-211, 1989

A.Title: Sequence analysis of cloned dengue virus type 2 genome (New Guinea-C strain).
A.Reference number: J50219; MUID:8923275f; PMID:2714651

A.Accession: J50219

A:Molecule type: genomic RNA

A.Residues: 1-3391 <R1>

A.Cross-references: UNIPROT:Q9O4T2; UNIPROT:Q9WLZ4; UNIPROT:Q9WDAG; UNIPROT:Q9JBD4; UNI
PROT:Q9ABDS; UNIPROT:Q9ABD8; UNIPROT:Q9WDA7; UNIPROT:Q92753; UNIPROT:Q92834; UNIPROT:
JBER; UNIPROT:Q9WE13; UNIPROT:Q9JSD7; UNIPROT:Q9MDA3; UNIPROT:O11875; UNIPROT:O92835; U
NPutnak, J.R.; Charles, S.C.; Padmanabhan, R.; Irte, K.; Hore, C.H.; Burke, D.S.
Virology 163, 93-103, 1988

A>Title: Functional and antigenic domains of the dengue-2 virus nonstructural glycoprote
A.Reference number: A28646; MUID:88160069; PMID:2964755

A.Accession: A28646

A:Molecule type: genomic RNA

A.Residues: 749-1227 <PUT>
Superfamily: yellow fever virus genome polyprotein

C:Keywords: ATP; envelope protein; glycoprotein; nonstructural protein; nucleotide binding site; capsid protein #status predicted <CAP>
 F:2-114/Product: membrane glycoprotein #status predicted <MEM>
 F:115-280/Product: nonterminal signal sequence #status predicted <SIG>
 F:115-205/Domain: membrane glycoprotein #status predicted <MEB>
 F:206-280/Product: envelope protein #status experimental <ENV>
 F:281-775/Domain: transmembrane #status predicted <TM1>
 F:775-775/Domain: transmembrane #status predicted <TM1>
 F:776-1127/Product: nonstructural protein NS1 #status experimental <NS1>
 F:1128-1345/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1135-1146/Domain: transmembrane #status predicted <TM2>
 F:1158-1173/Domain: transmembrane #status predicted <TM3>
 F:1346-1475/Product: nonstructural protein NS2B #status predicted <NSB>
 F:1476-2093/Product: nonstructural protein NS3 #status experimental <NS3>
 F:1668-1675/Region: nucleotide-binding motif A (P-loop)
 F:1755-1760/Region: nucleotide-binding motif B
 F:1759-1762/Region: DEAH motif
 F:2094-2379/Product: nonstructural protein NS4A #status predicted <NS4>
 F:2380-2491/Product: nonstructural protein NS4B #status predicted <NS4B>
 F:2492-3391/Product: nonstructural protein NS5 #status experimental <NS5>
 F:183,905,982,2305,2457,2704/Binding site: carbohydrate (Asn) (covalent) #status experimental <STA>
 F:247,433,1134,1174,2301,2485,2665,2714/Binding site: carbohydrate (Asn) (covalent) #status experimental <STA>

Query Match 85.0%; Score 34; DB 2; Length 3391;

Best Local Similarity 77.8%; Pred. No. 2.8e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALIAPLAF 9
 DB 49 ALVAFDRFL 57

Search completed: May 3, 2005, 06:14:39
 Job time : 29.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-4

Perfect score: 48

Sequence: 1 MIVEKATV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pirt: *
2: pirt: *
3: pirt: *
4: pirt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	1273	1	TDRILT
2	48	100.0	1291	1	A28334
3	48	100.0	1304	1	A46546
4	47	97.9	1237	2	A54080
5	46	95.8	1200	2	T43148
6	45	93.8	2294	2	167630
7	45	93.8	2466	2	167629
8	44	91.7	1691	1	D54689
9	44	85.4	1894	2	C54689
10	41	85.4	2490	1	A54971
11	39	81.2	680	2	JC8052
12	39	81.2	2450	2	S71625
13	37	77.1	252	2	H95854
14	37	77.1	593	1	A42690
15	36	75.0	597	2	B53978
16	36	75.0	694	2	A53978
17	36	75.0	1437	2	T31093
18	35.5	74.0	700	1	S12053
19	35	72.9	222	2	G86783
20	35	72.9	264	2	D71724
21	35	72.9	356	2	A97723
22	35	72.9	366	2	JM0049
23	35	72.9	414	1	QOEC49
24	35	72.9	414	2	H85512
25	35	72.9	414	2	B90662
26	35	72.9	432	1	A34845
27	35	72.9	432	1	JN0317
28	35	72.9	435	1	TPH0N1
29	35	72.9	535	2	A46101

30	35	72.9	548	2	B46101	protein-tyrosine-p
31	35	72.9	1301	1	A41622	protein-tyrosine-p
32	34.5	71.9	1912	2	A56178	protein-tyrosine-p
33	34	70.8	314	2	T45077	ornithine carbamoy
34	34	70.8	317	2	G75041	ornithine carbamoy
35	34	70.8	317	2	G71119	probable ornithine
36	34	70.8	377	1	A48711	protein-tyrosine-p
37	34	70.8	408	2	P97304	selenocysteine-ly
38	34	70.8	459	2	B95031	glycosyl hydrolase
39	34	70.8	499	2	D97902	beta-glucosidase (
40	34	70.8	850	2	A48753	NFAT transcription
41	34	70.8	921	2	G02326	transcription fact
42	34	70.8	3224	1	S58884	Ran-binding prote
43	33.5	69.8	582	2	A57068	protein-tyrosine-p
44	33.5	69.8	1262	1	B48758	protein-tyrosine-p
45	33.5	69.8	1290	2	A56493	leucocyte common a

ALIGNMENTS

RESULT 1

TDRILT

N/Alternate names: CD45; L-CA; Ly-5; T200

N/Contains: leukocyte common antigen precursor, splice form 1; leukocyte common antigen precursor, splice form 4 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 04-Dec-1986 #sequence revision 05-May-2000 #ext change 09-Jul-2004

C/Accession: A29450; B29450; C29450; D29450; A60241; A02247; I54569; A45854

R/Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

EMBL J 6, 1259-1264, 1987

A/Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) 1

A/Reference number: A51067; MUID:87275817; PMID:2440674

A/Accession: A29450

A/Molecule type: mRNA

A/Residues: 20-30,163-218 <BAR1>

A/Cross-references: UNIPROT:G64224; GB:M25820; GB:M24611; NID:G205153; GB:Y00065; GB:K0

A/Note: the translation in GenBank entry RATLCAI, PIDN:AAA1518.1, PID:G205154, release

A/Accession: B29450

A/Molecule type: mRNA

A/Residues: 19-30,122-218 <BAR2>

A/Cross-references: GB:M25821; GB:M24611; NID:G205155; PIDN:AAA1519.1; PID:G205156; GB

A/Note: the translation in GenBank entry RATLCAI, PIDN:AAA1518.1, PID:G205154, release

A/Accession: C29450

A/Molecule type: mRNA

A/Residues: 20-30,73-121,163-218 <BAR3>

A/Cross-references: GB:M25822; GB:M24611; NID:G205157; PIDN:AAA1520.1; PID:G205158; GB

A/Note: the translation in GenBank entry RATLCAI, PIDN:AAA1518.1, PID:G205154, release

A/Accession: D29450

A/Molecule type: mRNA

A/Residues: 28-218 <BAR4>

A/Cross-references: GB:M25823; GB:M24611; NID:G205159; PIDN:AAA1521.1; PID:G205160; GB

A/Note: the translation in GenBank entry RATLCAI, release 113.0, has the codon AGG for 56

R/Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

Adv. Exp. Med. Biol. 237, 3-7, 1988

A/Title: The leukocyte-common antigen (L-CA) family.

A/Reference number: A60241; MUID:89319817; PMID:2978200

A/Accession: A60241

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 30-161 <BAR5>

R/Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.

Cell 41, 83-93, 1985

A/Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans 1

A/Reference number: A02247; MUID:85201691; PMID:3158393

A/Accession: A02247

A/Molecule type: mRNA

A/Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>

A/Cross-references: GB:M10072; GB:M1859; NID:G205140; PIDN:AAA41513.1; PID:G205143

A/Note: the translation in GenBank entry RATLCAI, release 113.0, begins at non-initiat

A>Note: parts of this sequence were determined by protein sequencing
 R.McGill, M.N.; Shotton, D.M.; Barclay, A.N.
 Immunology 76, 310-317, 1992
 A>Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
 A:Reference number: 154569; PMID:92340120; PMID:1378817
 A:Accession: A5854
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-30, 163-180 <MC>
 A:Cross-references: GB:S40716; NID:G252015; PIDN:AA822648.1; PID:G252016
 R:Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A>Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are deriv
 A:Reference number: A45854; PMID:89233293; PMID:2523868
 A:Accession: A45854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JC>
 A:Cross-references: GB:M18347; GB:M18348; GB:M18349
 C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1273/Product: leukocyte common antigen precursor, splice form 4 #status predicted <
 F:24-546/Domain: extracellular #status predicted <EXT>
 F:24-30, 122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <MAT
 F:24-30, 153-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MAT
 F:24-30, 73-121, 163-218/Product: leukocyte common antigen, splice form 3 #status predicte
 F:547-568/Domain: transmembrane #status predicted <TM>
 F:565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:569-1273/Domain: intracellular #status predicted <INT>
 F:646-870/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:62, 142, 153, 164, 178, 200, 245, 271, 282, 327, 371, 374, 502/Binding site: carbohydrate (Asn) (C
 F:622/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:628/Binding site: substrate phosphate (Arg) #status predicted
 F:1063/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 100.0%; Score 48; DB 1; Length 1273;
 Best Local Similarity 100.0%; Pred. NO. 0.32; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

QY 1 MIMWOKATV 9
 |||||
 |||||
 Db 708 MIMWOKATV 716

RESULT 2
 A28334
 protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
 N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
 N:Contents: protein-tyrosine-phosphatase (T-cell variant)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text change 09-Jul-2004
 C:Accession: A28334; A29381; A61180; A60933; A35522; A4450; A28335; A23329; I57
 R:Thomas, M.L.; Reynolds, P.J.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
 A>Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
 A:Reference number: A28334; PMID:87260986; PMID:2955416
 A:Accession: A28334
 A:Molecule type: mRNA
 A:Residues: 1-1291 <THO>
 A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
 A>Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
 A:Reference number: A29381; PMID:86333686; PMID:2944116
 A:Accession: A29381
 A:Molecule type: mRNA
 A:Residues: 130, 170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, '
 A:Cross-references: GB:M14342; NID:G198914; PIDN:AAA39458.1; PID:G198915
 R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A>Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by

A:Reference number: A61180; PMID:92032882; PMID:1932742
 A:Accession: A61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 730-838 <YIA>
 R:Gomez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
 Immunogenetics 25, 263-266, 1987
 A>Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
 A:Reference number: A60933; PMID:87192931; PMID:3570377
 A:Accession: A60933
 A:Molecule type: Protein
 A:Residues: 'R', 289-298; 329, 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375; 595-608; 638-649; 669-
 R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
 J. Biol. Chem. 264, 6220-6229, 1989
 A>Title: Sequence conservation in potential regulatory regions of the mouse and human le
 A:Reference number: A35522; PMID:89197920; PMID:2522930
 A:Accession: A35522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <UOH>
 A:Cross-references: GB:M22456; NID:G198755; PIDN:AA846374.1; PID:G554185; GB:J04640; GB:
 R:Raschke, W.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
 A>Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
 A:Reference number: A29075; PMID:87092355; PMID:2948186
 A:Accession: A29075
 A:Molecule type: mRNA
 A:Residues: 961-1291 <RAS>
 A:Cross-references: GB:M5174; NID:G201105; PIDN:AAA40161.1; PID:G201106
 R:Tung, J.
 Immunogenetics 28, 271-277, 1988
 A>Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
 A:Reference number: I54450; PMID:8830145; PMID:3417340
 A:Accession: I54450
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 32-73 <RES>
 A:Cross-references: GB:M23241; NID:G340850; PIDN:AAA39460.1; PID:G548174
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A>Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishin
 A:Reference number: A28335; PMID:87260987; PMID:3037546
 A:Accession: A28335
 A:Molecule type: mRNA
 A:Residues: 1-30, 74-226 <SA2>
 A:Cross-references: GB:M14342
 R:Shen, F.W.; Saga, Y.; Littman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
 A:Reference number: A23329; PMID:86042665; PMID:3864163
 A:Accession: A23329
 A:Molecule type: mRNA
 A:Residues: 10-30, 170-263 <SHR>
 A:Cross-references: GB:M11934; NID:G198919; PIDN:AAA39461.1; PID:G198920
 R:Saga, Y.; Tung, J.
 Mol. Cell. Biol. 8, 4889-4895, 1988
 A>Title: Organization of the Ly-5 Gene.
 A:Reference number: I57644; PMID:89096862; PMID:3211131
 A:Accession: I57644
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 'MT', 1-22 <R82>
 A:Cross-references: GB:M23354; NID:G340890; PIDN:AAA39462.1; PID:G554192
 C:Genetics: Ly-5
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MAT
 F:24-564/Domain: extracellular #status predicted <EXT>
 F:24-30, 170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicte
 F:565-586/Domain: transmembrane #status predicted <TM>
 F:583-1223/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:587-1291/Domain: intracellular #status predicted <INT>

F:664-888/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: C
 F:840/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:846/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 48; DB 1; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXCATV 9
 DB 726 MIMEXCATV 734

RESULT 3

A:Accession: A46546
 leukocyte common antigen long splice form precursor - human
 N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprotein
 N/Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
 R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
 J. Exp. Med. 166, 1548-1566, 1987
 A>Title: Differential usage of three exons generates at least five different mRNAs encoded
 A/Reference number: A46546; MUID:88061067; PMID:2824653
 A/Accession: A46546
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1304 <STR>
 A/Cross-references: UNIPROT:P08575; GB:Y00638
 A/Experimental source: clone LCA.6/2
 A/Accession: B46546
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-32,99-264 <ST2>
 A/Cross-references: GB:Y00638
 A/Experimental source: clone LCA.111 and clone LCA.260
 A/Accession: C46546
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-31,193-264 <ST3>
 A/Cross-references: GB:Y00638
 A/Experimental source: clone LCA.1
 R/Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
 EMBO J. 6, 1251-1257, 1987
 A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
 A/Reference number: A91066; MUID:87275816; PMID:2956090
 A/Accession: A29449
 A/Molecule type: mRNA
 A/Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
 A/Cross-references: GB:Y00662; NID:934275; PIDN:CAA68269.1; PID:934276
 A/Experimental source: clones PHC-1 and lambdaHLG1
 A/Accession: B29449
 A>Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 32-192 <RA2>
 A/Experimental source: clone HLC-2
 R/Tsai, A.Y.; Streuli, M.; Saito, H.
 Mol. Cell. Biol. 9, 4550-4555, 1989
 A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative splicing
 A/Reference number: I57658; MUID:9066468; PMID:2531281
 A/Accession: I57658
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 146-192 <RES>
 A/Cross-references: GB:M29253; NID:9187020; PIDN:AAA59497.1; PID:9553521
 C/Genetics:
 A/Genes: GDB:PTPRC, CD45
 A/Cross-references: GDB:119768; OMIM:151460
 A/Map position: 1q31-1q32
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homology
 C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:575-899/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:551/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:557/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 48; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXCATV 9
 DB 737 MIMEXCATV 745

RESULT 4

A:Accession: A54080
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 02-Aug-1994 #sequence revision 02-Aug-1994 #text change 09-Jul-2004
 C/Accession: A54080; I50592
 R/Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
 J. Biol. Chem. 269, 14056-14063, 1994
 A>Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in
 A/Reference number: A54080; MUID:94245724; PMID:8188686
 A/Accession: A54080
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1237 <FAN>
 A/Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:9510510; PIDN:CAA79972.1; PID:9510
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homo
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:610-834/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:786/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 97.9%; Score 47; DB 2; Length 1237;
 Best Local Similarity 88.9%; Pred. No. 0.49;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXCATV 9
 DB 672 MIMEXCATV 680

RESULT 5

T43148
 probable protein-tyrosine-phosphatase (EC 3.1.3.48) - horn shark
 N/Alternate names: CD45 homolog
 C/Species: Heterodontus francisci (horn shark)
 C/Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 09-Jul-2004
 C/Accession: T43148
 R/Okumura, M.; Matthews, R.J.; Robb, B.; Bork, P.; Thomas, M.L.
 submitted to the EMBL Data Library, August 1995
 A/Reference number: Z22317
 A/Accession: T43148
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1200 <OKU>
 A/Cross-references: UNIPROT:Q91054; EMBL:U34750; NID:91304393; PID:91335805; PIDN:AAB01
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homo
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 95.8%; Score 46; DB 2; Length 1200;
 Best Local Similarity 77.8%; Pred. No. 0.74;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXCATV 9
 DB 637 MIMEXCATV 645

RESULT 6

167630
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 -
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: 167630
R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A:Reference number: 153483; PMID:94116679; PMID:8287977
A:Accession: 167630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2294 <RES>
A:Cross-references: UNIPROT:O12923; GB:D21211; NID:9452193; PIDN:BA04752.1; PID:9452194
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C:Keyword: phosphoric monoester hydrolase
F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F:1182-1258/Domain: protein 4.1 membrane-binding domain homology <GLG2>
F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 93.8%; Score 45; DB 2; Length 2294;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
Db 2105 MIMOKSTV 2113

RESULT 7
167629
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 -
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: 167629
R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A:Reference number: 153483; PMID:94116679; PMID:8287977
A:Accession: 167629
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2466 <RES>
A:Cross-references: UNIPROT:O12923; GB:D21210; NID:9452191; PIDN:BA04751.1; PID:9452192
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C:Keyword: phosphoric monoester hydrolase
F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F:1354-1430/Domain: GLGF domain homology <GLG2>
F:2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 93.8%; Score 45; DB 2; Length 2466;
Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
Db 2277 MIMOKSTV 2285

RESULT 8
D54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precursor
N:Alternate names: MPTP delta type D
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form A
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: D54689; A54689
R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized
A:Reference number: A54689; PMID:93360986; PMID:8355697
A:Accession: D54689
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-1691 <MI2>
A:Cross-references: UNIPROT:O64487
A:Experimental source: brain
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:136537)
A:Accession: A54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-398,799-1691 <MI2>
A:Experimental source: brain
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBI:136524)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
C:Keyword: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:42-95/Domain: immunoglobulin homology <IMM3>
F:114-196/Domain: fibronectin type III repeat homology <FN3A>
F:1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1449-1671/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1333/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1623/Binding site: Cys (phosphocysteine intermediate) #status predicted
F:1629/Binding site: substrate phosphate (Arg) #status predicted

Query Match 91.7%; Score 44; DB 1; Length 1691;
Best Local Similarity 86.9%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
Db 1224 MIMOKATV 1232

RESULT 9
C54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor
N:Alternate names: MPTP delta type B/C
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C:Species: Mus musculus (house mouse)
C:Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C:Accession: C54689; B54689
R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized
A:Reference number: A54689; PMID:93360986; PMID:8355697
A:Accession: C54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1894 <MI2>
A:Cross-references: UNIPROT:O64487
A:Experimental source: brain; splice form B
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:137487)
A:Accession: B54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MI2>
A:Experimental source: brain; splice form C
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBI:136530)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
C:Keyword: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:45-107/Domain: immunoglobulin homology <IMM1>
F:245-299/Domain: immunoglobulin homology <IMM2>
F:317-399/Domain: fibronectin type III repeat homology <FN3A>
F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1542/Binding site: substrate phosphate (Arg) #status predicted
F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 91.7%; Score 44; DB 2; Length 1894;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIWEOKATV 9
DB 1427 MIWEOKATV 1435

RESULT 10

A:Accession: A54971
A:Residues: 1-2490 <BAN>
A:Cross-references: UNIPROT:Q12923; GB:U12128
A:Note: sequence shown follows authors' translation at positions 62-63
R:Saras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gonen, L.J.
J. Biol. Chem. 269, 24082-24089, 1994
A:Title: Cloning and characterization of PTPBL1, a protein tyrosine phosphatase with siml
A:Reference number: A55114; PMID:95014139; PMID:7929060
A:Accession: A55114
A:Molecule type: mRNA
A:Residues: 1-61, 'GS', 64-839, 'D', 841-1055, 1075-1133, 'RH', 1136-1210, 'I', 1212-1383, 1389-15
A:Cross-references: GB:X80289; NID:9515030; PIDN:CA56563.1; PID:9515031
R:Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A:Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.
A:Reference number: I59595; PMID:95232528; PMID:7536343
A:Accession: I59595
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1279-1868 <RES>
A:Cross-references: GB:I34583; NID:9806291; PIDN:AA41755.1; PID:9806292
R:Nakawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A:Reference number: I53483; PMID:9411679; PMID:8287977
A:Accession: I53483
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-61, 'GS', 64-839, 'D', 841-1210, 'I', 1212-1383, 1389-2229, 'QM', 2302-2490 <RE2>
A:Cross-references: GB:D21209; NID:9452189; PIDN:BA404750.1; PID:9452190
C:Genetics:
A:Gene: GDB:PTPN13
A:Cross-references: GDB:306348; OMIM:600267
A:Map position: 4q21.3-4q21.3
C:Suprafamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F:1099-1175/Domain: GLGF domain homology <GLG1>
F:1373-1454/Domain: GLGF domain homology <GLG2>
F:1511-1590/Domain: GLGF domain homology <GLG3>
F:1799-1870/Domain: GLGF domain homology <GLG4>
F:1893-1967/Domain: GLGF domain homology <GLG5>
F:2242-2461/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:2413/Active site: Cys (phosphocysteine intermediate) #status predicted
F:2419/Binding site: substrate phosphate (Arg) #status predicted

Query Match 85.4%; Score 41; DB 1; Length 2490;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIWEOKATV 9

DB 2301 MIWEOKSTV 2309

RESULT 11

JC8052
C:Species: Oryzias latipes (Japanese medaka)
C>Date: 09-May-2004 #sequence_revision 09-May-2004 #text_change 09-May-2004
C:Accession: JC8052
R:Okubo, K., and Aida, K.
Biochem. Biophys. Res. Commun. 312, 531-536, 2003
A:Title: Gonadotropin-releasing hormone gene products downregulate the expression of th
A:Reference number: JC8051; PMID:14680798
A:Accession: JC8052
A:Molecule type: mRNA
A:Residues: 1-680 <OKU>
A:Cross-references: DDBJ:AB094509
A:Experimental source: (Brain)
C:Comment: This protein is capable of both driving neuromodulatory effects of gonadotrop
ifying potassium channel.
C:Genetics:
A:Gene: pcg epsilon
C:Keywords: brain; gonadotropin-releasing hormone; protein tyrosine phosphatase

Query Match 81.2%; Score 39; DB 2; Length 680;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIWEOKAT 8
DB 205 MIWEOKKT 212

RESULT 12

S71625
A:Accession: S71625
A:Cross-references: UNIPROT:O64512; UNIPROT:O62370; EMBL:DB3966; NID:91232103; PIDN:BA4
A:Residues: 1-2450 <CHI>
A:Cross-references: UNIPROT:O64512; UNIPROT:O62370; EMBL:DB3966; NID:91232103; PIDN:BA4
A:Experimental source: strain DBM/2; cell line MEL 745A
R:Wolf, B.B.; Brown, M.D.
FEBS Lett. 376, 177-180, 1995
A:Title: Epidermal growth factor-binding protein activates soluble and receptor-bound s
A:Reference number: S67987; PMID:96105375; PMID:7498536
A:Accession: S67987
A:Molecule type: protein
A:Residues: 1098-1102 <MOI>
A:Experimental source: submaxillary glands
R:Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A:Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.
A:Reference number: I59595; PMID:95232528; PMID:7536343
A:Accession: I59595
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1329-1354, 'K', 1356-1447, 'R', 1449-1454 <RES>
A:Cross-references: GB:I34582; NID:9806297; PIDN:AA42056.1; PID:9806298
A:Accession: I81209
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1336-1354, 'K', 1356-1447, 'R', 1449-1454 <RE2>
A:Cross-references: GB:I34581; NID:9806295; PIDN:AA42055.1; PID:9806296
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.

submitted to the EMBL Data Library, June 1993

A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatases

A:Reference number: S40280

A:Molecule type: S40290

A:Residues: 2266-2372 <HEN>

A:Cross-references: EMBL:223059; NID:9438155; PIDN:CAA80594.1; PID:9438156

C:Genetics:

A:Gene: Ptpn13

A:Map position: 5

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C:Keywords: phosphoprotein, phosphoric monoester hydrolase; transmembrane protein; tyros

F:566-860/Domain: protein 4.1 membrane-binding domain homology <B41>

F:1089-1165/Domain: GLGF domain homology <GLG1>

F:1361-1437/Domain: GLGF domain homology <GLG2>

F:1495-1574/Domain: GLGF domain homology <GLG3>

F:1769-1840/Domain: GLGF domain homology <GLG4>

F:1863-1937/Domain: GLGF domain homology <GLG5>

F:2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:2374/Active site: Cys (phosphocysteine intermediate) #status predicted

F:2380/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 81.2%; Score 39; DB 2; Length 2450;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9

DB 2262 MWBONSTV 2270

RESULT 13

H95854

hypothetical membrane protein (imported) - Sinorhizobium meliloti (strain 1021) megaplas

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: H95854

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N₂-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: H95854

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-252 <KUR>

A:Cross-references: UNIPROT:Q92X58; GB:AL591965; PIDN:CAC48504.1; PID:G15139976; GSPDB:C

A:Experimental source: strain 1021, megaplasmid pSymB

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

petla, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kies, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weiss, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Cross-references: annotation

C:Genetics:

A:Gene: Smb20104

A:Genome: plasmid

Query Match

Best Local Similarity 77.1%; Score 37; DB 2; Length 252;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9

DB 236 MIMBOKATV 244

RESULT 14

A42690

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 9 - human

N:Alternate names: PTPase MEG2

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C:Accession: A42690

R:Gu, M.; Marshawsky, I.; Majerus, P.W.

Proc. Natl. Acad. Sci. U.S.A. 89, 2980-2984, 1992

A:Title: Cloning and expression of a cytosolic megakaryocyte protein-tyrosine-phosphatase

A:Reference number: A42690; MUID:92212952; PMID:1557404

A:Accession: A42690

A:Molecule type: mRNA

A:Residues: 1-593 <GUA>

A:Cross-references: UNIPROT:P43378; GB:M83738; NID:9190745; PIDN:AAA60226.1; PID:9190746

C:Genetics:

A:Gene: GDB:PTPN9

A:Map position: 1q32.1-1q32.1

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:48-237/Domain: cellular retinaldehyde-binding protein homology <CRB>

F:327-563/Domain: protein-tyrosine-phosphatase homology <PTP>

F:515/Active site: Cys (phosphocysteine intermediate) #status predicted

F:521/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 77.1%; Score 37; DB 1; Length 593;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9

DB 389 MWBOKATV 397

RESULT 15

B53978

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX10 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B53978

R:Del Vecchio, R.L.; Tonke, N.K.

J. Biol. Chem. 269, 19639-19645, 1994

A:Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph

A:Reference number: A53978; MUID:94308257; PMID:8034733

A:Accession: B53978

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-597

A:Cross-references: UNIPROT:Q91871; GB:L33099; NID:9495671; PIDN:AAA21728.1; PID:9495672

A:Experimental source: ovary

A:Note: sequence extracted from NCBI backbone (NCBI:149759, NCBI:149760)

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>

F:328-564/Domain: protein-tyrosine-phosphatase homology <PTP>

F:516/Active site: Cys (phosphocysteine intermediate) #status predicted

F:522/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 75.0%; Score 36; DB 2; Length 597;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9

DB 390 MWBOKATV 398

Search completed: May 3, 2005, 06:15:05
Job time: 14.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:29:17 ; Search time 48 Seconds
(without alignments)
72.518 Million cell updates/sec

Title: US-10-003-983C-7
Perfect score: 44
Sequence: 1 LIAFGFAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	5	ABG31977 Human CD4
2	44	100.0	10	5	ABG31985 Human CD4
3	44	100.0	23	2	AAW35875 Leader se
4	44	100.0	34	8	ADP24555 PRO poly
5	44	100.0	42	3	AAV64915 Human 5'
6	44	100.0	60	3	AAW00095 Human sec
7	44	100.0	87	3	AAV64916 Human 5'
8	44	100.0	153	3	AAV64914 Human 5'
9	44	100.0	641	4	AAW23689 Human EST
10	44	100.0	641	4	ABU07333 Human exp
11	44	100.0	664	4	AAW39282 Human pol
12	44	100.0	664	4	ABU07334 Human exp
13	44	100.0	1143	6	ABU05240 Human exp
14	44	100.0	1143	6	ABU05245 Human exp
15	44	100.0	1143	7	ADL16232 Human pro
16	44	100.0	1143	4	ADQ18845 Human sof
17	44	100.0	1149	4	AAW41048 Human pol
18	44	100.0	1149	6	ABU05242 Human exp
19	44	100.0	1192	8	ADR39747 Human kin
20	44	100.0	1256	8	ADM67187 Human adi
21	44	100.0	1256	8	ADP12966 Protein e
22	44	100.0	1258	8	ADQ39376 Human wyo
23	44	100.0	1304	6	ABU05243 Human exp
24	44	100.0	1304	6	ABU05241 Human exp
25	44	100.0	1304	6	ABU05244 Human exp

26	44	100.0	1304	7	ADL16230	Adl16230 Human pro
27	44	100.0	1304	7	ADP65158	Adp65158 Human pro
28	44	100.0	1304	8	ADM67209	Adm67209 Human adi
29	44	100.0	1304	8	ABO84455	AbO84455 Human can
30	44	100.0	1304	8	ADQ39380	Adq39380 Human myo
31	44	100.0	1306	8	ADQ39375	Adq39375 Human myo
32	40	90.9	400	6	ABU22641	Abu22641 Protein e
33	40	90.9	567	6	ABU21519	Abu21519 Protein e
34	39	88.6	230	6	ADA34931	Ada34931 Actinotoda
35	39	88.6	467	7	ADH87882	Adh87882 Enterococ
36	38	86.4	1157	8	ABO84453	AbO84453 Mouse can
37	38	86.4	1291	7	ADL16234	Adl16234 Mouse pro
38	38	86.4	1343	8	ADM67208	Adm67208 Murine ad
39	37	84.1	164	3	AAQ44168	Aaq44168 Arabidops
40	37	84.1	171	3	AAQ44167	Aaq44167 Arabidops
41	37	84.1	198	3	AAQ44166	Aaq44166 Arabidops
42	37	84.1	1237	2	AAW44729	Aaw44729 Chicken p
43	37	84.1	1237	2	AAW89347	Aaw89347 Chicken t
44	36	81.8	338	7	ABO61284	AbO61284 Klebsiell
45	36	81.8	610	6	ABU19540	Abu19540 Protein e

ALIGNMENTS

RESULT 1	ABG31977	standard; peptide; 9 AA.
ID	ABG31977	
XX	ABG31977;	
AC	XX	
XX	XX	
DT	05-NOV-2002	(first entry)
XX	XX	
DE	Human CD45 HLA-binding peptide, huCD45/7.	
XX	XX	
XX	Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL; antigen-presenting cell; APC; major histocompatibility complex; MHC; antigen; allogenic; T cell receptor; TCR; cancer; tumour; allogenic stem cell transplantation; CFU-GM; leukaemia; colony forming unit-granulocyte macrophage; immunotherapeutic; haematopoietic; malignant.	
KW	XX	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	WO200244207-A1.	
PD	06-JUN-2002.	
XX	XX	
PF	30-NOV-2000; 2000WO-GB004566.	
XX	XX	
PR	30-NOV-2000; 2000WO-GB004566.	
XX	XX	
PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.	
XX	XX	
PI	Stauss HJ, Amrolia PJ,	
XX	XX	
DR	WPI; 2002-599413/64.	
XX	XX	
PT	Novel peptide comprising leukocyte antigen binding peptide of human CD45 polypeptide, useful for producing activated cytotoxic T lymphocytes, for killing cancerous cells e.g. leukemia.	
PT	XX	
PS	Claim 2; Page 38; 56pp; English.	
XX	XX	
CC	The invention discloses a peptide comprising the human leukocyte antigen (HLA)-binding peptide of human CD45 polypeptide, its portion or variant, provided that the peptide is not the intact human CD45 polypeptide. The peptides are useful for producing activated cytotoxic T lymphocyte (CTL) in vitro which involves contacting the CTL with an antigen-presenting cell, where its major histocompatibility complex (MHC) class I molecules are loaded with the peptide, to activate, in an antigen specific manner, where the CTL and the antigen presenting cell are allogenic with respect to the class I MHC molecule that is presenting peptides of CD45. The	

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animal models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/7,
CC comprising an HLA-binding peptide of human CD45
XX
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAFGFAFL 9
Db 1 LIAFGFAFL 9

RESULT 2
ABG31985
ID ABG31985 standard; peptide; 10 AA.
AC ABG31985;
XX
XX

DT 05-NOV-2002 (first entry)
XX
XX Human CD45 HLA-binding peptide, huCD45/6.

XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
KW antigen-presenting cell; APC; major histocompatibility complex; MHC;
KW antigen; allogenic; T cell receptor; TCR; cancer; tumour;
KW allogenic stem cell transplantation; CFU-GM; leukaemia;
KW colony forming unit-granulocyte macrophage; immunotherapeutic;
KW haematopoietic; malignant.
XX
XX

OS Homo sapiens..

PN MO200244207-A1.

PD 06-JUN-2002.

XX 30-NOV-2000; 2000WO-GB004566.

PR 30-NOV-2000; 2000WO-GB004566.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Stauss HU, Amrolia PU;

XX WPI; 2002-599413/64.

PT Novel peptide comprising leukocyte antigen binding peptide of human CD45
PT polypeptide, useful for producing activated cytotoxic T lymphocytes, for
PT killing cancerous cells e.g. leukemia.
XX

PS Claim 2; Page 38; 56pp; English.

XX The invention discloses a peptide comprising the human leukocyte antigen
CC (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,
CC provided that the peptide is not the intact human CD45 polypeptide. The
CC peptides are useful for producing activated cytotoxic T lymphocyte (CTL)

CC in vitro which involves contacting the CTL with an antigen-presenting
CC cell, where its major histocompatibility complex (MHC) class I molecules
CC are loaded with the peptide, to activate, in an antigen specific manner,
CC where the CTL and the antigen presenting cell are allogenic with respect
CC to the class I MHC molecule that is presenting peptides of CD45. The
CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animal models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/6,
CC comprising an HLA-binding peptide of human CD45
XX
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 44; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAFGFAFL 9
Db 2 LIAFGFAFL 10

RESULT 3
AAW35875
ID AAW35875 standard; peptide; 23 AA.
AC AAW35875;
XX
XX

DT 27-APR-1998 (first entry)

XX Leader sequence for use in T lymphocyte veto molecule.

XX T lymphocyte veto molecule; chimeric molecule; leader sequence;
KW targeting polypeptide; suppression; immune response; treatment;
KW autoimmune disease; allergy; immunological disorder;
KW transplant rejection.
XX
XX

OS Synthetic.

PN MO9737687-A1.

PD 16-OCT-1997.

XX 10-APR-1997; 97WO-US005943.

PR 10-APR-1996; 96US-00630172.

XX (NABE-) NAT DEWISH CENT IMMUNOLOGY & RESPIRATORY.

XX Staerz UD;

XX WPI; 1997-512419/47.

PT T lymphocyte veto molecule comprising response cell activating protein -
PT linked to molecule that targets stimulator cell marker, used for
PT selective suppression of immune response, e.g. prevention of graft
PT rejection or treatment of auto-immune disease.
XX

PS Disclosure; Page 90; 309pp; English.

XX

CC A novel T lymphocyte veto molecule is a chimeric molecule comprising a
 CC protein linked to a targeting polypeptide, e.g. the present sequence,
 CC that binds a molecule, which differentiates a host cell from a tissue,
 CC graft-cell or selectively targets a stimulator cell involved in the
 CC autoimmune response. A veto molecule, in which the protein binds a
 CC molecule that targets stimulator cells, can be used to suppress an immune
 CC response and therefore treat autoimmune diseases, e.g. systemic lupus
 CC erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
 CC diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
 CC thyroiditis, Addison's or Grave's diseases and rheumatoid arthritis,
 CC allergies and other immunological disorders. Where the protein binds a
 CC molecule that differentiates graft and host cells, the veto molecule can
 CC be used to reduce transplant rejection. The veto molecule provides
 CC specific regulation of particulate-stimulator cells that can kill graft
 CC cells or respond to autoantigens, but leave other stimulator cells
 CC unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
 CC affecting the other. The veto molecule can be administered locally to
 CC maintain generalised immunosuppression

XX Sequence 23 AA;

Query Match 100.0%; Score 44; DB 2; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.25; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
 DB 7 LIAFGFAFL 15

RESULT 4
 ADP24555
 ID ADP24555 standard; protein; 34 AA.

XX ADP24555;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:1173.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 XX osteopathic; antidiabetic; dermatologic; antipsoriatic; antiallergic;
 XX antisthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GENT) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 XX Wu TD;

XX WPI; 2004-419628/39.
 XX N-PSDB; ADP24554.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 XX renal disease, or demyelinating diseases of the central or peripheral
 XX nervous system.

XX Claim 7: SEQ ID NO 1733; 2940bp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 XX polypeptide encoded by it. A protein of the invention has
 XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX Sequence 34 AA;

Query Match 100.0%; Score 44; DB 8; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
 DB 7 LIAFGFAFL 15

RESULT 5
 AA64915
 ID AA64915 standard; protein; 42 AA.

XX AA64915;

XX 01-FEB-2000 (first entry)

XX Human 5' EST related polypeptide SEQ ID NO:1076.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
 XX gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
 XX location; development; protein synthesis; stability; regulation;
 XX identification.

XX Homo sapiens.

XX WO9953051-A2.

XX 21-OCT-1999.

XX 09-APR-1999; 99WO-IB000712.

XX 09-APR-1998; 98US-00057719.

XX 28-APR-1998; 98US-00069047.

XX (GENT) GENSET.

XX Dumas Mline Edwards J, Duclert A, Giordano J;

XX WPI; 2000-038446/03.

XX N-PSDB; AA642529.

XX Novel secreted protein 5' expressed sequence tag sequences used in
 XX diagnostic, forensic, gene therapy, and chromosome mapping procedures.
 XX Claim 3; Page 680; 837bp; English.

CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AA64651 to AA65438 represent the EST-related proteins corresponding to AA242265 to AA243052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a cell. The polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AA242249 to AA242264 and AA64644 to AA64650 represent sequences used in the exemplification of the present invention

XX Sequence 42 AA;

Query Match 100.0%; Score 44; DB 3; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIAFGFAPL 9
 |||||
 9 LIAFGFAPL 17

Db

RESULT 6
 AAG00095
 ID AAG00095 standard; protein; 60 AA.

XX AAG00095;

XX 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 4176.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GSEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX N-PSDB; AAC00101.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 4176; 71bp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT

CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors

XX Sequence 60 AA;

Query Match 100.0%; Score 44; DB 3; Length 60;

Best Local Similarity 100.0%; Pred. No. 0.65;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIAFGFAPL 9
 |||||
 9 LIAFGFAPL 17

Db

RESULT 7
 AA64916
 ID AA64916 standard; protein; 87 AA.

XX AA64916;

XX 01-FEB-2000 (first entry)

XX Human 5' EST related polypeptide SEQ ID NO:1077.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation;

XX Identification.

XX Homo sapiens.

XX WO953051-A2.

XX 21-OCT-1999.

XX 09-APR-1999; 99WO-IB000712.

XX 09-APR-1998; 98US-00057719.

XX 28-APR-1998; 98US-00069047.

XX (GSEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-038446/03.

XX N-PSDB; AA242530.

XX Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures.

XX Claim 3; Page 680; 837bp; English.

XX AA242265 to AA243075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AA64651 to AA65438 represent the EST-related proteins corresponding to AA242265 to AA243052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a cell. The polypeptide into a membrane, or importing a polypeptide into a cell. The

CC proteins encoded by the EST sequences may be useful in treating a variety
CC of human conditions. Secreted proteins have therapeutic value, and the
CC identification of new secreted proteins is valuable. AA242249 to AA242264
CC and AA64644 to AA64650 represent sequences used in the exemplification
CC of the present invention

XX Sequence 87 AA;

Query Match 100.0%; Score 44; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
Db 9 LIAFGFAFL 17

RESULT 8
AA64914
ID AA64914 standard; protein; 153 AA.
XX
AC AA64914;

DT 01-FEB-2000. (first entry)

XX Human 5' EST related polypeptide SEQ ID NO:1075.

KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
KW location; development; protein synthesis; stability; regulation;
KW identification.

XX Homo sapiens.

PN WO953051-A2.

PD 21-OCT-1999.

PF 09-APR-1999; 99WO-IB000712.

PR 09-APR-1998; 98US-00057719.

PR 28-APR-1998; 98US-00069047.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclet A, Giordano J;

DR MPI; 2000-038446/03.

DR N-PSDB; AA242528.

PT Novel secreted protein 5' expressed sequence tag sequences used in
PT diagnostic, forensic, gene therapy, and chromosome mapping procedures.

XX Claim 3; Page 679; 837p; English.

CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AA64651 to AA65438
CC represent the EST-related proteins corresponding to AA242265 to AA243052.
CC The 5' ESTs can be used for producing secreted human gene products. They
CC can be used to identify and isolate 5' untranslated regions (UTRs) and
CC upstream regulatory regions which control the location, development
CC stage, rate, and quantity of protein synthesis, as well as stability of
CC mRNA. The ESTs are also useful as probes for chromosome mapping, and to
CC obtain full length cDNA clones. The ESTs can also be used in forensic
CC procedures to identify individuals, or in diagnostic procedures to
CC identify individuals having genetic diseases resulting from abnormal gene
CC expression. The products may also be used in gene therapy protocols. The
CC nucleic acids encoding signal peptides can be used for directing
CC extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC proteins encoded by the EST sequences may be useful in treating a variety
CC of human conditions. Secreted proteins have therapeutic value, and the
CC identification of new secreted proteins is valuable. AA242249 to AA242264

CC and AA64644 to AA64650 represent sequences used in the exemplification
CC of the present invention

XX Sequence 153 AA;

Query Match 100.0%; Score 44; DB 3; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
Db 9 LIAFGFAFL 17

RESULT 9
AAM23689
ID AAM23689 standard; protein; 641 AA.
XX
AC AAM23689;

DT 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1214.

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.

XX Homo sapiens.

PN WO200154477-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US002687.

PR 25-JUN-2000; 2000US-00491404.

PR 17-JUL-2000; 2000US-00617746.

PR 03-AUG-2000; 2000US-00631451.

PR 15-SEP-2000; 2000US-00663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Wehrman T;

DR MPI; 2001-476164/51.

DR N-PSDB; AAH98348.

PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.

XX Claim 20; Page 875-876; 1275p; English.

CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention

XX Sequence 641 AA;

Query Match 100.0%; Score 44; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
Db 9 LIAFGFAFL 17

```
RESULT 10
AB007333
ID AB007333 standard; protein; 641 AA.
XX
AC AB007333;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2034.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR MPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2034; 134bp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_poc_sequences
XX
SQ Sequence 641 AA;
XX
XX
Query Match 100.0%; Score 44; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 7.2; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 11
AAM39262
ID AAM39262 standard; protein; 664 AA.
XX
AC AAM39262;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2407.
XX
KW Human; nocotropic; immunosuppressant; cyostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's, Parkinson's disease, Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
XX
PR 21-JAN-2000; 2000US-00488725.
XX
PR 25-APR-2000; 2000US-00552317.
XX
PR 20-JUN-2000; 2000US-00598042.
XX
PR 19-JUL-2000; 2000US-00620312.
XX
PR 03-AUG-2000; 2000US-00653450.
XX
PR 14-SEP-2000; 2000US-00662191.
XX
PR 19-OCT-2000; 2000US-00693036.
XX
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Aundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang Z, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Dmanac RT;
XX
DR MPI; 2001-442253/47.
XX
DR N-PSDB; AAI58418.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2407; 1007bp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM3642-AAM42213) with nocotropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 664 AA;
XX
XX
Query Match 100.0%; Score 44; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	LLAFGPAFL	9
Db	9	LLAFGPAFL	17

RESULT 12
ABU07334
ID ABU07334 standard; protein; 664 AA

KM Translational profiling; expressed protein tag; EPI; kinase; phosphatase
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS	Homo sapiens.
XX	
PN	W0200278524-A2.

PF	28-MAR-2002;	2002WO-US009671
XX	28-MAR-2001;	2001US-0279495P
PR	21-MAY-2001;	2001US-0292544P
PR	08-AUG-2001;	2001US-0310801P
PR	01-OCT-2001;	2001US-0326370P
PR	04-DEC-2001;	2001US-0336780P
PR	20-FEB-2002;	2002US-0358985P

PA (ZYCO-) ZYCOS INC.

PI Chicz RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

PS Example 2; SEQ ID NO 2035; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC myeloma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC http://wipo.int/publ/published_pat_sequences

SQ Sequence 664 AA;

Query Match	100.0%	Score 44	DB 6	Length 664
Similarity	100.0%	Pred. No.	7.5	
Best Local				
Matches	9	Conservative	0	Mismatches 0

Qy	1	LIAFGFAFL	9
Db	9	LIAFGFAFL	17

RESULT 13
ABU05240
ID ABU05240 standard; protein; 1143 AA

KM Translational profiling; expressed protein tag; ERT; kinase; phosphatase
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS	Homo sapiens.
XX	
PN	WO200278524-A2.

PF	28-MAR-2002;	2002NO-US009671
XX	28-MAR-2001;	2001US-0279495P
PR	21-MAY-2001;	2001US-0292544P
PR	08-AUG-2001;	2001US-0310801P
PR	01-OCT-2001;	2001US-0336370P
PR	04-DEC-2001;	2001US-0336780P
PR	20-FEB-2002;	2002US-0358985P

PA (ZYCO-) ZYCOS INC.

PI Chicz RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

PS Example 2; SEQ ID NO 1906; 134pp; English

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (BPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC http://wipo.int/pubd/published_pct_sequences

SQ Sequence 1143 AA;

Query Match	100.0%	Score 44	DB 6	Length 1143
Best Local Similarity	100.0%	Pred. No. 13		
Matches 9	Conservative 0	Mismatches 0	Indels 0	Gaps 0

OY 1 LIAFGFAFL 9
| | | | |
| | | | |
Db 7 LIAFGFAFL 15

RESULT 14

ABU05245
ID ABU05245 standard; protein; 1143 AA.

AC ABU05245;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1911.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCOX INC.

PI Chicz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

XX Example 2; SEQ ID NO 1911; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPo at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1143 AA;

Query Match 100.0%; Score 44; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAFGFAFL 9
| | | | |
| | | | |
Db 7 LIAFGFAFL 15

RESULT 15

ADL16232
ID ADL16232 standard; protein; 1143 AA.

AC ADL16232;

DT 06-MAY-2004 (first entry)

DE Human protein tyrosine phosphatase #27.

XX cytosolic; immunosuppressive; antiallergic;
XX protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
XX inducible signalling pathway; cell proliferation; cancer;
XX guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX cell-cycle abnormality; enzyme.

OS Homo sapiens.

PN WO2003068984-A2.

PD 21-AUG-2003.

PF 13-FEB-2003; 2003WO-EP001446.

PR 13-FEB-2002; 2002US-0356810P.

PR 12-FEB-2003; 2003US-00366547.

PR (COLD-) COLD SPRING HARBOR LAB.

PA (CERT-) CERTYR INC.

PI Tonks NK, Tzu-Ching M, Cool DE;

XX WPI; 2003-712572/67.

XX N-PSDB; ADL16231.

XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX screening for specific modulators, potential agents for treating e.g.
XX cancer or autoimmune disease.

XX Disclosure; SEQ ID NO 81; 238pp; English.

XX The invention relates to a method for identifying a protein tyrosine
XX phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX subjecting a sample, including a cell that contains at least one PTP, to
XX conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX anaerobically, in presence of a sulfhydryl-reactive agent (II) that
XX irreversibly modifies the thiol group of an invariant Cys in the active
XX site of PTP; and (iii) determining, under reducing conditions, the level
XX of dephosphorylation, caused by PTP, of a labelled substrate (III), where
XX dephosphorylation indicates that an active PTP is present. No details
XX of tests for these activities are given. The method is used to identify
XX reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX are involved. These agents are potentially useful, in human or veterinary
XX medicine, for treating abnormal cell proliferation or growth (cancer);
XX guest vs. host disease; autoimmune diseases; allergy or other
XX immunosuppressed states; metabolic disorders and cell-cycle
XX abnormalities. This sequence represents one of the PTP enzyme of the
XX invention.

XX Sequence 1143 AA;

Query Match 100.0%; Score 44; DB 7; Length 1143;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LIAFGFAFL 9
| | | | |
| | | | |

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DB          7 LLAFGFAFL 15

RESULT 16
ADQ18845
ID      ADQ18845 standard; protein; 1143 AA.
XX
XX      ADQ18845;
AC
XX      26-AUG-2004 (first entry)
XX
XX      Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
DE
XX      soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
XX      Homo sapiens.
XX      OS
XX      MO20040408938-AA.
XX      PN
XX      10-JUN-2004.
PD
XX      26-NOV-2003; 2003WO-US038193.
XX      PF
XX      26-NOV-2002; 2002US-0429739P.
XX      PR
XX      (PROT-) PROTEIN DESIGN LABS INC.
XX      PA
XX      Aziz N, Ginsburg WM, Zlotnick A;
XX      PI
XX      WPI; 2004-441208/41.
XX      DR
XX
XX      Early detection of soft tissue sarcoma comprises determining expression
PT      of a gene in a first soft tissue sample and a normal soft tissue sample
PT      and comparing the gene expression, also useful in treating soft tissue
PT      sarcoma.
XX
XX      Example 2; SEQ ID NO 1664; 210pp; English.
XX
XX      The invention relates to a novel method for detecting soft tissue sarcoma
CC      which comprises obtaining a first soft tissue sample from an individual
CC      and a normal soft tissue sample from the same or different individual,
CC      determining the expression of a gene in both samples and comparing the
CC      expression of the gene in both soft tissue samples, where a higher level
CC      of protein expression in the first soft tissue sample indicates the
CC      presence of soft tissue sarcoma. The method of the invention has
CC      cyrostatic applications and may be useful for detecting soft tissue
CC      sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC      acid sequences may be useful in diagnostic and screening applications.
CC      The current sequence is that of a human soft tissue sarcoma-upregulated
CC      protein of the invention. The current sequence is not shown within the
CC      specification per se but was submitted in CD format by the inventor.
XX
XX      Sequence 1143 AA;
SQ

Query Match          100.0%; Score 44; DB 8; Length 1143;
Best Local Similarity 100.0%; Pred. No. 13;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0

QY      1 LLAFGFAFL 9
        |||||
        |||||
        |||||
DB      7 LLAFGFAFL 15

RESULT 17
AA041048
ID      AA041048 standard; protein; 1149 AA.
XX
XX      AA041048;
AC
XX      22-OCT-2001 (first entry)
XX      DT
XX
XX      Human polypeptide SEQ ID NO 5979.
XX

```

KW	Human; nootropic; immunosuppressant; cytototoxic; gene therapy; cancer;
KM	peripheral nervous system; neuropathy; central nervous system; CNS;
KM	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM	chemokine; thrombolytic; drug screening; arthritis; inflammation;
KM	leukaemia.
OS	Homo sapiens.
XX	
PN	WO200153312-A1.
XX	
PD	26-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US034263.
XX	
PR	23-DEC-1999; 99US-00471275.
XX	
PR	21-JAN-2000; 2000US-00488725.
XX	
PR	25-APR-2000; 2000US-00552317.
XX	
PR	20-JUN-2000; 2000US-00588042.
XX	
PR	19-JUL-2000; 2000US-00620312.
XX	
PR	03-AUG-2000; 2000US-00653450.
XX	
PR	14-SEP-2000; 2000US-00662191.
XX	
PR	19-OCT-2000; 2000US-00693036.
XX	
PR	29-NOV-2000; 2000US-00727344.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
XX	
PI	Tang Y, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
XX	
PI	Zhou F, Goodrich R, Dimaac RT;
XX	
XX	
DR	WPI; 2001-442253/47.
XX	
DR	N-PSDB; AAI60204.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders such
XX	
PT	as central nervous system injuries.
XX	
PS	Example 2; SEQ ID NO 5979; 10078pp; English.
XX	
PS	
XX	
CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX	
CC	encoded polypeptides (AAM36642-AAM42213) with nootropic,
XX	
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
XX	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
XX	
CC	of the invention may be used to treat diseases of the peripheral nervous
XX	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
XX	
CC	localised neuropathies and central nervous system diseases, such as
XX	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX	
CC	utilisation of the activities such as: immune system suppression,
XX	
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX	
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX	
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
XX	
CC	C.N.S disorders. Note: The sequence data for this patent did not form
XX	
CC	part of the printed specification
XX	
SQ	Sequence 1149 AA;
XX	
Query Match	100.0%; Score 44; DB 4; Length 1149;
XX	
Best Local Similarity	100.0%; Pred. No. 13;
XX	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	
OY	1 LLAFGFAFL 9
XX	
XX	
Db	12 LLAFGFAFL 20
XX	
RESULT 18	
XX	
ABU05242	
XX	
ID	ABU05242 standard; protein; 1149 AA.
XX	
AC	ABU05242;
XX	
DT	29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPR) #1908.
XX XX
XX KW Translational profiling; expressed protein tag; EPR; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS
XX Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOs INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX XX
XX PS Example 2; SEQ ID NO 1908; 134pp; English.
XX XX
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC myeloma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPR) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1149 AA;
OY Query Match 100.0%; Score 44; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 12 LIAFGFAFL 20
1 LIAFGFAFL 9
|||||
12 LIAFGFAFL 20
RESULT 19
ID ADR39747 standard; protein; 1192 AA.
XX ADR39747;
XX AC
XX DT 18-NOV-2004 (first entry)

XX DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
XX XX
XX KW human, kinase and phosphatase protein; KPP; enzyme; cytosatic;
KW antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thymometric; gene therapy; cell proliferative disorder; cancer;
KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KW KPP-20.
XX OS
XX Homo sapiens.
XX PN WO2004074453-A2.
XX PD 02-SEP-2004.
XX XX
XX PF 20-FEB-2004; 2004WO-US005092.
XX XX
XX PR 20-FEB-2003; 2003US-0449059P.
XX PR 19-MAR-2003; 2003US-0456932P.
XX PR 28-MAR-2003; 2003US-0458844P.
XX PR 09-APR-2003; 2003US-0461678P.
XX PR 17-APR-2003; 2003US-0463937P.
XX PA (INCYTE) INCYTE CORP.
XX PI Rankumar J, Marguis JP, Swarnakar A, Chawla NK, Tran UK;
XX PI Becha SD, Lee SY, Hatella AJA, Richardson TW, Khare R, Jiang X;
XX PI Jackson AA, Yang J, Gorvad AB;
XX DR WPI; 2004-635568/61.
XX DR N-PSDB; ADR39793.
XX XX
XX PT New human kinases and phosphatases (KPP) for diagnosing, treating and
XX PT preventing diseases or conditions associated with aberrant KPP expression
XX PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX PS Claim 1; SEQ ID NO 20; 299pp; English.
XX XX
XX CC The present sequence represents the human kinase and phosphatase protein
XX CC (KPP), designated KPP-20. The human KPP sequences from the present
XX CC invention have cytosatic, antiarteriosclerotic, anticonvulsant,
XX CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
XX CC antiinflammatory and thymometric activities, and can be used in gene
XX CC therapy. The human KPP proteins and polynucleotides can be used in
XX CC diagnosing, treating and preventing diseases or conditions associated
XX CC with the decreased expression or overexpression of KPP, such as cell
XX CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
XX CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
XX CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
XX CC disorders, or infections. They can also be used in assessing the effects
XX CC of exogenous compounds on the expression of nucleic acid and amino acid
XX CC sequences of KPP. The KPP or its fragments are useful in screening
XX CC compounds for effectiveness as agonist or antagonist of the polypeptides,
XX CC or in altering the expression of the target polynucleotide and compounds
XX CC that specifically bind to or modulate the activity of the polypeptide.
XX SQ Sequence 1192 AA;
OY Query Match 100.0%; Score 44; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 9 LIAFGFAFL 17
1 LIAFGFAFL 9
|||||
9 LIAFGFAFL 17
RESULT 20
ID ADM67187 standard; protein; 1256 AA.
XX ADM67187

PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JJ, Iakubova O;
 XX
 DR WPI: 2004-533949/51.
 DR N-PSDB; ADQ38548.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1039; 145pp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has carrier activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1258 AA;
 XX
 Query Match 100.0%; Score 44; DB 8; Length 1258;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LIAFGFAFL 9
 DB 9 LIAFGFAFL 17
 XX
 RESULT 23
 ABU05243
 ID ABU05243 standard; protein; 1304 AA.
 XX
 AC ABU05243;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1909.
 XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI: 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1909; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1304 AA;
 XX
 Query Match 100.0%; Score 44; DB 6; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LIAFGFAFL 9
 DB 7 LIAFGFAFL 15
 XX
 RESULT 24
 ABU05241
 ID ABU05241 standard; protein; 1304 AA.
 XX
 AC ABU05241;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1907.
 XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-036780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
SQ The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 44; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLAFGFAFL 9
Db 7 LLAFGFAFL 15
XX
RESULT 25
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
DT 29-JUN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1910.
XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-036780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1910; 134pp; English.
XX
SQ The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 44; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLAFGFAFL 9
Db 7 LLAFGFAFL 15
XX
RESULT 26
ADL16230
ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #26.
XX

KW cytosolic; immunosuppressive; antiallergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signaling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003068984-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-EP001446.
 XX
 PR 13-FEB-2002; 2002US-0356810P.
 XX
 PR 12-FEB-2003; 2003US-00366547.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (CEPT-) CEPTYR INC.
 XX
 PI Tonks NK, Tzu-Ching M, Cool DE;
 PI WPI; 2003-712572/67.
 DR N-PSDB; ADL16229.
 XX
 PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 79; 238pp; English.
 XX
 CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulphydryl-reactive agent (ii) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signaling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 XX
 SQ Sequence 1304 AA;
 QY
 DB 1 LIAFGPFL 9
 7 LIAFGPFL 15
 100.0%; Score 44; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 27
 ADP65158
 ID ADP65158 standard; protein; 1304 AA.
 AC ADP65158;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
 XX
 KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072827-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 31-OCT-2002; 2002WO-US035433.
 XX
 PR 31-OCT-2001; 2001US-0336220P.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA Hirsch R, Thorton SL;
 PI WPI; 2003-712740/67.
 DR GENBANK; NP_002829.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analysis of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 XX
 SQ Sequence 1304 AA;
 QY
 DB 1 LIAFGPFL 9
 7 LIAFGPFL 15
 100.0%; Score 44; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 28
 ADM67209
 ID ADM67209 standard; protein; 1304 AA.
 AC ADM67209;
 XX

DT	03-JUN-2004	(first entry)
XX		
DE	Human adipocyte specific leukocyte common antigen protein Segid 563.	
XX		
XX	human; adipocyte specific; adipose tissue; anti-obesity;	
KW	high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;	
KV	adipogenesis; hypertension; cardiovascular disease; anorectic;	
KW	antidiabetic; hypotensive; leukocyte common antigen.	
XX		
OS	Homo sapiens.	
PN	WO2004011618-A2.	
XX		
PD	05-FEB-2004.	
XX		
PF	29-JUL-2003; 2003WO-US0233684.	
XX		
PR	29-JUL-2002; 2002US-0398785P.	
XX	12-JUN-2003; 2003US-0478206P.	
PA	(HMGE-) HMGEIN INC.	
PI	Chada K, Chouinard R, Ashar H, Sayed AMD;	
DR	WPI: 2004-143846/14.	
XX	N-PSDB; ADM66930.	
XX		
PT	Identifying adipocyte specific genes, useful for treating obesity or	
PT	diabetes, and for identifying drug targets, by differential gene	
PT	expression analysis between adipose tissue or stromal vascular tissue of	
XX	mice of different genotypes.	
XX		
PS	Disclosure; SEQ ID NO 563; 91pp; English.	
XX		
CC	This invention relates to a novel method for identifying genes that are	
CC	over-expressed in adipose tissue and as such it provides targets for anti-	
CC	-obesity pharmaceutical compositions. Specifically, it refers to a high	
CC	mobility group I-C protein (HMGI-C) that is associated with obesity and	
CC	is epistatic to leptin, furthermore, it refers to the ob gene where an	
CC	autosomal recessive trait is linked to obesity and diabetes. The present	
CC	invention describes performing differential gene expression analysis	
CC	between the white adipose tissue (WAT) or stromal vascular tissue (SVT)	
CC	of any two different mice selected from a group consisting of wild-type,	
CC	HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using	
CC	this method novel nucleotides and the encoded proteins thereof were	
CC	identified that are adipocyte specific, and as such can be used for	
CC	preventing adipogenesis, diagnosing and treating diabetes, obesity,	
CC	hypertension and cardiovascular disease, as well as screening for	
CC	compounds that can modulate or prevent adipogenesis and treat diabetes or	
CC	obesity. These compositions exhibit anorectic, antidiabetic and	
CC	hypotensive activities. This polypeptide sequence is a human homologue of	
CC	a murine adipocyte specific protein sequence of the invention.	
XX		
SEQ	Sequence 1304 AA;	
Query Match	100.0%; Score 44; DB 8; Length 1304;	
Best Local Similarity	100.0%; Pred. No. 15;	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 LLAFGFAFL 9	
DB	7 LLAFGFAFL 15	
RESULT 29		
ID	ABO84455 standard; protein; 1304 AA.	
XX	ABO84455;	
AC		
XX		
DT	18-NOV-2004 (first entry)	
XX		
DE	Human cancer-associated protein HP13-011.2.	

Db 7 LIAFGFAPL 15

RESULT 30

ADQ39380
ID ADQ39380 standard; protein; 1304 AA.

AC ADQ39380;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.

KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin J, Iakubova O;

PI WPI; 2004-533949/51.

DR N-PSDB; ADQ38552.

PS Claim 10; SEQ ID NO 1043; 145pp; English.

CC The invention relates to a novel method for identifying an individual who

CC has an altered risk for developing myocardial infarction. The method

CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's

CC nucleic acids, where the presence of the SNP is correlated with an

CC altered risk for myocardial infarction in the individual. The invention

CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in

CC the specification or its complement and encoding any one of the amino

CC acid sequences given in the specification; an isolated polypeptide

CC comprising an amino acid sequence given in the specification; an antibody

CC that specifically binds to the polypeptide or its antigen-binding

CC fragment; an amplified polynucleotide containing an SNP given in the

CC specification and which is between about 16 and 1000 nucleotides in

CC length; a kit for detecting an SNP in a nucleic acid, comprising the

CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a

CC nucleic acid molecule; a method of detecting a variant polypeptide; and a

CC method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiant activity.

CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or

CC decreased risk for developing myocardial infarction and for preparing a

CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-

CC associated gene containing one or more SNP's of the invention. Note: This

CC sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.

CC

XX

SQ Sequence 1304 AA;

Query Match 100.0%; Score 44; DB 8; Length 1304;

Beet Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIAFGFAPL 9

Db 7 LIAFGFAPL 15

RESULT 31

ADQ39375
ID ADQ39375 standard; protein; 1306 AA.

AC ADQ39375;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.

KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin J, Iakubova O;

PI WPI; 2004-533949/51.

DR N-PSDB; ADQ38547.

PS Claim 10; SEQ ID NO 1038; 145pp; English.

CC The invention relates to a novel method for identifying an individual who

CC has an altered risk for developing myocardial infarction. The method

CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's

CC nucleic acids, where the presence of the SNP is correlated with an

CC altered risk for myocardial infarction in the individual. The invention

CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in

CC the specification or its complement and encoding any one of the amino

CC acid sequences given in the specification; an isolated polypeptide

CC comprising an amino acid sequence given in the specification; an antibody

CC that specifically binds to the polypeptide or its antigen-binding

CC fragment; an amplified polynucleotide containing an SNP given in the

CC specification and which is between about 16 and 1000 nucleotides in

CC length; a kit for detecting an SNP in a nucleic acid, comprising the

CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a

CC nucleic acid molecule; a method of detecting a variant polypeptide; and a

CC method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiant activity.

CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or

CC decreased risk for developing myocardial infarction and for preparing a

CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-

CC associated gene containing one or more SNP's of the invention. Note: This

CC sequence was not shown in the specification. The sequence has come from

CC

XX

CC an electronic sequence listing downloaded from the WPO website.

XX
SQ Sequence 1306 AA;

Query Match 100.0%; Score 44; DB 8; Length 1306;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLAFGPAFL 9
Db 9 LLAFGPAFL 17

Search completed: May 3, 2005, 07:35:37
Job time : 70 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:28:27 ; Search time 42.973 Seconds
(without alignments)
90.001 Million cell updates/sec

Title: US-10-003-983C-15

Perfect score: 49
Sequence: 1 KLLAFGFAPL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760361 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	10	5	ABG31985 Human CD4
2	49	100.0	23	8	AAW35875 Leader se
3	49	100.0	34	8	ADP24555 PRO polyp
4	49	100.0	42	3	AAV64915 Human 5'
5	49	100.0	60	3	AAAG00095 Human sec
6	49	100.0	87	3	AAV64916 Human 5'
7	49	100.0	153	3	AAV64914 Human 5'
8	49	100.0	641	4	AAW23689 Human EST
9	49	100.0	641	6	ABU07333 Human exp
10	49	100.0	664	4	AAW39262 Human pol
11	49	100.0	664	6	ABU07334 Human exp
12	49	100.0	1143	6	ABU05240 Human exp
13	49	100.0	1143	6	ABU05245 Human exp
14	49	100.0	1143	7	ADL16232 Human pro
15	49	100.0	1143	8	ADQ18845 Human sol
16	49	100.0	1149	4	AAW41048 Human pol
17	49	100.0	1149	6	ABU05242 Human exp
18	49	100.0	1192	8	ADP39747 Human kin
19	49	100.0	1256	8	ADW67187 Human adl
20	49	100.0	1256	8	ADP12966 Protein e
21	49	100.0	1258	8	ADQ39376 Human myo
22	49	100.0	1304	6	ABU05243 Human exp
23	49	100.0	1304	6	ABU05241 Human exp
24	49	100.0	1304	6	ABU05244 Human exp
25	49	100.0	1304	7	ADL16230 Human pro

26	49	100.0	1304	7	ADP65158 Human pro
27	49	100.0	1304	8	ADW67209 Human adl
28	49	100.0	1304	8	ABO84455 Human can
29	49	100.0	1304	8	ADQ39380 Human myo
30	49	100.0	1306	8	ADQ39375 Human myo
31	44	89.8	1306	9	ABG31977 Human CD4
32	43	87.8	1157	8	ABO84453 Human can
33	43	87.8	1291	7	ADL16234 Mouse pro
34	43	87.8	1243	8	ADW67208 Murine ad
35	42	85.7	1237	2	AAW44729 Chicken p
36	42	85.7	1237	2	AAW89347 Chicken t
37	40	81.6	400	6	ABU22641 Protein e
38	40	81.6	567	6	ABU21519 Protein e
39	39	79.6	230	6	ADN34931 Acinetoba
40	39	79.6	467	7	ADH87882 Enterococ
41	38	77.6	78	7	ADM26258 Hyperther
42	38	77.6	289	6	ABU39540 Protein e
43	37	75.5	164	3	AAW44168 Arabidops
44	37	75.5	171	3	AAW44167 Arabidops
45	37	75.5	198	3	AAW44166 Arabidops

ALIGNMENTS

RESULT 1
ID ABG31985 standard; peptide, 10 AA.
XX
AC ABG31985;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CD45 HLA-binding peptide, huCD45/6.
XX
KW Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
KW antigen-presenting cell; APC; major histocompatibility complex; MHC;
KW antigen; allogeneic; T cell receptor; TCR; cancer; tumour;
KW allogenic stem cell transplantation; CFU-GM; leukaemia;
KW colony forming unit-granulocyte macrophage; immunotherapeutic;
KW haematopoietic; malignant.
XX
OS Homo sapiens.
XX
PN WO200244207-A1.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2000; 2000WO-GB004566.
XX
PR 30-NOV-2000; 2000WO-GB004566.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Staus HJ, Amrolia PJ;
XX
DR WPI; 2002-599413/64.
XX
PT Novel peptide comprising leukocyte antigen binding peptide of human CD45
PT polypeptide, useful for producing activated cytotoxic T lymphocytes, for
PT killing cancerous cells e.g. leukemia.
XX
PS Claim 2; Page 38; 56pp; English.
XX
XX The invention discloses a peptide comprising the human leukocyte antigen
XX (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,
XX provided that the peptide is not the intact human CD45 polypeptide. The
XX peptides are useful for producing activated cytotoxic T lymphocyte (CTL)
XX in vitro which involves contacting the CTL with an antigen-presenting
XX cell, where its major histocompatibility complex (MHC) class I molecules
XX are loaded with the peptide, to activate, in an antigen specific manner,
XX where the CTL and the antigen presenting cell are allogenic with respect
XX to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
 CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
 CC for killing, and in the manufacture of a medicament for, target cells
 CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
 CC recognising cells expressing the CD45 peptides, is useful for killing
 CC target cells (cancer cells) in a patient which involves obtaining CTLs
 CC from the patient, introducing into the CTLs the polynucleotide encoding
 CC the TCR and then introducing the cells thus produced into the patient who
 CC has undergone an allogeneic stem cell transplantation. Tumour reactive
 CC CTLs have been shown to mediate tumour regression in animal models by
 CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
 CC colony formation. The cancer is leukaemia which expresses the CD45
 CC polypeptide. The method is useful as an immunotherapeutic for treating a
 CC patient with haematopoietic malignancy or to target and kill cells which
 CC express the CD45 polypeptide. The advantage this method provides is that
 CC the CTLs destroy the malignant haematopoietic cells but not the
 CC transplanted cells. The sequence presented is the peptide, huCD45/6,
 CC comprising an HLA-binding peptide of human CD45
 CC
 XX SQ Sequence 10 AA:

Query Match, 100.0%; Score 49; DB 5; Length 10;
 Best Local Similarity, 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLARGFAPL 10
 DB 1 KLLARGFAPL 10

RESULT 2
 AAM35875
 ID AAM35875 standard; peptide; 23 AA.

AC AAM35875;
 DT 27-APR-1998 (first entry)

DE Leader sequence for use in T lymphocyte veto molecule.

XX T lymphocyte veto molecule; chimeric molecule; leader sequence;
 KW targeting polypeptide; suppression; immune response; treatment;
 KM autoimmune disease; allergy; immunological disorder;
 KM transplant rejection.

XX Synthetic.

OS WO9737687-A1.

XX 16-OCT-1997.

PD 10-APR-1997; 97WO-US005943.

XX 10-APR-1996; 96US-00630172.

XX (NAJL-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

PA Straetz UD;

PI WPI; 1997-512419/47.

XX T lymphocyte veto molecule comprising response cell activating protein -
 PT linked to molecule that targets stimulator cell marker, used for
 PT selective suppression of immune response, e.g. prevention of graft
 PT rejection or treatment of auto-immune disease.

PS Disclosure; Page 90; 309pp; English.

XX A novel T lymphocyte veto molecule is a chimeric molecule comprising a
 CC protein linked to a targeting polypeptide, e.g. the present sequence,
 CC that binds a molecule, which differentiates a host cell from a tissue
 CC graft cell, or selectively targets a stimulator cell involved in the
 CC autoimmune response. A veto molecule, in which the protein binds a

CC molecule that targets stimulator cells, can be used to suppress an immune
 CC response and therefore treat autoimmune diseases, e.g. systemic lupus
 CC erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
 CC diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
 CC thyroiditis, Addison's or Grave's diseases and rheumatoid arthritis,
 CC allergies and other immunological disorders. Where the protein binds a
 CC molecule that differentiates graft and host cells, the veto molecule can
 CC be used to reduce transplant rejection. The veto molecule provides
 CC specific regulation of particular stimulator cells that can kill graft
 CC cells or respond to autoantigens, but leave other stimulator cells
 CC unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
 CC affecting the other. The veto molecule can be administered locally to
 CC minimise generalised immunosuppression
 CC
 XX SQ Sequence 23 AA:

Query Match, 100.0%; Score 49; DB 2; Length 23;
 Best Local Similarity, 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLARGFAPL 10
 DB 6 KLLARGFAPL 15

RESULT 3
 ADP24555
 ID ADP24555 standard; protein; 34 AA.

XX ADP24555;

DT 18-NOV-2004 (first entry)

DE PRO polypeptide SEQ ID NO:1733.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KM antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX Unidentified.

XX WO2004041170-A2.

PD 21-MAY-2004.

PF 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GENTH) GENENTECH INC.

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI,

PI Wu TD;

DR WPI; 2004-419628/39.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.

PS Claim 7; SEQ ID NO 1733; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

CC Sequence 34 AA:

Query Match 100.0%; Score 49; DB 8; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAFL 10
 DB 6 KLLAFGFAFL 15

RESULT 4

ID AAY64915 standard; protein; 42 AA.

AC AAY64915;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:1076.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
 KW gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
 KM location; development; protein synthesis; stability; regulation;
 XX identification.

OS Homo sapiens.

PN WO953051-A2.

PD 21-OCT-1999; 99WO-IB000712.

PF 09-APR-1999; 99WO-IB000712.

PR 09-APR-1998; 98US-00057719.

PR 28-APR-1998; 98US-00069047.

XX (GEST) GENSET.

PI Dumas Mline Edwards J, Duclert A, Giordano J;

DR WPI; 2000-038446/03.

DR N-PSDB; AA242529.

PT Novel secreted protein 5' expressed sequence tag sequences used in
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures.
 XX Claim 3; Page 680; 837BP; English.

CC AA24265 to AA243075 represent novel 5' expressed sequence tag (EST)
 CC sequences, corresponding to human secreted proteins. AAY64651 to AAY65438
 CC represent the EST-related proteins corresponding to AA24265 to AA243052.
 CC The 5' ESTs can be used for producing secreted human gene products. They
 CC can be used to identify and isolate 5' untranslated regions (UTRs) and

CC upstream regulatory regions which control the location, development
 CC stage, rate, and quantity of protein synthesis, as well as stability of
 CC mRNA. The ESTs are also useful as probes for chromosome mapping, and to
 CC obtain full length cDNA clones. The ESTs can also be used in forensic
 CC procedures to identify individuals, or in diagnostic procedures to
 CC identify individuals having genetic diseases resulting from abnormal gene
 CC expression. The products may also be used in gene therapy protocols. The
 CC nucleic acids encoding signal peptides can be used for directing
 CC extracellular secretion of a polypeptide or the insertion of a cell.
 CC polypeptide into a membrane, or importing a polypeptide into a cell. The
 CC proteins encoded by the EST sequences may be useful in treating a variety
 CC of human conditions. Secreted proteins have therapeutic value, and the
 CC identification of new secreted proteins is valuable. AA24249 to AA24264
 CC and AAY64644 to AAY64650 represent sequences used in the exemplification
 CC of the present invention

CC Sequence 42 AA:

Query Match 100.0%; Score 49; DB 3; Length 42;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAFL 10
 DB 8 KLLAFGFAFL 17

RESULT 5

ID AAG00095 standard; protein; 60 AA.

AC AAG00095;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 4176.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-00200610.

PR 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

PI Dumas Mline Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

DR N-PSDB; AAC00101.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX Claim 13; SEQ ID NO 4176; 71pp + Sequence Listing; English.

CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs

CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX Sequence 60 AA;

Query Match 100.0%; Score 49; DB 3; Length 60;

Best Local Similarity 100.0%; Pred. No. 0.081; 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAFL 10

DB 8 KLLAFGFAFL 17

RESULT 6
AA64916
ID AAY64916 standard; protein; 87 AA.

XX AAY64916;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:1077.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
XX gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
XX location; development; protein synthesis; stability; regulation;
XX identification.

OS Homo sapiens.

PN WO953051-A2.

PD 21-OCT-1999.

PF 09-APR-1999; 99WO-IB000712.

PR 09-APR-1998; 98US-00057719.

PR 28-APR-1998; 98US-00069047.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-038446/03.

DR N-PSDB; AA242530.

PT Novel secreted protein 5' expressed sequence tag sequences used in
PT diagnostic, forensic, gene therapy, and chromosome mapping procedures.

PS Claim 3; Page 680; 837pp; English.

XX AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AAY64651 to AAY65438
CC represent the EST-related proteins corresponding to AA242265 to AA243052.
CC The 5' ESTs can be used for producing secreted human gene products. They
CC can be used to identify and isolate 5' untranslated regions (UTRs) and
CC upstream regulatory regions which control the location, development
CC stage, rate, and quantity of protein synthesis, as well as stability of
CC mRNA. The ESTs are also useful as probes for chromosome mapping, and to
CC obtain full length cDNA clones. The ESTs can also be used in forensic
CC procedures to identify individuals, or in diagnostic procedures to
CC identify individuals having genetic diseases resulting from abnormal gene
CC expression. The products may also be used in gene therapy protocols. The
CC nucleic acids encoding signal peptides can be used for directing
CC extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC proteins encoded by the EST sequences may be useful in treating a variety
CC of human conditions. Secreted proteins have therapeutic value, and the
CC identification of new secreted proteins is valuable. AA242249 to AA242264
CC and AAY64644 to AAY64650 represent sequences used in the exemplification
CC of the present invention

XX Sequence 87 AA;

Query Match 100.0%; Score 49; DB 3; Length 87;

Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAFL 10

DB 8 KLLAFGFAFL 17

RESULT 7
AA64914
ID AAY64914 standard; protein; 153 AA.

XX AAY64914;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:1075.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
XX gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
XX location; development; protein synthesis; stability; regulation;
XX identification.

OS Homo sapiens.

PN WO953051-A2.

PD 21-OCT-1999.

PF 09-APR-1999; 99WO-IB000712.

PR 09-APR-1998; 98US-00057719.

PR 28-APR-1998; 98US-00069047.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-038446/03.

DR N-PSDB; AA242528.

PT Novel secreted protein 5' expressed sequence tag sequences used in
PT diagnostic, forensic, gene therapy, and chromosome mapping procedures.

PS Claim 3; Page 679; 837pp; English.

XX AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AAY64651 to AAY65438
CC represent the EST-related proteins corresponding to AA242265 to AA243052.
CC The 5' ESTs can be used for producing secreted human gene products. They
CC can be used to identify and isolate 5' untranslated regions (UTRs) and
CC upstream regulatory regions which control the location, development
CC stage, rate, and quantity of protein synthesis, as well as stability of
CC mRNA. The ESTs are also useful as probes for chromosome mapping, and to
CC obtain full length cDNA clones. The ESTs can also be used in forensic
CC procedures to identify individuals, or in diagnostic procedures to
CC identify individuals having genetic diseases resulting from abnormal gene
CC expression. The products may also be used in gene therapy protocols. The
CC nucleic acids encoding signal peptides can be used for directing
CC extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC proteins encoded by the EST sequences may be useful in treating a variety
CC of human conditions. Secreted proteins have therapeutic value, and the
CC identification of new secreted proteins is valuable. AA242249 to AA242264
CC and AAY64644 to AAY64650 represent sequences used in the exemplification
CC of the present invention

XX Sequence 153 AA;


```
XX AC AAM39262;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 2407.
XX
XX KM Human; neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KM peripheral nervous system; neuropathy; central nervous system; CNS;
XX KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX KM leukaemia.
XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX
XX PF 26-DEC-2000; 2000MO-US034263.
XX
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
XX PI Wang Z, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX PI Zhou P, Goodrich R, Drmanac RT;
XX
XX DR WPI: 2001-442253/47.
XX DR N-PSDB; AAI58418.
XX
XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX PT as central nervous system injuries.
XX
XX PS Example 4; SEQ ID NO 2407; 10078bp; English.
XX
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX CC encoded polypeptides (AAM38642-AAM42213) with neurotrophic.
XX CC immunosuppressant and cyostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localized neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression.
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemia and
XX CC C.N.S disorders. Note: The sequence data for this patent did not form
XX CC part of the printed specification
XX
XX SQ Sequence 664 AA;
```

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Query Match 100.0%; Score 49; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KILAFAPFL 10
DB 8 KILAFAPFL 17
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RESULT 11
ABU07334
ID ABU07334 standard; protein; 664 AA.
XX AC ABU07334;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #2035.
XX
XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KM protease; protease inhibitor; transporter; cytoskeletal protein;
XX KM receptor; transcription factor; cancer; MHC;
XX KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002MO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX PA (ZYCO-) ZYCO INC.
XX
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
XX DR WPI: 2003-040607/03.
XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukaemia.
XX
XX PS Example 2; SEQ ID NO 2035; 134bp; English.
XX
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 664 AA;
```

```
Query Match 100.0%; Score 49; DB 6; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KILAFAPFL 10
DB 8 KILAFAPFL 17
```

```
RESULT 12
ABU05240
ID ABU05240 standard; protein; 1143 AA.
XX
AC ABU05240;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1906.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;
XX
Query Match 100.0%; Score 49; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 13
ABU05245
ID ABU05245 standard; protein; 1143 AA.
XX
AC ABU05245;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1911.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1911; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;
XX
Query Match 100.0%; Score 49; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 14

ADL16232 standard; protein; 1143 AA.

ADL16232;

06-MAY-2004 (first entry)

Human protein tyrosine phosphatase #27.

cytostatic; immunosuppressive; anti-allergic;

protein tyrosine phosphatase; reversible oxidation; dephosphorylation;

inducible signaling pathway; cell proliferation; cancer;

guest vs. host disease; autoimmune disease; allergy; metabolic disorder;

cell-cycle abnormality; enzyme.

Homo sapiens.

MO2003068984-A2.

21-AUG-2003.

13-FEB-2003; 2003WO-EP001446.

13-FEB-2002; 2002US-0356810P.

12-FEB-2003; 2003US-00365547.

(COLD-) COLD SPRING HARBOR LAB.

(CEPT-) CEPTYR INC.

Tonke NK, Tzu-Ching M, Cool DE;

WPI; 2003-712572/67.

N-PSDB; ADL16231.

Identifying reversibly oxidized protein tyrosine phosphatase, useful in

screening for specific modulators, potential agents for treating e.g.

cancer or autoimmune disease.

Disclosure; SEQ ID NO 81; 238pp; English.

The invention relates to a method for identifying a protein tyrosine

phosphatase (PTP) that is reversibly oxidized in a cell by: (i)

subjecting a sample, including a cell that contains at least one PTP, to

conditions that cause reversible oxidation of PTP; (ii) isolating PTP

anaerobically, in presence of a sulphydryl-reactive agent (II) that

irreversibly modifies the thiol group of an invariant Cys in the active

site of PTP; and (iii) determining, under reducing conditions, the level

of dephosphorylation, caused by PTP, of a labelled substrate (III), where

dephosphorylation indicates that an active PTP is present. No details

of tests for these activities are given. The method is used to identify

reversibly oxidized PTP, also to identify agents that: (a) reversibly

modify such PTP; or (b) alter inducible signalling pathways in which PTP

are involved. These agents are potentially useful, in human or veterinary

medicine, for treating abnormal cell proliferation or growth (cancer);

guest vs. host disease; autoimmune disease; allergy or other

immunosuppressed states; metabolic disorders and cell-cycle

abnormalities. This sequence represents one of the PTP enzyme of the

invention.

Sequence 1143 AA;

Query Match 100.0%; Score 49; DB 7; Length 1143;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAFL 10

Db 6 KLLAFGFAFL 15

RESULT 15

ADQ18845

ID ADQ18845 standard; protein; 1143 AA.

ADQ18845;

26-AUG-2004 (first entry)

Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.

soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

Homo sapiens.

MO2004048938-A2.

10-JUN-2004.

26-NOV-2003; 2003WO-US038193.

26-NOV-2002; 2002US-0429739P.

(PROT-) PROTEIN DESIGN LABS INC.

Aziz N, Ginsburg WM, Zlotnick A;

WPI; 2004-441208/41.

Early detection of soft tissue sarcoma comprises determining expression

of a gene in a first soft tissue sample and a normal soft tissue sample

and comparing the gene expression, also useful in treating soft tissue

sarcoma.

Example 2; SEQ ID NO 1664; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma

which comprises obtaining a first soft tissue sample from an individual

and a normal soft tissue sample from the same or different individual,

determining the expression of a gene in both samples and comparing the

expression of the gene in both soft tissue samples, where a higher level

of protein expression in the first soft tissue sample indicates the

presence of soft tissue sarcoma. The method of the invention has

cytostatic applications and may be useful for detecting soft tissue

sarcoma, possibly via gene therapy or vaccine production. The nucleic

acid sequences may be useful in diagnostic and screening applications.

The current sequence is that of a human soft tissue sarcoma-upregulated

protein of the invention. The current sequence is not shown within the

specification per se but was submitted in CD format by the inventor.

Sequence 1143 AA;

Query Match 100.0%; Score 49; DB 8; Length 1143;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAFL 10

Db 6 KLLAFGFAFL 15

RESULT 16

AAM41048

AAM41048 standard; protein; 1149 AA.

Query Match 100.0%; Score 49; DB 8; Length 1143;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAFL 10

Db 6 KLLAFGFAFL 15

Human polypeptide SEQ ID NO 5979.

Human; noctropic; immunosuppressive; cytostatic; gene therapy; cancer;

peripheral nervous system; neuropathy; central nervous system; CNS;

Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KM Leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
XX
PR 21-JAN-2000; 2000US-00488725.
XX
PR 25-APR-2000; 2000US-00552317.
XX
PR 20-JUN-2000; 2000US-00598042.
XX
PR 19-JUL-2000; 2000US-00620312.
XX
PR 03-AUG-2000; 2000US-00653450.
XX
PR 14-SEP-2000; 2000US-00662191.
XX
PR 19-OCT-2000; 2000US-00693036.
XX
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
XX
DR N-PSDB; AAI60204.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5979; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA438642-AA42213) with nootropic.
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1149 AA;
XX
Query Match 100.0%; Score 49; DB 4; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLLAFGFAPL 10
DB 11 KLLAFGFAPL 20
RESULT 17
ABU05242
ID ABU05242 standard; protein; 1149 AA.
XX
AC ABU05242;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1908.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1908; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1149 AA;
XX
Query Match 100.0%; Score 49; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLLAFGFAPL 10
DB 11 KLLAFGFAPL 20
RESULT 18
ADR39747
ID ADR39747 standard; protein; 1192 AA.
XX
AC ADR39747;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
XX
KW human; kinase and phosphatase protein; KPP; enzyme; cytoskeletal;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;

KM cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
 KM thyromimetic; gene therapy; cell proliferative disorder; cancer;
 KM atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
 KM stroke; immune disorder; inflammatory disorder; AIDS; allergy;
 KM developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
 KM KPP-20.
 XX
 OS Homo sapiens.
 XX
 PN WO2004074453-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005092.
 XX
 PR 20-FEB-2003; 2003US-0449059P.
 XX
 PR 19-MAR-2003; 2003US-0456932P.
 XX
 PR 28-MAR-2003; 2003US-0458844P.
 XX
 PR 09-APR-2003; 2003US-0461678P.
 XX
 PR 17-APR-2003; 2003US-0463937P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Ramkumar J, Margulis JP, Swarnakar A, Chawla NK, Tran UK;
 PI Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
 PI Jackson AA, Yang J, Gorvad AE;
 XX
 DR WPI; 2004-635568/61.
 DR N-PSDB; ADR39793.
 XX
 PT New human kinases and phosphatases (KPP) for diagnosing, treating and
 PT preventing diseases or conditions associated with aberrant KPP expression
 PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
 XX
 Claim 1; SEQ ID NO 20; 299pp; English.
 XX
 CC The present sequence represents the human kinase and phosphatase protein
 CC (KPP), designated KPP-20. The human KPP sequences from the present
 CC invention have cytosolic, antitumorocytotoxic, anticonvulsant,
 CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
 CC antiinflammatory and thyromimetic activities, and can be used in gene
 CC therapy. The human KPP proteins and polynucleotides can be used in
 CC diagnosing, treating and preventing diseases or conditions associated
 CC with the decreased expression or overexpression of KPP, such as cell
 CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
 CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
 CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
 CC disorders, or infections. They can also be used in assessing the effects
 CC of exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of KPP. The KPP or its fragments are useful in screening
 CC compounds for effectiveness as agonist or antagonist of the polypeptides,
 CC or in altering the expression of the target polynucleotide and compounds
 CC that specifically bind to or modulate the activity of the polypeptide.
 XX
 SQ Sequence 1192 AA;
 XX
 Query Match 100.0%; Score 49; DB 8; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAPL 10
 |||||
 Db 8 KLLAFGFAPL 17
 |||||
 RESULT 19
 ID ADM67187 standard; protein; 1256 AA.
 XX
 AC ADM67187;
 XX
 DT 03-JUN-2004 (first entry)
 XX

DB Human adipocyte specific PTPase receptor type C protein Segid 541.
 XX
 XX human; adipocyte specific; adipose tissue; anti-obesity;
 KM high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
 KM adipogenesis; hypertension; cardiovascular disease; anorectic;
 KM antidiabetic; hypotensive; PTPase receptor type C.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011618-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-US023684.
 XX
 PR 29-JUL-2002; 2002US-0398785P.
 XX
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMG1-) HMG1 INC.
 XX
 PI Chada K, Chouinard R, Ashar H, Sayed AMD;
 PI WPI; 2004-143846/14.
 DR N-PSDB; ADM65908.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 XX Disclosure; SEQ ID NO 541; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti
 CC -obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMG1-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 XX
 SQ Sequence 1256 AA;
 XX
 Query Match 100.0%; Score 49; DB 8; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAPL 10
 |||||
 Db 6 KLLAFGFAPL 15
 |||||
 RESULT 20
 ID ADP12966 standard; protein; 1256 AA.
 XX
 AC ADP12966;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Protein encoding reference mRNA sequence #51.
 XX
 KM transplant rejection; immune system; rheumatoid arthritis; lupus;
 XX

KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX Homo sapiens.
 OS
 XX
 PN WO2004042346-A2.
 XX
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 XX 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M,
 PI Rosenberg S;
 DR WPI; 2004-400724/37.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2975; 1762pp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprising detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection, in an
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein encoded by an mRNA sequence of the invention which show altered
 CC expression in renal transplantation and expression.
 XX
 SQ Sequence 1256 AA;
 Query Match 100.0%; Score 49; DB 8; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAPL 10
 Db 6 KLLAFGFAPL 15
 XX
 XX
 AC ADQ39376;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiac; gene therapy; human.
 XX
 XX Homo sapiens.
 OS
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.

XX
 PR 20-DEC-2002; 2002US-0634778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JT, Takubova O;
 XX
 DR WPI; 2004-533949/51.
 DR N-PSDB; ADQ38548.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1039; 145pp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiac activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1258 AA;
 Query Match 100.0%; Score 49; DB 8; Length 1258;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAPL 10
 Db 8 KLLAFGFAPL 17
 XX
 XX
 AC ABU05243;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1909.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

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XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002MO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX PT WPI; 2003-040607/03.
XX DR
XX XX
XX XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1909; 134bp; English.
XX XX
XX XX The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1304 AA;
XX
XX Query Match 100.0%; Score 49; DB 6; Length 1304;
XX Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLLAFGFAFL 10
Db 6 KLLAFGFAFL 15
XX
XX RESULT 23
XX ABU05241
XX ID ABU05241 standard; protein; 1304 AA.
XX AC ABU05241;
XX XX
XX XX 29-JAN-2003 (first entry)
XX XX
XX XX Human expressed protein tag (EPT) #1907.
XX XX
XX XX Translational profiling; expressed protein tag; EPT: kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
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XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002MO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX PT WPI; 2003-040607/03.
XX DR
XX XX
XX XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1907; 134bp; English.
XX XX
XX XX The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1304 AA;
XX
XX Query Match 100.0%; Score 49; DB 6; Length 1304;
XX Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLLAFGFAFL 10
Db 6 KLLAFGFAFL 15
XX
XX RESULT 24
XX ABU05244
XX ID ABU05244 standard; protein; 1304 AA.
XX AC ABU05244;
XX XX
XX XX 29-JAN-2003 (first entry)
XX XX
XX XX Human expressed protein tag (EPT) #1910.
XX XX
XX XX Translational profiling; expressed protein tag; EPT: kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
```

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XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOs INC.
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX PT WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1910; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC melanoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1304 AA;
XX
XX Query Match 100.0%; Score 49; DB 6; Length 1304;
XX Best Local Similarity 100.0%; Pred. No. 1.8;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLLAFGFAPL 10
XX |||||
XX 6 KLLAFGFAPL 15
XX
XX Db
XX
XX RESULT 25
XX ID ADL16230
XX ADL16230 standard; protein; 1304 AA.
XX
XX AC ADL16230;
XX
XX DE 06-MAY-2004 (first entry)
XX
XX XX Human protein tyrosine phosphatase #26.
XX
XX XX cytosolic; immunosuppressive; antiallergic;
XX KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
XX KM inducible signalling pathway; cell proliferation; cancer;
XX KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX KM cell-cycle abnormality; enzyme.

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XX OS Homo sapiens.
XX PN WO2003068984-A2.
XX PD 21-AUG-2003.
XX PF 13-FEB-2003; 2003WO-EP001446.
XX PR 13-FEB-2002; 2002US-0356810P.
XX PR 12-FEB-2003; 2003US-00366547.
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PA (CEPT-) CEPTYR INC.
XX PI Tonks NK, Tzu-Ching M, Cool DE;
XX PT WPI; 2003-712572/67.
XX PT N-PSDB; ADL16229.
XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX PT screening for specific modulators, potential agents for treating e.g.
XX PT cancer or autoimmune disease.
XX PS Disclosure; SEQ ID NO 79; 238pp; English.
XX CC The invention relates to a method for identifying a protein tyrosine
XX CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX CC subjecting a sample, including a cell that contains at least one PTP, to
XX CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
XX CC irreversibly modifies the thiol group of an invariant Cys in the active
XX CC site of PTP; and (iii) determining, under reducing conditions, the level
XX CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
XX CC dephosphorylation indicates that an active PTP is present. No details
XX CC of tests for these activities are given. The method is used to identify
XX CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX CC are involved. These agents are potentially useful, in human or veterinary
XX CC medicine, for treating abnormal cell proliferation or growth (cancer);
XX CC guest vs. host disease; autoimmune diseases; allergy or other
XX CC immunosuppressed states; metabolic disorders and cell-cycle
XX CC abnormalities. This sequence represents one of the PTP enzyme of the
XX CC invention.
XX SQ Sequence 1304 AA;
XX
XX Query Match 100.0%; Score 49; DB 7; Length 1304;
XX Best Local Similarity 100.0%; Pred. No. 1.8;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KLLAFGFAPL 10
XX |||||
XX 6 KLLAFGFAPL 15
XX
XX Db
XX
XX RESULT 26
XX ID ADP65158
XX ADP65158 standard; protein; 1304 AA.
XX
XX AC ADP65158;
XX
XX DE 12-AUG-2004 (first entry)
XX
XX XX Human protein tyrosine phosphatase, receptor type, C, isoform 1.
XX
XX XX autoimmune disease; arthritis; gene expression analysis;
XX KM rheumatoid arthritis; collagen-induced; immunosuppressive; antineumatic;
XX KM antiallergic; osteopathic; antigout; antiinflammatory; dermatological;
XX KM immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
XX KM fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
XX KM immune; human.

```

OS Homo sapiens.
 XX WO2003072827-A1.
 PN
 XX
 PD 04-SEP-2003.
 XX
 PF 31-OCT-2002; 2002WO-US035433.
 XX
 PR 31-OCT-2001; 2001US-0336220P.
 XX
 (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA
 XX Hirech R, Thornton SL;
 PI
 XX MPI; 2003-712740/67.
 DR GENBANK; NP_002829.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analyzing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analyzing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antijoint, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 CC
 SQ Sequence 1304 AA;
 XX
 XX
 Query Match 100.0%; Score 49; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAFL 10
 |||||
 DB 6 KLLAFGFAFL 15
 |||||
 RESULT 27
 ADM67209
 ID ADM67209 standard; protein; 1304 AA.
 XX
 AC ADM67209;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human adipocyte specific leukocyte common antigen protein SeqID 563.
 XX
 KW human; adipocyte specific; adipose tissue; anti-obesity;

KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; leukocyte common antigen.
 OS Homo sapiens.
 XX WO2004011618-A2.
 PN
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-US023684.
 XX
 PR 29-JUL-2002; 2002US-0398785P.
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMG-) HMGNE INC.
 XX
 XX Chada K, Chouinard R, Ashar H, Sayed AMD;
 PI
 XX MPI; 2004-143846/14.
 DR N-PSDB; ADM65930.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 PS Disclosure; SEQ ID NO 563; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 CC
 SQ Sequence 1304 AA;
 XX
 XX
 Query Match 100.0%; Score 49; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAFL 10
 |||||
 DB 6 KLLAFGFAFL 15
 |||||
 RESULT 28
 ABO84455
 ID ABO84455 standard; protein; 1304 AA.
 XX
 AC ABO84455;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human cancer-associated protein HP13-011.2.
 XX
 KW Human; cancer-associated protein; cyrostatic; cancer; leukaemia;
 KW lymphoma; CAP.
 XX
 OS Homo sapiens.

XX MO2004074320-A2.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 17-FEB-2004; 2004WO-US004730.
PF
XX 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGES DISCOVERY INC.
PI
XX Morris DW, Morris DW, Malandro MS;
PI
XX WPI; 2004-652914/63.
DR N-PSDB; ABD32626.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
XX claim 18; seqid 147; 310pp; English.
PS
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1304 AA;
SO
Query Match 100.0%; Score 49; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID ADQ39380 standard; protein; 1304 AA.
XX
XX ADQ39380;
AC
XX 18-NOV-2004 (first entry)
DT
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
DE
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiant; gene therapy; human.
XX
XX Homo sapiens.
OS
XX
XX MO2004058052-A2.
PN
XX
XX 15-JUL-2004.
PD
XX
XX 22-DEC-2003; 2003WO-US040978.
PF
XX
XX 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
PA
XX
XX Cargill M, Devlin JJ, Iakubova O;
PI
XX WPI; 2004-533949/51.
DR N-PSDB; ADQ38552.
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1043; 145pp; English.
PS
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cariant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
XX Sequence 1304 AA;
SO
Query Match 100.0%; Score 49; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 KLLAFGFAFL 15

RESULT 30
ADQ39375
ID ADQ39375 standard; protein; 1306 AA.
XX
AC ADQ39375;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
KW cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN MO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PP 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JT, Yakubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PSDB; ADQ38547.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1038; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1306 AA;

Query Match 100.0%; Score 49; DB 8; Length 1306;

Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLLAFGFAFL 10
DB 8 KLLAFGFAFL 17

Search completed: May 3, 2005, 07:35:37
Job time : 44.973 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-1

Perfect score: 44

Sequence: 1 PLYDVIAST 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	1304	1 A46546	leukocyte common a
2	43	97.7	1200	2 T43148	probable protein-c
3	38	86.4	445	2 B82735	argininosuccinate
4	38	86.4	1291	1 A28334	protein-tyrosine-P
5	37	84.1	681	2 S33116	structural protein
6	37	84.1	681	2 A45705	type I transmembr
7	36	81.8	1817	2 AD2165	two-component hydr
8	35	79.5	1237	2 A54080	protein-tyrosine-P
9	35	79.5	1273	1 TDR171	leukocyte common a
10	34	77.3	222	2 T30423	hypothetical prote
11	34	77.3	652	2 T20549	hypothetical prote
12	33	75.0	170	2 B81938	probable membrane
13	33	75.0	221	2 T33414	hypothetical prote
14	33	75.0	265	2 S67653	probable membrane
15	33	75.0	330	2 E69831	conserved hypothet
16	33	75.0	442	2 T33412	hypothetical prote
17	33	75.0	597	2 B53978	protein-tyrosine-P
18	33	75.0	3176	2 CGH13A	collagen alpha 3(V
19	32	72.7	159	2 AF1372	protein involved
20	32	72.7	159	2 AD1742	protein involved
21	32	72.7	347	2 T15149	hypothetical prote
22	32	72.7	473	2 T22830	hypothetical prote
23	32	72.7	563	2 H95212	ABC transporter, p
24	32	72.7	563	2 A98077	hypothetical prote
25	32	72.7	714	1 ALBSGR	cyclomaltodextrin
26	32	72.7	936	2 T06190	lipoxigenase (BC 1
27	32	72.7	954	2 T22369	hypothetical prote
28	32	72.7	4085	2 S28600	hypothetical prote
29	31	70.5	78	2 C64472	hypothetical prote

30	31	70.5	161	2 A69732	PBSX prophage ORF
31	31	70.5	193	2 D81009	conserved hypothet
32	31	70.5	193	2 E82031	probable integral
33	31	70.5	247	2 D69437	hypothetical prote
34	31	70.5	374	2 S28285	hypothetical prote
35	31	70.5	490	2 B82971	cardiolipin syntha
36	31	70.5	495	1 S46284	calcium-dependent
37	31	70.5	501	2 G85097	hypothetical prote
38	31	70.5	510	2 T22835	hypothetical prote
39	31	70.5	547	2 T06758	hypothetical prote
40	31	70.5	577	2 S64613	probable membrane
41	31	70.5	629	2 T05089	hypothetical prote
42	31	70.5	770	2 T22944	hypothetical prote
43	31	70.5	784	2 T22939	hypothetical prote
44	31	70.5	865	2 T30998	hypothetical prote
45	30	68.2	91	2 T17867	hypothetical prote

ALIGNMENTS

RESULT 1
A46546
Leukocyte common antigen long splice form precursor - human
N:Alternate names: CD45, protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 09-Jul-2004
C/Accession: A46546; B46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A:Reference number: A46546; MUID:88061067; PMID:2824653+
A/Accession: A46546
A/Status: preliminary
A/Molecule type: mRNA
A:Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.6/2
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A:Residues: 1-32,99-264 <ST2>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.111 and clone LCA.260
A/Accession: C46546
A/Status: preliminary
A/Molecule type: mRNA
A:Residues: 1-31,193-264 <ST3>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.1
A/Ralph, S.D.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A:Reference number: A91065; MUID:87275816; PMID:2956090
A/Accession: A29449
A/Molecule type: mRNA
A:Residues: 1-31,193-649,'L',651-869,'G',871-872,'A',874-1206,'P',1208-1304 <RAL>
A/Cross-references: GB:Y00662; MUID:934275; PDB:CA68269.1; PID:934276
A/Experimental source: clones pHLC-1 and lambdaHLC1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A:Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Tsai, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative ;
A:Reference number: I57658; MUID:90066468; PMID:2531281
A/Accession: I57658
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A:Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:G187020; PIDN:AA59497.1; PID:G553521
 A:Gene: GDB:PTPRC; CD45
 A:Cross-references: GDB:119768; OMIM:151460
 A:Map position: 1q31-q32
 C:Superfamily: leukocyte common antigen, leukocyte common antigen cytosolic domain homolog
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:675-699/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:857/Binding site: substrate phosphate (ATG) #status predicted

Query Match
 Best Local Similarity 100.0%; Score 44; DB 1; Length 1304;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDVIAT 9
 Db 1218 FLYDVIAT 1226

RESULT 2
 T43148
 probable protein-tyrosine-phosphatase (EC 3.1.3.48) - horn shark
 N:Alternate names: CD45 homolog
 C:Species: Heterodontus francisci (horn shark)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T43148
 R:Okumura, M.; Matthews, R.J.; Robb, B.; Bork, P.; Thomas, M.L.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: Z22317
 A:Accession: T43148
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-1200 <OK>
 A:Cross-references: UNIPROT:Q91054; EMBL:U34750; NID:G1304393; PID:G1335605; PIDN:AA010
 C:Superfamily: leukocyte common antigen, leukocyte common antigen cytosolic domain homol
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match
 Best Local Similarity 97.7%; Score 43; DB 2; Length 1200;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLYDVIAT 9
 Db 1114 FLYDVIAT 1122

RESULT 3
 B82735
 argininosuccinate lyase XP1003 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: B82735
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20355717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: B82735
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-445 <SIM>
 A:Cross-references: UNIPROT:Q9P8H5; GB:AE003938; GB:AE003849; NID:G9105955; PIDN:AA0381
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Britson, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Teshako, M.H.; Valada, H.; Van Stuyve, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Gene: XFI003
 C:Superfamily: argininosuccinate lyase

Query Match
 Best Local Similarity 86.4%; Score 38; DB 2; Length 445;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FLYDVIAT 9
 Db 38 FLYDVIAT 46

RESULT 4
 A28334
 protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
 N:Alternate names: 200k leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
 N:Contents: protein-tyrosine-phosphatase (T-cell variant)
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A28334; A29381; A61180; A60933; A33522; A29075; I54450; A28335; A23329; I57
 R:Thomas, M.L.; Reynolds, P.J.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
 A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
 A:Reference number: A28334; MUID:87260986; PMID:2955416
 A:Accession: A28334
 A:Molecule type: mRNA
 A:Residues: 1-1291 <THO>
 A:Cross-references: UNIPROT:P06600; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
 A:Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
 A:Reference number: A29381; MUID:86313686; PMID:2944116
 A:Accession: A29381
 A:Molecule type: mRNA
 A:Residues: 1-30,170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, '
 A:Cross-references: GB:M14342; NID:G198914; PIDN:AA39458.1; PID:G198915
 R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
 A:Reference number: A61180; MUID:92032882; PMID:1932742
 A:Accession: A61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 730-838 <YIA>
 R:Gomez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
 Immunogenetics 25, 263-266, 1987
 A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
 A:Reference number: A60933; MUID:87192931; PMID:3570377
 A:Accession: A60933
 A:Molecule type: protein
 A:Residues: 'R', 289-298; 'V', 331-335, 'Y', 'R', 364-370, 'X', 372-375; 595-608; 638-649; 669-
 R:Johnson, N.A.; Meyer, C.W.; Pingel, J.T.; Thomas, M.L.
 J. Biol. Chem. 264, 6220-6229, 1989
 A:Title: Sequence conservation in potential regulatory regions of the mouse and human le
 A:Reference number: A33522; MUID:89197920; PMID:2522930
 A:Accession: A33522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <ONH>
 A:Cross-references: GB:M22456; NID:G198755; PIDN:AA646374.1; PID:G554185; GB:U04640; GB:
 R:Roach, W.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
 A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
 A:Reference number: A29075; MUID:87092355; PMID:2948186
 A:Accession: A29075
 A:Molecule type: mRNA

A;Residues: 961-1291 <RAS>
 A;Cross-references: GB:M15174; NID:g201105; PIDN:AAA40161.1; PID:g201106
 R;Tung, J.
 Immunogenetics 28, 271-277, 1988
 A;Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in other
 A;Reference number: I54450; MUID:8830145; PMID:3417340
 A;Accession: I54450
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 32-73 <RES>
 A;Cross-references: GB:M23241; NID:g340850; PIDN:AAA39460.1; PID:g548174
 R;Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A;Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishes
 A;Reference number: A28335; MUID:87260987; PMID:3037546
 A;Accession: A28335
 A;Molecule type: mRNA
 A;Residues: 1-30,74-226 <SA2>
 A;Cross-references: GB:M14342
 R;Shen, F.W.; Saga, Y.; Litman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
 A;Reference number: A23329; MUID:86042665; PMID:3864163
 A;Accession: A23329
 A;Molecule type: mRNA
 A;Residues: 10-30,170-263 <SHE>
 A;Cross-references: GB:M11934; NID:g198919; PIDN:AAA39461.1; PID:g198920
 R;Saga, Y.; Tung, J.
 Mol. Cell. Biol. 8, 4889-4895, 1988
 A;Title: Organization of the Ly-5 Gene.
 A;Reference number: I57644; MUID:89096862; PMID:3211131
 A;Accession: I57644
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: MT,1-22 <RE2>
 A;Cross-references: GB:M23354; NID:g340890; PIDN:AAA39462.1; PID:g554192
 C;Genetics:
 A;Gene: Ly-5
 C;Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;1-24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MAT>
 F;24-564/Domain: extracellular #status predicted <EXT>
 F;24-30,170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicted
 F;565-586/Domain: transmembrane #status predicted <TM>
 F;587-1293/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F;564-888/Domain: intracellular #status predicted <INT>
 F;564-150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: c
 F;840/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;846/Binding site: substrate phosphate (Arg) #status predicted

Query Match 86.4%; Score 38; DB 1; Length 1291;
 Best Local Similarity 87.5%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIVAS 8
 DB 1206 FLYDVIVAS 1213

RESULT 5
 S33316
 structural protein - Marburg virus
 C;Species: Marburg virus
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S33316; S32775
 R;Bukreyev, A.A.; Volchkov, V.E.; Blinov, V.M.; Netesov, S.V.
 FEBS Lett. 323, 183-187, 1993
 A;Title: The GP-protein of Marburg virus contains the region similar to the 'immunosuppr
 A;Reference number: S33316; MUID:93265932; PMID:8495737
 A;Accession: S33316
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-661 <BUK>
 A;Cross-references: UNIPROT:P35254; EMBL:X68493; NID:g296960; PIDN:CAA48507.1; PID:g296
 C;Keywords: transmembrane protein

Query Match 84.1%; Score 37; DB 2; Length 681;
 Best Local Similarity 88.9%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIVAST 9
 DB 144 FLYDVIVAST 152

RESULT 6
 A45705
 type I transmembrane glycoprotein - Marburg virus
 C;Species: Marburg virus
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A45705
 R;Will, C.; Muhlbacher, E.; Linder, D.; Slenczka, W.; Klenk, H.D.; Feldmann, H.
 J. Virol. 67, 1203-1210, 1993
 A;Title: Marburg virus gene 4 encodes the virion membrane protein, a type I transmembr
 A;Reference number: A45705; MUID:93172334; PMID:8437211
 A;Accession: A45705
 A;Status: preliminary
 A;Molecule type: nucleic acid
 A;Residues: 1-661 <WIL>
 A;Cross-references: UNIPROT:P35253; GB:Z12132; GB:S55429; NID:g541780; PIDN:CAA78117.1;
 A;Experimental source: strain Musoke
 A;Note: sequence extracted from NCBI backbone (NCBIN:125332, NCBI:P:127598)
 C;Keywords: glycoprotein; transmembrane protein

Query Match 84.1%; Score 37; DB 2; Length 681;
 Best Local Similarity 88.9%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIVAST 9
 DB 144 FLYDVIVAST 152

RESULT 7
 AD2165
 two-component hybrid sensor and regulator all2875 (imported) - Nostoc sp. (strain PCC 71
 C;Species: Nostoc sp. PCC 7120
 A;Date: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AD2165
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi
 Nakasaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A;Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium An
 A;Reference number: UNIPROT:O8Y751; GB:BA000019; PIDN:BAW4574.1; PID:g17131969; GSPDB:(
 A;Accession: AD2165
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1817 <KTR>
 A;Cross-references: UNIPROT:O8Y751; GB:BA000019; PIDN:BAW4574.1; PID:g17131969; GSPDB:(
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: all2875

Query Match 81.8%; Score 36; DB 2; Length 1817;
 Best Local Similarity 87.5%; Pred. No. 55;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYDVIVAST 9
 DB 1519 LYDVIVAST 1526

RESULT 8
 A54080

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
 A/Accession: A54080; 150592
 J/Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
 J. Biol. Chem. 269, 14056-14063, 1994
 A/Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in
 A/Reference number: A54080; PMID:94245724; PMID:8186866
 A/Accession: A54080
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1237 <FAN>
 A/Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:9510510; PIDN:CAA79972.1; PID:95105
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C/Keyword: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F/528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F/510-834/Domain: protein-tyrosine-phosphatase homology <PTP>
 F/786/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F/792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 79.5%; Score 35; DB 2; Length 1237;
 Best Local Similarity 77.8%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
 Db 1153 FLYDTIART 1161

RESULT 9
 TDRILT
 leukocyte common antigen precursor, splice form 4 - rat
 N/Alternate names: CD45, L-CA, Ly-5, T200
 N/Contains: leukocyte common antigen precursor, splice form 1; leukocyte common antigen
 .1.3.48)
 C/Species: Rattus norvegicus (Norway rat).
 C/Date: 04-Dec-1986 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 A/Accession: A29450; B29450; C29450; D29450; A60241; A02247; I54569; A45854
 R/Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 EMBO J. 6, 1259-1264, 1987
 A/Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) is
 A/Reference number: A91067; PMID:87275817; PMID:2440674
 A/Accession: A29450
 A/Molecule type: mRNA
 A/Residues: 20-30,163-218 <BAR1>
 A/Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:9205153; GB:Y00065; GB:X03
 A/Experimental source: splice form 1
 A/Note: the translation in Genbank entry RATLCAI, PIDN:AAA41518.1, PID:9205154, release
 A/Accession: B29450
 A/Molecule type: mRNA
 A/Residues: 19-30,122-218 <BAR2>
 A/Cross-references: GB:M25821; GB:M24611; NID:9205155; PIDN:AAA41519.1; PID:9205156; GB:
 A/Experimental source: splice form 2
 A/Accession: C29450
 A/Molecule type: mRNA
 A/Residues: 20-30,73-121,163-218 <BAR3>
 A/Cross-references: GB:M25822; GB:M24611; NID:9205157; PIDN:AAA41520.1; PID:9205158; GB:
 A/Experimental source: splice form 3
 A/Accession: D29450
 A/Molecule type: mRNA
 A/Residues: 28-218 <BAR4>
 A/Cross-references: GB:M25823; GB:M24611; NID:9205159; PIDN:AAA41521.1; PID:9205160; GB:
 A/Experimental source: splice form 4
 A/Note: the sequence in Genbank entry RATLCAIV, release 113.0, has the codon AGG for 56-
 R/Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 Adv. Exp. Med. Biol. 237, 3-7, 1988
 A/Title: The leukocyte-common antigen (L-CA) family.
 A/Reference number: A60241; PMID:89319817; PMID:2978200
 A/Accession: A60241
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 30-161 <BAR5>
 R/Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.

Cell 41, 83-93, 1985
 A/Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans th
 A/Reference number: A02247; PMID:85201691; PMID:3158393
 A/Accession: A02247
 A/Molecule type: mRNA
 A/Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>
 A/Cross-references: GB:M10072; GB:M81859; NID:9205140; PIDN:AAA41513.1; PID:9205143
 A/Note: the translation in Genbank entry RATLCAI, release 113.0, begins at non-initiatio
 R/McCall, M.N.; Shotton, D.M.; Barclay, A.N.
 Immunology 76, 310-317, 1992
 A/Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
 A/Reference number: I54569; PMID:92340120; PMID:1378817
 A/Accession: I54569
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-30,163-180 <MCC>
 A/Cross-references: NID:9252015; PIDN:AA822648.1; PID:9252016
 R/Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A/Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are deriv
 A/Reference number: A45854; PMID:89233293; PMID:1252868
 A/Accession: A45854
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JAC>
 A/Cross-references: GB:M18347; GB:M18348; GB:M18349
 C/Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C/Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-1273/Product: leukocyte common antigen precursor, splice form 4 #status predicted <
 F/24-546/Domain: extracellular #status predicted <EXT>
 F/24-30,122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <MAT
 F/24-30,163-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MAT
 F/24-30,73-121,163-218/Product: leukocyte common antigen, splice form 3 #status predicte
 F/547-568/Domain: transmembrane #status predicted <TM>
 F/565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F/566-1273/Domain: intracellular #status predicted <INT>
 F/568-870/Domain: protein-tyrosine-phosphatase homology <PTP>
 F/62,142,151,154,178,200,245,271,282,327,371,374,502/Binding site: carbohydrate (Asn) (C
 F/822/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F/828/Binding site: substrate phosphate (Arg) #status predicted
 F/1063/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 79.5%; Score 35; DB 1; Length 1273;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 8
 Db 1188 FLYDIWAS 1195

RESULT 10
 T30423
 hypothetical protein ORF75 - lymphantria dispar nuclear polyhedrosis virus
 N/Alternate names: Ld-bro-g
 C/Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 A/Accession: T30423
 R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
 Virology 253, 17-34, 1999
 A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
 A/Reference number: Z20836; PMID:99124785; PMID:9887315
 A/Accession: T30423
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-222 <KUZ>
 A/Cross-references: UNIPROT:Q9YMQ2; EMBL:AF081810; PIDN:AAC70261.1

Query Match 77.3%; Score 34; DB 2; Length 222;
 Best Local Similarity 66.7%; Pred. No. 15;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FLYDVIASNT 9
|||:|
Db 105 FLYDVIASNT 113

RESULT 11

T20549

hypothetical protein F07C6.4a - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T20549; T23677

R/Steward, C.
submitted to the EMBL Data Library, February 1996

A/Reference number: Z19290

A/Accession: T20549

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-652 <W12>

A/Cross-references: UNIPROT:Q81093; EMBL:Z69659; PIDN:CAA93487.1; GSPDB:GN00022; CESP:FO

A/Experimental source: clone F07C6

R/Lighting, J.
submitted to the EMBL Data Library, October 1996

A/Reference number: Z19780

A/Accession: T23677

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-652 <W12>

A/Cross-references: EMBL:Z81102; PIDN:CA03206.1; GSPDB:GN00022; CESP:F07C6.4a

A/Experimental source: clone M02B1

C/Genetics:

A/Map position: 4

A/Introns: 27/3; 65/2; 98/2; 126/3; 152/2; 203/2; 280/2; 333/1; 381/3; 417/3; 494/1; 550

Query Match

Best Local Similarity 77.3%; Score 34; DB 2; Length 652;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYDVIASNT 9

|||:|

Db 77 FLYDVIASNT 84

RESULT 12

B81938

probable membrane protein NMA0915 [imported] - *Neisseria meningitidis* (strain Z2491 seroC/Species: *Neisseria meningitidis*

C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: B81938

R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: B81938

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-170 <PAR>

A/Cross-references: UNIPROT:Q9JVB1; GB:AL162754; GB:AL157959; NID:G7379424; PIDN:CA08419

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Map position: 4

A/Introns: 25/1; 44/1; 128/3; 167/3; 191/3

Query Match

Best Local Similarity 75.0%; Score 33; DB 2; Length 170;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLYDVIASNT 9

|||:|

Db 153 FLYDVIASNT 161

RESULT 13

T33414

hypothetical protein C04E12.3 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T33414

R/Pullon, R.; Wohldmann, P.; Bauer, C.; Gibson, A.

submitted to the EMBL Data Library, July 1998

A/Description: The sequence of C. elegans cosmid C04E12.

A/Reference number: Z23341

A/Accession: T33414

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-221 <FUL>

A/Cross-references: UNIPROT:O76677; EMBL:AF078785; PIDN:AACT3089.1; GSPDB:GN00023; CESP

A/Experimental source: strain Bristol N2; clone C04E12

C/Genetics:

A/Map position: 5

A/Introns: 25/1; 44/1; 128/3; 167/3; 191/3

Query Match

Best Local Similarity 75.0%; Score 33; DB 2; Length 221;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIASNT 9

|||:|

Db 76 FLYDVIASNT 84

RESULT 14

S67653

probable membrane protein YDL111c - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: hypothetical protein D2315

C/Species: *Saccharomyces cerevisiae*

C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004

C/Accession: S67653; S67407; S72095

R/Ballester, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Ba

submitted to the Protein Sequence Database, July 1996

A/Reference number: S67629

A/Accession: S67653

A/Molecule type: DNA

A/Residues: 1-265 <BAL>

A/Cross-references: UNIPROT:Q12277; EMBL:Z74159; NID:g1431159; PID:e253227; PID:g143116c

A/Experimental source: strain S288C

R/Dobkovic, J.; Salz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimin

submitted to the EMBL Data Library, February 1996

A/Reference number: S67406

A/Accession: S67407

A/Molecule type: DNA

A/Residues: 1-265 <BOS>

A/Cross-references: EMBL:X95644; NID:g1199535; PID:e223184; PID:g1199537

R/Salz, J.E.; Bittiger, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F.

Yeast 12, 1077-1084, 1996

A/Title: The sequence of a 20.3 kb DNA fragment from the left arm of *Saccharomyces cere*

A/Reference number: S72094; MUID:97051597; PMID:8896274

A/Accession: S72095

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-265 <SAT>

A/Cross-references: EMBL:X95644; NID:g1199535; PID:e223184; PID:g1199537

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

C/Genetics:

A/Map position: 4L

A/Introns: 25/1; 44/1; 128/3; 167/3; 191/3

A/Description: required for processing of the 5.8S rRNA

C/Keywords: transmembrane protein

P:177-193/Domain: transmembrane #status predicted <TM>

Query Match 75.0%; Score 33; DB 2; Length 265;
 Best Local Similarity 66.7%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
 :|||:||||
 10 YLYDSLAST 18

RESULT 15

E69831

conserved hypothetical protein ynfP - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: E69831

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emmerson, P.T.; Errington, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetler, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Raeger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
 A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tepsstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69831

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-330 <KUN>

A:Cross-references: UNIPROT:O07615; GB:Z99109; GB:AL009126; NID:G2633260; PIDN:CAB12872.

A:Experimental source: strain 168

C:Genetics:

A:Gene: ynfP

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match

75.0%; Score 33; DB 2; Length 330;

Best Local Similarity 85.7%; Pred. No. 37;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YDVIAST 9
 |||:||||
 DB 176 YDVVAST 182

Search completed: May 3, 2005, 06:14:16
 Job time : 27.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 06:25:02 ; Search time 44 Seconds
(without alignments)
79.110 Million cell updates/sec

Title: US-10-003-983C-1

Perfect score: 44

Sequence: 1 FLVDVIAST 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	5	ABG31971 Human CD4
2	44	100.0	273	7	ADd22989 Human pro
3	44	100.0	764	8	ABO84454 Human can
4	44	100.0	960	8	ADQ39377 Human myo
5	44	100.0	1114	6	ABU05246 Human exp
6	44	100.0	1114	6	ABU05239 Human exp
7	44	100.0	1143	6	ABU05240 Human exp
8	44	100.0	1143	6	ABU05245 Human exp
9	44	100.0	1143	7	ADL16232 Human pro
10	44	100.0	1143	7	ADQ18845 Human pol
11	44	100.0	1149	4	AA41048 Human pol
12	44	100.0	1149	6	ABU05242 Human exp
13	44	100.0	1192	8	ADR39747 Human kin
14	44	100.0	1219	8	ADQ39378 Human myo
15	44	100.0	1256	8	ADM67187 Human adi
16	44	100.0	1256	8	ADP12966 Protein e
17	44	100.0	1258	8	ADQ39376 Human myo
18	44	100.0	1267	8	ADQ39379 Human myo
19	44	100.0	1304	6	ABU05243 Human exp
20	44	100.0	1304	6	ABU05241 Human exp
21	44	100.0	1304	5	ABU05244 Human exp
22	44	100.0	1304	7	ADL16230 Human pro
23	44	100.0	1304	7	ADP65158 Human pro
24	44	100.0	1304	8	ADM67209 Human adi
25	44	100.0	1304	8	ABO84455 Human can

26	44	100.0	1304	8	ADQ39380 Human myo
27	44	100.0	1306	8	ADQ39375 Human myo
28	39	88.6	260	8	ADJ92685 Human leu
29	38	86.4	277	4	AAB59393 Murine pr
30	38	86.4	333	4	AA678291 Mouse CD4
31	38	86.4	397	8	ADN26688 Bacterial
32	38	86.4	405	8	ADN26828 Bacterial
33	38	86.4	444	8	ADN26856 Bacterial
34	38	86.4	1157	8	ABO84453 Mouse can
35	38	86.4	1291	7	ADL16234 Mouse pro
36	38	86.4	1343	8	ADM67208 Murine ad
37	37	84.1	610	6	ABJ18473 ChimERIC
38	37	84.1	642	3	AA77133 Marburg v
39	37	84.1	675	6	ABR42248 Marburg v
40	37	84.1	678	6	ABR42247 Marburg v
41	37	84.1	681	3	AA77127 Marburg v
42	37	84.1	681	3	AA770075 Marburg v
43	37	84.1	681	3	AAE00707 Marburg v
44	37	84.1	681	6	ABJ18476 ChimERIC
45	37	84.1	681	6	ABJ18474 ChimERIC

ALIGNMENTS

RESULT 1
ID ABG31971 standard; peptide, 9 AA.
XX AC ABG31971;
XX DT 05-NOV-2002 (first entry)
XX DE Human CD45 HLA-binding peptide, huCD45/1218.
XX XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
XX XX antigen-presenting cell; APC; major histocompatibility complex; MHC;
XX XX antigen; allogenic; T cell receptor; TCR; cancer; tumour;
XX XX allogenic stem cell transplantation; CFU-GM; leukaemia;
XX XX colony forming unit-granulocyte macrophage; immunotherapeutic;
XX XX haematopoietic; malignant.
XX OS Homo sapiens.
XX PN WO200244207-A1.
XX PD 06-JUN-2002.
XX PF 30-NOV-2000; 2000WO-GB004566.
XX PR 30-NOV-2000; 2000WO-GB004566.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Staus HJ, Amrolia PJ;
XX WPI; 2002-599413/64.
XX PS Claim 2, Page 38; 56pp; English.
XX CC The invention discloses a peptide comprising the human leukocyte antigen
XX CC (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,
XX CC provided that the peptide is not the intact human CD45 polypeptide. The
XX CC peptides are useful for producing activated cytotoxic T lymphocyte (CTL)
XX CC in vitro which involves contacting the CTL with an antigen-presenting
XX CC cell, where its major histocompatibility complex (MHC) class I molecules
XX CC are loaded with the peptide, to activate, in an antigen specific manner,
XX CC where the CTL and the antigen presenting cell are allogenic with respect
XX CC to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animal models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/1218,
CC comprising an HLA-binding peptide of human CD45
XX
SO Sequence 9 AA;
Query Match 100.0%; Score 44; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIAST 9
DB 1 FLYDVIAST 9
RESULT 2
ADD22989
ID ADD22989 standard; protein; 273 AA.
XX
AC ADD22989;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, CD45-D2.
XX
KW Human; enzyme; protein tyrosine phosphatase; PTPN1; cytosolic;
KW gene therapy; retroviral vector; phosphotyrosine; pp60(V-src);
XX breast cancer; leukaemia; CD45-D2.
XX
OS Homo sapiens.
XX
PN US2003113294-A1.
XX
PD 19-JUN-2003.
XX
PF 12-NOV-2002; 2002US-00293231.
XX
PR 14-MAR-1990; 90US-00494036.
PR 01-MAR-1991; 91US-00663579.
PR 16-AUG-1993; 93US-00107420.
PR 04-DEC-1996; 96US-00759536.
PR 22-JAN-1999; 99US-00235251.
PR 03-MAY-2001; 2001US-00848294.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX
XX PI Tonks NK;
XX
XX DR WPI; 2003-810871/76.
XX
XX PT New isolated RNA encoding protein tyrosine phosphatase designated as
XX PTPN1 useful for treating malignancies such as breast cancer, leukemia.
XX
XX PS Disclosure; Fig 4B; 12pp; English.
XX
XX CC The invention relates to an isolated RNA encoding a protein tyrosine
XX phosphatase designated as PTPN1 appearing as ADD22982. Also included is a
XX retroviral vector comprising the RNA. The RNA is useful for treating or

CC preventing a condition in which abnormally high levels of phosphotyrosine
CC occur in a mammalian cell (which involves introducing into the mammalian
CC cell and agent which comprises DNA or RNA encoding all or a portion of a
CC PTPN1, under conditions sufficient to express PTPN1 where the polypeptide
CC can catalyse dephosphorylation of tyrosyl residues that are
CC phosphorylated through action of a protein tyrosine kinase. The RNA is
CC also useful for reversing a malignant phenotype of a mammalian cell which
CC is associated with tyrosyl phosphorylation catalysed by a protein
CC tyrosine kinase. The DNA or RNA is delivered via a recombinant retrovirus
CC or a recombinant vaccinia virus. At least one tyrosyl residue that is
CC dephosphorylated by the protein tyrosine phosphatase polypeptide can be
CC aberrantly phosphorylated by pp60(V-src). The RNA is useful for treating
CC or preventing malignancies such as breast cancer and leukaemia. The
CC present sequence is a PTP similar to PTPN1.
XX
SQ Sequence 273 AA;
Query Match 100.0%; Score 44; DB 7; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIAST 9
DB 253 FLYDVIAST 261
RESULT 3
AB084454
ID AB084454 standard; protein; 764 AA.
XX
XX AB084454;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP13-011.1.
XX
KW Human; cancer-associated protein; cytosolic; cancer; leukaemia;
KW lymphoma; CAP.
XX
OS Homo sapiens.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX PI Morris DW, Morris DW, Malandro MS;
XX
XX DR WPI; 2004-652914/63.
XX
XX DR N-PSDB; ABD32625.
XX
XX PT New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.
XX
XX PS claim 18; seqid 145; 310pp; English.
XX
XX CC The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
XX in the specification, or its complement. The nucleic acids encode cancer-
XX associated proteins. Also included are an expression vector comprising
XX the isolated nucleic acid cited above, a host cell comprising the above
XX recombinant nucleic acid or expression vector, a microarray for detecting

CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
SQ Sequence 764 AA;

Query Match 100.0%; Score 44; DB 8; Length 764;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
|||
Db 678 FLYDVIAST 686

RESULT 4
AD039377
ID AD039377 standard; protein; 960 AA.
XX
XX AD039377;
XX

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1040.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM Cardiant; gene therapy; human.

XX Homo sapiens.

XX WO2004058052-A2.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

XX (APPL-) APPLERA CORP.

XX Cargill M, Devlin JT, Iakubova O;

DR WPI; 2004-533949/51.

DR N-PSDB; AD038549.

PT Identifying an individual who has an altered risk for developing
myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.
XX Claim 10; SEQ ID NO 1040; 145bp; English.

XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide
XX comprising an amino acid sequence given in the specification; an antibody
XX that specifically binds to the polypeptide or its antigen-binding
XX fragment; an amplified polynucleotide containing an SNP given in the
XX specification and which is between about 16 and 1000 nucleotides in
XX length; a kit for detecting an SNP in a nucleic acid, comprising the
XX polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX method for identifying an agent useful in treating or preventing
XX myocardial infarction. The novel detection method has cardiant activity.
XX The nucleic acids of the invention may be used in gene therapy. The
XX method is useful in identifying an individual who has an increased or
XX decreased risk for developing myocardial infarction and for preparing a
XX composition for treating or preventing myocardial infarction. This
XX sequence represents the protein of a human myocardial infarction-
XX associated gene containing one or more SNPs of the invention. Note: This
XX sequence was not shown in the specification. The sequence has come from
XX an electronic sequence listing downloaded from the WIPO website.

Query Match 100.0%; Score 44; DB 8; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
|||
Db 874 FLYDVIAST 882

RESULT 5
ABU05246
ID ABU05246 standard; protein; 1114 AA.
XX
XX ABU05246;
XX

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1912.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOs INC.
XX PA Chicz RM, Tomlinson AJ, Urban RG;
XX PI WPI; 2003-040607/03.
XX DR
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS Example 2; SEQ ID NO 1912; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX (ZYCO-) ZYCOs INC.
XX PA Chicz RM, Tomlinson AJ, Urban RG;
XX PI WPI; 2003-040607/03.
XX DR
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS Example 2; SEQ ID NO 1905; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 44; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
DB 1028 FLYDVIAST 1036

RESULT 6
ABU05239
ID ABU05239 standard; protein; 1114 AA.
XX
XX AC ABU05239;
XX
XX DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1905.
XX
XX

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.
XX OS
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.

XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX

XX 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.

Query Match 100.0%; Score 44; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
DB 1028 FLYDVIAST 1036

RESULT 7
ABU05240
ID ABU05240 standard; protein; 1143 AA.
XX
XX AC ABU05240;
XX
XX DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1906.
XX
XX

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.
XX OS
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.

XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX

XX 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.


```
XX (ZYCO-) ZYCO INC.
PA
XX Chiciz RM, Tomlinson AJ, Urban RG;
PI
XX WPI; 2003-040607/03.
DR
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1906; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;
```

```
Query Match 100.0%; Score 44; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FLYDVIAS 9
Db 1057 FLYDVIAS 1065
```

```
RESULT 8
ABU05245
ID ABU05245 standard; protein; 1143 AA.
XX
XX ABU05245;
AC
XX
XX 29-JAN-2003 (first entry)
DT
XX
XX Human expressed protein tag (EPT) #1911.
DE
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX Homo sapiens.
OS
XX
XX WO200278524-A2.
PN
XX
XX 10-OCT-2002.
PD
XX
XX 28-MAR-2002; 2002WO-US009671.
PF
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
```

```
XX (ZYCO-) ZYCO INC.
PA
XX Chiciz RM, Tomlinson AJ, Urban RG;
PI
XX WPI; 2003-040607/03.
DR
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1911; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;
```

```
Query Match 100.0%; Score 44; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FLYDVIAS 9
Db 1057 FLYDVIAS 1065
```

```
RESULT 9
ADL16232
ID ADL16232 standard; protein; 1143 AA.
XX
XX ADL16232;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human protein tyrosine phosphatase #27.
DE
XX
XX cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
XX Homo sapiens.
OS
XX
XX WO2003068984-A2.
PN
XX
XX 21-AUG-2003.
PD
XX
XX 13-FEB-2003; 2003WO-EP001446.
PF
XX
XX 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-00366547.
PR (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
XX
```

```

Query Match      100.0%; Score 44; DB 7; Length 1143;
Best Local Similarity 100.0%; Pred.No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      1 FLYDIYAST 9
        |||||
Db      1057 FLYDIYAST 1065

RESULT 10
ADQ18845
ADQ18845 strand; protein; 1143 AA.
AC      ADQ18845;
XX
XX
DT      26-AUG-2004 (first entry)
XX
XX
DE      Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
XX
XX      soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
XX      Homo sapiens.
XX
XX      WO2004048938-A2.
XX
XX      10-JUN-2004.
PD
XX
XX
PF      26-NOV-2003; 2003WO-US038193.
XX
XX      26-NOV-2002; 2002US-0429739P.
PR
XX
XX      (PROT-) PROTEIN DESIGN LABS INC.
XX
XX      Aziz N, Ginsburg MM, Zlotnik A;
PI
XX      WPI; 2004-441208/41.
DR
XX
XX
PT      Early detection of soft tissue sarcoma comprises determining expression
PT      of a gene in a first soft tissue sample and a normal soft tissue sample
PT      and comparing the gene expression, also useful in treating soft tissue
PT      sarcoma.

```

Query Match	Similarity	Score	DB	Length
Best Local	100.0%	Pred. No.	1.9	0
Matches	9	Conservative	0	Indels
				Gaps
Qy	1 FLYDVIASST 9			
Db	1057 FLYDVIASST 1065			

XX	
AC	AA041048;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 5979.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; hematologic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemocarcin;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukemia.

PA (HYSE-) HYSEQ INC

xx Tang Y¹, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Qi;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
 PI Zhou P, Goodrich R, Demanac RT;
 xx
 DR WPI; 2001-442253/47.
 DR N-PSDB; AA160204.

XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5979; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AM157798-AM161369) and the
CC encoded polypeptides (AM38642-AM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1149 AA;

Query Match 100.0%; Score 44; DB 4; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
| | | | | | | | | |
Db 1063 FLYDVIAST 1071

RESULT 12
ABU05242
ID ABU05242 standard; protein; 1149 AA.
XX
AC ABU05242;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1908.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

PS Example 2; SEQ ID NO 1908; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1149 AA;

Query Match 100.0%; Score 44; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
| | | | | | | | | |
Db 1063 FLYDVIAST 1071

RESULT 13
ADR39747
ID ADR39747 standard; protein; 1192 AA.
XX
AC ADR39747;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
XX
KW human; kinase and phosphatase protein; KPP; enzyme; cytoslastic;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; anti-allergic; anti-inflammatory;
KW thymorectic; gene therapy; cell proliferative disorder; cancer;
KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KW KPP-20.
XX
OS Homo sapiens.
XX
PN WO2004074453-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004MO-US005092.
XX
PR 20-FEB-2003; 2003US-0449059P.
XX
PR 19-MAR-2003; 2003US-0456932P.
XX
PR 28-MAR-2003; 2003US-0458844P.
XX
PR 09-APR-2003; 2003US-0461678P.
XX
PR 17-APR-2003; 2003US-0461937P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Raktumar J, Marguis JP, Swarnaker A, Chawla NK, Tran UK;
PI Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
PI Jackson AA, Yang J, Gorvad AB;
XX
DR WPI; 2004-635568/61.
XX
DR N-PSDB; ADR39793.
XX

PT New human kinases and phosphatases (KPP) for diagnosing, treating and
PT preventing diseases or conditions associated with aberrant KPP expression
PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX
XX
XX Claim 1; SEQ ID NO 20; 299pp; English.
XX
CC The present sequence represents the human kinase and phosphatase protein
CC (KPP), designated KPP-20. The human KPP sequences from the present
CC invention have cytosolic, antiarteriosclerotic, anticonvulsant,
CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thymomimetic activities, and can be used in gene
CC therapy. The human KPP proteins and polynucleotides can be used in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KPP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They can also be used in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
XX
SQ Sequence 1192 AA;
XX
Query Match 100.0%; Score 44; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 FLYDVIAT 9
DB 1106 FLYDVIAT 1114
XX
RESULT 14
ADQ39378
ID ADQ39378 standard; protein; 1219 AA.
XX
XX ADQ39378;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
XX Myocardial; gene therapy; human.
XX
XX Homo sapiens.
XX
XX OS
XX
XX PN WO2004056052-A2.
XX
XX PD 15-JUL-2004.
XX
XX PF 22-DEC-2003; 2003WO-US040978.
XX
XX PR 20-DEC-2002; 2002US-0434778P.
XX
XX PR 10-MAR-2003; 2003US-0453135P.
XX
XX PR 30-APR-2003; 2003US-0466412P.
XX
XX PR 23-SEP-2003; 2003US-0504955P.
XX
XX PA (APPL-) APPLERA CORP.
XX
XX PI Cargill M, Devlin J, Jakubova O;
XX
XX DR MPI; 2004-533949/51.
XX
XX DR N-PSDB; ADQ38550.
XX
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX
XX PS Claim 10; SEQ ID NO 1041; 145pp; English.

XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1219 AA;
XX
Query Match 100.0%; Score 44; DB 8; Length 1219;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 FLYDVIAT 9
DB 1133 FLYDVIAT 1141
XX
RESULT 15
ADM67187
ID ADM67187 standard; protein; 1256 AA.
XX
XX ADM67187;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human adipocyte specific PRPase receptor type C protein segid 541.
XX
XX human; adipocyte specific; adipose tissue; anti-obesity;
XX
XX high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
XX
XX adipogenesis; hypertension; cardiovascular disease; anorectic;
XX
XX antidiabetic; hypotensive; PRPase receptor type C.
XX
XX OS
XX
XX PN WO2004011618-A2.
XX
XX PD 05-FEB-2004.
XX
XX PF 29-JUL-2003; 2003WO-US023684.
XX
XX PR 29-JUL-2002; 2002US-0398785P.
XX
XX PR 12-JUN-2003; 2003US-0478206P.
XX
XX PA (HMGCE-) HMGCE INC.
XX
XX PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
XX DR MPI; 2004-143846/14.
XX
XX DR N-PSDB; ADM66908.
XX

PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 541; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group 1-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
XX
SQ Sequence 1256 AA;
XX
Query Match 100.0%; Score 44; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIAST 9
DB 1170 FLYDVIAST 1178
XX
RESULT 16
ADP12966
ID ADP12966 standard; protein; 1256 AA.
XX
AC ADP12966;
XX
DT 12-AUG-2004 (first entry)
XX
DE Protein encoding reference mRNA sequence #51.
XX
XX transapant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
XX Homo sapiens.
XX
OS WO2004042346-A2.
XX
PN 21-MAY-2004.
XX
PD 24-APR-2003; 2003WO-US012946.
XX
PF 24-APR-2002; 2002US-00131831.
XX
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Mohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR MPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.

PS Claim 65; SEQ ID NO 2975; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein encoded by an mRNA sequence of the invention which show altered
CC expression in renal transplantation and expression.
XX
SQ Sequence 1256 AA;
XX
Query Match 100.0%; Score 44; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIAST 9
DB 1170 FLYDVIAST 1178
XX
RESULT 17
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.
XX
XX ADQ39376;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiac; gene therapy; human.
XX
OS Homo sapiens.
XX
OS WO2004058052-A2.
XX
PN 15-JUL-2004.
XX
PD 22-DEC-2003; 2003WO-US040978.
XX
PF 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
XX
PR 30-APR-2003; 2003US-0466412P.
XX
PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JT, Iakubova O;
XX
DR MPI; 2004-533949/51.
XX
DR N-PSDB; ADQ38548.
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1039; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention

CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1258 AA;

Query Match 100.0%; Score 44; DB 8; Length 1258;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAS 9
DB 1172 FLYDVIAS 1180

XX RESULT 18

ADQ39379 standard; protein; 1267 AA.

XX ADQ39379;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.

DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KM cardiant; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

XX 15-UTU-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin JT, Iakubova O;

DR WPI, 2004-53949/51.

DR N-PSDB; ADQ38551.

PT Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

PS Claim 10; SEQ ID NO 1042; 145pp; English.

XX The invention relates to a novel method for identifying an individual who

CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1267 AA;

Query Match 100.0%; Score 44; DB 8; Length 1267;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAS 9
DB 1181 FLYDVIAS 1189

XX RESULT 19

ABU05243 standard; protein; 1304 AA.

XX ABU05243;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1909.

DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;

KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;

KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN WO200278524-A2.

XX 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCO INC.

PI Chiciz RM, Tomlinson AJ, Urban RG;

```
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1909; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
XX Query Match 100.0%; Score 44; DB 6; Length 1304;
XX Best Local Similarity 100.0%; Pred. No. 2.1;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIYST 9
XX |||||
DB 1218 FLYDVIYST 1226
XX
RESULT 20
ABU05241
ID ABU05241 standard; protein; 1304 AA.
XX
AC ABU05241;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1907.
XX
XX Translational profiling: expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
OS
XX WO200278524-A2.
PN
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
PA
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
```

```
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1907; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
XX Query Match 100.0%; Score 44; DB 6; Length 1304;
XX Best Local Similarity 100.0%; Pred. No. 2.1;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIYST 9
XX |||||
DB 1218 FLYDVIYST 1226
XX
RESULT 21
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1910.
XX
XX Translational profiling: expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
OS
XX WO200278524-A2.
PN
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
PA
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
```


DR MPI; 2003-040607/03.
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1910; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 1304 AA;
 XX
 Query Match 100.0%; Score 44; DB 6; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLYDVIAT 9
 DB 1218 FLYDVIAT 1226
 ADL16230
 ID ADL16230 standard; protein; 1304 AA.
 XX
 AC ADL16230;
 XX
 DT 06-MAY-2004 (first entry)
 DE Human protein tyrosine phosphatase #26.
 XX
 KW cytoskeletal; immunosuppressive; antiallergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signaling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003068984-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-EP001446.
 XX
 PR 13-FEB-2002; 2002US-0356810P.
 XX
 PR 12-FEB-2003; 2003US-0036547.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PA (CEPT-) CEPTYR INC.
 XX
 PI Tonke NK, Tzu-Ching M, Cool DE;
 XX
 DR MPI; 2003-712572/67.
 DR N-PSDB; ADL16229.
 XX

PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 79; 238pp; English.
 XX
 CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulfhydryl-reactive agent (iii) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 CC
 SQ Sequence 1304 AA;
 XX
 Query Match 100.0%; Score 44; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FLYDVIAT 9
 DB 1218 FLYDVIAT 1226
 ADP65158
 ID ADP65158 standard; protein; 1304 AA.
 XX
 AC ADP65158;
 XX
 DT 12-AUG-2004 (first entry)
 DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
 XX
 KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;
 KW antirheumatic; osteopathic; antigout; anti-inflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072827-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 31-OCT-2002; 2002WO-US035433.
 XX
 PR 31-OCT-2001; 2001US-0336220P.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Hirsch R, Thorton SL;
 XX
 DR MPI; 2003-712740/67.
 DR GENBANK; NP_002829.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

PT gout.
XX
XX Disclosure; Page; 56pp; English.
PS
CC The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
SQ Sequence 1304 AA;
XX
XX
Query Match 100.0%; Score 44; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIAST 9
DB 1218 FLYDVIAST 1226
RESULT 24
ADM67209
ID ADM67209 standard; protein; 1304 AA.
XX
AC ADM67209;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human adipocyte specific leukocyte common antigen protein SegID 563.
XX
XX human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KM adipogenesis; hypertension; cardiovascular disease; anorectic;
KM anti-diabetic; hypotensive; leukocyte common antigen.
XX
XX Homo sapiens.
OS
XX
XX WO2004011618-A2.
PN
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
XX
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGF-) HMGF INC.
XX
XX Chada K, Chouinard R, Ashar H, Sayed AMD;
PI
XX WPI; 2004-143846/14.
DR

DR N-PSDB; ADM66930.
XX
XX Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 563; 91pp; English.
XX
XX This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti-
CC obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, anti-diabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
XX
SQ Sequence 1304 AA;
XX
XX
Query Match 100.0%; Score 44; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVIAST 9
DB 1218 FLYDVIAST 1226
RESULT 25
ABO84455
ID ABO84455 standard; protein; 1304 AA.
XX
XX ABO84455;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP13-011.2.
XX
XX Human; cancer-associated protein; cyrostatic; cancer; leukaemia;
KW lymphoma; CAP.
XX
XX Homo sapiens.
OS
XX
XX WO2004074320-A2.
PN
XX
PD 02-SEP-2004.
XX
XX
XX 17-FEB-2004; 2004WO-US004730.
XX
XX
XX 14-FEB-2003; 2003US-00367094.
XX
XX 14-MAR-2003; 2003US-00388838.
XX
XX 15-APR-2003; 2003US-00417375.
XX
XX 13-JUN-2003; 2003US-00461862.
XX
XX 15-SEP-2003; 2003US-00663431.
XX
XX 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
PI
XX WPI; 2004-652914/63.
XX
XX N-PSDB; ABD32626.
DR

XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
XX claim 18; seqid 147; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1304 AA;
SQ

Query Match 100.0%; Score 44; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
DB 1218 FLYDVIAST 1226

RESULT 26
ADQ39380
ID ADQ39380 standard; protein; 1304 AA.
XX
XX ADQ39380;
AC
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
XX WO2004058052-A2.
PN
XX
XX 15-JUL-2004.
PD
XX
XX 22-DEC-2003; 2003WO-US040978.
PF
XX
XX 20-DEC-2002; 2002US-0434778P.
PR

PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLEERA CORP.
PA
XX Cargill M, Devlin J, Iakubova O;
XX
XX
DR MPI: 2004-533949/51.
DR N-PSDB; ADQ38552.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1043; 145pp; English.
XX
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
XX Sequence 1304 AA;
SQ

Query Match 100.0%; Score 44; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLYDVIAST 9
DB 1218 FLYDVIAST 1226

RESULT 27
ADQ39375
ID ADQ39375 standard; protein; 1306 AA.
XX
XX ADQ39375;
AC
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
XX WO2004058052-A2.
PN
XX

PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakubova O;
XX
XX WPI; 2004-533949/51.
DR N-PSDB; ADQ38547.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1038; 145bp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acid, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1306 AA;
Query Match 100.0%; Score 44; DB 8; Length 1306;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLYDVYAST 9
|||
1220 FLYDVYAST 1228

Search completed: May 3, 2005, 07:29:23
Job time : 71 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:28:27 ; Search time 38.6757 Seconds
(without alignments)
90.001 Million cell updates/sec

Title: US-10-003-983C-2

Perfect score: 40

Sequence: 1 ALIAFLAFL 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	5	ABG31972 Human CD4
2	40	100.0	641	4	AAM23689 Human EST
3	40	100.0	641	6	ABU07333 Human exp
4	40	100.0	664	4	AAM39262 Human pol
5	40	100.0	664	6	ABU07334 Human exp
6	40	100.0	764	8	ABO84454 Human can
7	40	100.0	960	8	ADQ39377 Human myo
8	40	100.0	1114	6	ABU05246 Human exp
9	40	100.0	1114	6	ABU05239 Human exp
10	40	100.0	1143	6	ABU05240 Human exp
11	40	100.0	1143	6	ABU05245 Human exp
12	40	100.0	1143	7	ADL16232 Human pro
13	40	100.0	1143	7	ADL16232 Human pro
14	40	100.0	1149	4	AAM41048 Human pol
15	40	100.0	1149	4	ABU05242 Human exp
16	40	100.0	1192	8	ADR39747 Human kin
17	40	100.0	1219	8	ADQ39378 Human myo
18	40	100.0	1256	8	ADM67187 Human adi
19	40	100.0	1256	8	ADP12966 Protein e
20	40	100.0	1258	8	ADQ39376 Human myo
21	40	100.0	1267	8	ADQ39379 Human myo
22	40	100.0	1304	6	ABU05243 Human exp
23	40	100.0	1304	6	ABU05241 Human exp
24	40	100.0	1304	6	ABU05244 Human exp
25	40	100.0	1304	7	ADL16230 Human pro

26	40	100.0	1304	7	ADP65158 Human pro
27	40	100.0	1304	8	ADM67209 Human adi
28	40	100.0	1304	8	ABO84455 Human can
29	40	100.0	1304	8	ADQ39380 Human myo
30	40	100.0	1306	8	ADQ39375 Human myo
31	36	90.0	151	3	AAG54654 Zea mays
32	36	90.0	170	3	AAG54653 Zea mays
33	36	90.0	354	4	AAU33849 Staphyloc
34	36	90.0	444	4	AAU36890 Staphyloc
35	36	90.0	444	6	ABU16251 Protein e
36	36	90.0	444	6	ABM71958 Staphyloc
37	34	85.0	113	5	ABM71252 Dengue v1
38	34	85.0	129	7	ADH86015 Enterococ
39	34	85.0	139	6	ADA54401 Human pro
40	34	85.0	139	7	ADJ71107 Human hea
41	34	85.0	431	4	AAG82736 S. epider
42	34	85.0	466	5	ABP38510 Staphyloc
43	34	85.0	466	6	ABU42861 Protein e
44	34	85.0	466	8	ADS05274 Staphyloc
45	34	85.0	1127	2	AAM09409 Dengue v1

ALIGNMENTS

RESULT 1	
ID	ABG31972 standard; peptide; 9 AA.
XX	XX
AC	ABG31972;
XX	XX
DT	05-NOV-2002 (first entry)
XX	XX
DE	Human CD45 HLA-binding peptide, huCD45/576.
XX	XX
KW	Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL; antigen-presenting cell; APC; major histocompatibility complex; MHC; antigen; allogenic; T cell receptor; TCR; cancer; tumour;
KW	allogenic stem cell transplantation; CFU-GM; leukaemia;
KW	colony forming unit-granulocyte macrophage; immunotherapeutic;
KW	haematopoietic; malignant.
XX	XX
OS	Homo sapiens.
XX	XX
PN	MO200244207-A1.
XX	XX
PD	06-JUN-2002.
XX	XX
PF	30-NOV-2000; 2000MO-GB004566.
XX	XX
PR	30-NOV-2000; 2000MO-GB004566.
XX	XX
PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX	XX
PI	Stauss HJ, Amrolia PJ;
XX	XX
DR	WPI, 2002-599413/64.
XX	XX
PT	Novel peptide comprising leukocyte antigen binding peptide of human CD45 polypeptide, useful for producing activated cytotoxic T lymphocytes, for killing cancerous cells e.g. leukemia.
PT	Claim 2; Page 38; 56pp; English.
XX	XX
PS	XX
CC	The invention discloses a peptide comprising the human leukocyte antigen (HLA)-binding peptide of human CD45 polypeptide, its portion or variant, provided that the peptide is not the intact human CD45 polypeptide. The peptides are useful for producing activated cytotoxic T lymphocyte (CTL) in vitro which involves contacting the CTL with an antigen-presenting cell, where its major histocompatibility complex (MHC) class I molecules are loaded with the peptide, to activate, in an antigen specific manner, where the CTL and the antigen presenting cell are allogenic with respect to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animal models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/576,
CC comprising an HLA-binding peptide of human CD45
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
1 |||||
Db 1 ALIAFLAFL 9

RESULT 2
ID AAM23689 standard; protein; 641 AA.

AC AAM23689;

DT 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1214.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.

OS Homo sapiens.

PN WO200154477-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001MO-US002687.

PR 25-JAN-2000; 2000US-00491404.

PR 17-JUL-2000; 2000US-00617746.

PR 03-AUG-2000; 2000US-00631451.

PR 15-SEP-2000; 2000US-00663870.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

DR WPI; 2001-476164/51.

DR N-PSDB; AAH98348.

PT Isolated polypeptide for treatment of diseases, diagnostics, raising

PS antibodies and research use.

XX Claim 20; Page 875-876; 1275pp; English.

CC The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention

SQ Sequence 641 AA;

Query Match 100.0%; Score 40; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
417 |||||
Db 417 ALIAFLAFL 425

RESULT 3
ID ABU07333 standard; protein; 641 AA.

AC ABU07333;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #2034.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002MO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-036780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCO INC.

PI Chiciz RM, Tomlinson AJ, Urban RG;

PI WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.

XX Example 2; SEQ ID NO 2034; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a

XX fragment of a kinase, phosphatase, protease, protease inhibitor.

XX transporter, cytoskeletal protein, receptor or transcription factor. The

XX polypeptide is useful as an immunogenic composition for eliciting in a

XX mammal an immunogenic response directed against any of the purified

XX polypeptide. The purified polypeptide, or the antibody that binds to this

XX polypeptide, is useful for treating cancer. The polypeptide is also

XX useful for identifying compounds that binds to a naturally processed

XX class I or class II MHC-binding polypeptide. The polypeptides and

XX polynucleotides are particularly useful for treating or preventing

XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 641 AA;

SO Query Match

Best Local Similarity 100.0%; Score 40; DB 6; Length 641;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9

|||||

Db 417 ALIAFLAFL 425

RESULT 4

AAM39262

ID AAM39262 standard; protein; 664 AA.

XX AC AAM39262;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 2407.

XX KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000MO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662191.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,

XX PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,

XX PI Zhou P, Goodrich R, Dmanac RT;

XX DR WPI; 2001-442253/47.

XX DR N-PSDB; AAI58418.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such

XX PS as central nervous system injuries.

XX XX Example 4; SEQ ID NO 2407; 10078bp; English.

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: immune system suppression,

CC Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification

XX Sequence 664 AA;

SO Query Match

Best Local Similarity 100.0%; Score 40; DB 4; Length 664;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9

|||||

Db 417 ALIAFLAFL 425

RESULT 5

ABU07334

ID ABU07334 standard; protein; 664 AA.

XX AC ABU07334;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #2035.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002MO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCO INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

XX PT cytoskeletal proteins, receptors or transcription factors), useful for

XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

XX PT leukemia.

XX PS Example 2; SEQ ID NO 2035; 134bp; English.

XX XX The invention describes a purified polypeptide, which comprises a

XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,

XX CC transporter, cytoskeletal protein, receptor or transcription factor. The

XX CC polypeptide is useful as an immunogenic composition for eliciting in a

XX CC mammal an immunogenic response directed against any of the purified

XX CC polypeptide. The purified polypeptide, or the antibody that binds to this

XX CC polypeptide, is useful for treating cancer. The polypeptide is also

XX CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 664 AA;

XX Query Match 100.0%; Score 40; DB 6; Length 664;
 XX Best Local Similarity 100.0%; Pred. No. 25;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
 DB 417 ALIAFLAFL 425

RESULT 6
 ABO84454
 ID ABO84454 standard; protein; 764 AA.
 XX AC ABO84454;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human cancer-associated protein HPI3-011.1.
 XX KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
 XX KW lymphoma; CAP.
 XX OS Homo sapiens.
 XX PN WO2004074320-A2.
 XX PD 02-SEP-2004.
 XX PF 17-FEB-2004; 2004WO-US004730.
 XX PR 14-FEB-2003; 2003US-00367094.
 XX PR 14-MAR-2003; 2003US-0038838.
 XX PR 15-APR-2003; 2003US-00417375.
 XX PR 13-JUN-2003; 2003US-00461862.
 XX PR 15-SEP-2003; 2003US-00663431.
 XX PR 15-DEC-2003; 2003US-00737318.
 XX PA (SAGR-) SAGRES DISCOVERY INC.
 XX PI Morris DW, Morris DW, Malandro MS;
 XX DR WPI; 2004-652914/63.
 XX DR N-PSDB; ABD32625.
 XX PT New isolated cancer-associated polynucleotides and polypeptides useful
 XX PT for diagnosing, preventing or treating cancers, especially lymphoma and
 XX PT leukemia, or in screening for agents that modulate cancer.
 XX claim 16; seqid 145; 310pp; English.

XX The invention relates to an isolated nucleic acid comprising at least 10
 XX contiguous nucleotides of any of the 233 polynucleotide sequences given
 XX in the specification, or its complement. The nucleic acids encode cancer-
 XX associated proteins. Also included are an expression vector comprising
 XX the isolated nucleic acid cited above, a host cell comprising the above
 XX recombinant nucleic acid or expression vector, a microarray for detecting
 XX a cancer-associated (CA) nucleic acid comprising at least one probe
 XX comprising at least 10 contiguous nucleotides of any of the above-
 XX mentioned nucleotide sequences, an isolated polypeptide (encoded within
 XX an open reading frame of a CA sequence selected from any of the 95
 XX polynucleotide sequences as mentioned in the specification, or its

CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 764 AA;

XX Query Match 100.0%; Score 40; DB 8; Length 764;
 XX Best Local Similarity 100.0%; Pred. No. 28;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
 DB 36 ALIAFLAFL 44

RESULT 7
 ADQ39377
 ID ADQ39377 standard; protein; 960 AA.
 XX AC ADQ39377;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1040.
 XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 XX KW cardiac; gene therapy; human.
 XX OS Homo sapiens.
 XX PN WO2004058052-A2.
 XX PD 15-JUL-2004.
 XX PF 22-DEC-2003; 2003WO-US040978.
 XX PR 20-DEC-2002; 2002US-0434778P.
 XX PR 10-MAR-2003; 2003US-0453135P.
 XX PR 30-APR-2003; 2003US-0466412P.
 XX PR 23-SEP-2003; 2003US-0504955P.
 XX PA (APPL-) APPLERA CORP.
 XX PI Cargill M, Devlin JT, Iakoubova O;
 XX DR WPI; 2004-533949/51.
 XX DR N-PSDB; ADQ38549.
 XX PT Identifying an individual who has an altered risk for developing
 XX PT myocardial infarction by detecting a single nucleotide polymorphism in
 XX PT the individual's nucleic acids.
 XX claim 10; SEQ ID NO 1040; 145pp; English.

XX The invention relates to a novel method for identifying an individual who

CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction.
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

SO Sequence 960 AA;

Query Match 100.0%; Score 40; DB 8; Length 960;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
 |||||
 DB 232 ALIAFLAFL 240

RESULT 8
 ABU05246
 ID ABU05246 standard; protein; 1114 AA.
 XX
 AC ABU05246;
 XX
 DT 29-JAN-2003 (first entry)
 XX

DE Human expressed protein tag (EPT) #1912.
 XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX

OS Homo sapiens.
 XX

PN WO200278524-A2.
 XX

PD 10-OCT-2002.
 XX

PF 28-MAR-2002; 2002WO-US009671.
 XX

PR 28-MAR-2001; 2001US-0279495P.
 XX

PR 21-MAY-2001; 2001US-0292544P.
 XX

PR 08-AUG-2001; 2001US-0310801P.
 XX

PR 01-OCT-2001; 2001US-0326370P.
 XX

PR 04-DEC-2001; 2001US-0336780P.
 XX

PR 20-FEB-2002; 2002US-0358985P.
 XX

PA (ZYCO-) ZYCOS INC.
 XX

PI Chicx RM, Tomlinson AJ, Urban RG;
 XX

DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX

PS Example 2; SEQ ID NO 1912; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 1114 AA;

Query Match 100.0%; Score 40; DB 6; Length 1114;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
 |||||
 DB 386 ALIAFLAFL 394

RESULT 9
 ABU05239
 ID ABU05239 standard; protein; 1114 AA.
 XX
 AC ABU05239;
 XX
 DT 29-JAN-2003 (first entry)
 XX

DE Human expressed protein tag (EPT) #1905.
 XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX

OS Homo sapiens.
 XX

PN WO200278524-A2.
 XX

PD 10-OCT-2002.
 XX

PF 28-MAR-2002; 2002WO-US009671.
 XX

PR 28-MAR-2001; 2001US-0279495P.
 XX

PR 21-MAY-2001; 2001US-0292544P.
 XX

PR 08-AUG-2001; 2001US-0310801P.
 XX

PR 01-OCT-2001; 2001US-0326370P.
 XX

PR 04-DEC-2001; 2001US-0336780P.
 XX

PR 20-FEB-2002; 2002US-0358985P.
 XX

PA (ZYCO-) ZYCOS INC.
 XX

PI Chicx RM, Tomlinson AJ, Urban RG;
 XX

DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1905; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;

Query Match 100.0%; Score 40; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 386 ALIAFLAFL 394

RESULT 10
ABU05240
ID ABU05240 standard; protein; 1143 AA.
XX
XX AC ABU05240;
XX
XX DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1906.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX
XX PR 21-MAY-2001; 2001US-0292544P.
XX
XX PR 08-AUG-2001; 2001US-0310801P.
XX
XX PR 01-OCT-2001; 2001US-0326370P.
XX
XX PR 04-DEC-2001; 2001US-0336780P.
XX
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX

DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1906; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;

Query Match 100.0%; Score 40; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 415 ALIAFLAFL 423

RESULT 11
ABU05245
ID ABU05245 standard; protein; 1143 AA.
XX
XX AC ABU05245;
XX
XX DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1911.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX
XX PR 21-MAY-2001; 2001US-0292544P.
XX
XX PR 08-AUG-2001; 2001US-0310801P.
XX
XX PR 01-OCT-2001; 2001US-0326370P.
XX
XX PR 04-DEC-2001; 2001US-0336780P.
XX
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX

DR WPI; 2003-040607/03.
 XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1911; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 1143 AA;
 Query Match 100.0%; Score 40; DB 6; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALIAPLAF 9
 |||||
 415 ALIAPLAF 423
 DB
 RESULT 12
 ADL16232
 ID ADL16232 standard; protein; 1143 AA.
 XX
 AC ADL16232;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human protein tyrosine phosphatase #27.
 XX
 KW cytosolic; immunosuppressive; antiallergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signalling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003068984-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-BP001446.
 XX
 PR 13-FEB-2002; 2002US-0356810P.
 PR 12-FEB-2003; 2003US-0036547.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (CEPT-) CEPTYR INC.
 XX
 PI Tonks NK, Tzu-Ching M, Cool DE;
 DR WPI; 2003-712572/67.
 DR N-PSDB; ADL16231.
 CC

PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 81; 238pp; English.
 XX
 CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulphydryl-reactive agent (iii) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
 CC dephosphorylation indicates that an active PTP is present.. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 CC
 XX
 SQ Sequence 1143 AA;
 Query Match 100.0%; Score 40; DB 7; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALIAPLAF 9
 |||||
 415 ALIAPLAF 423
 DB
 RESULT 13
 ADQ18845
 ID ADQ18845 standard; protein; 1143 AA.
 XX
 AC ADQ18845;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
 XX
 KW soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human.
 KW
 OS Homo sapiens.
 XX
 PN WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038193.
 XX
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Ginsburg WM, Zlotnick A;
 PI
 DR WPI; 2004-441208/41.
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 PS Example 2; SEQ ID NO 1664; 210pp; English.
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

CC Sequence 1143 AA;

Query Match 100.0%; Score 40; DB 8; Length 1143;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALIAFLAFL 9

Db 415 ALIAFLAFL 423

RESULT 14

AA041048
ID AA041048 standard; protein; 1149 AA.

AC AA041048;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 5979.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.

XX Homo sapiens.

XX WO20015312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00596042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI60204.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX Example 2; SEQ ID NO 5979; 10078bp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AA038642-AA042213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

CC Sequence 1149 AA;

Query Match 100.0%; Score 40; DB 4; Length 1149;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALIAFLAFL 9

Db 420 ALIAFLAFL 428

RESULT 15

AB05242
ID AB05242 standard; protein; 1149 AA.

AC AB05242;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1908.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

XX Example 2; SEQ ID NO 1908; 134bp; English.

XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The

CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC melanoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1149 AA;
Query Match 100.0%; Score 40; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
Db 420 ALIAFLAFL 428
RESULT 16
ADR39747 100.0%; Score 40; DB 6; Length 1192;
ID ADR39747 standard; protein; 1192 AA.
XX ADR39747;
AC
XX
DT 18-NOV-2004 (first entry)
DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
XX
XX human; kinase and phosphatase protein; KPP; enzyme; cytosolic;
XX antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
XX cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
XX thymomimetic; gene therapy; cell proliferative disorder; cancer;
XX atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
XX stroke; immune disorder; inflammatory disorder; AIDS; allergy;
XX developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX KPP-20.
OS Homo sapiens.
XX
XX WO2004074453-A2.
XX
XX 02-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005092.
XX
XX 20-FEB-2003; 2003US-0449059P.
XX
XX 19-MAR-2003; 2003US-0456932P.
XX
XX 28-MAR-2003; 2003US-0458644P.
XX
XX 09-APR-2003; 2003US-0461678P.
XX
XX 17-APR-2003; 2003US-0463937P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Ramkumar J, Marguis JP, Swarnakar A, Chawla NK, Tran UK,
XX Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
XX Jackson AA, Yang J, Gorvad AE;
XX WPI; 2004-635568/61.
XX
XX N-PSDB; ADR39793.
XX
XX New human kinases and phosphatases (KPP) for diagnosing, treating and
XX preventing diseases or conditions associated with aberrant KPP expression
XX e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX
XX Claim 1; SEQ ID NO 20; 299pp; English.

XX The present sequence represents the human kinase and phosphatase protein
CC (KPP), designated KPP-20. The human KPP sequences from the present
CC invention have cytosolic, antiarteriosclerotic, anticonvulsant,
CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thymomimetic activities, and can be used in gene
CC therapy. The human KPP proteins and polynucleotides can be used in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KPP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies, and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They can also be used in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
XX
SQ Sequence 1192 AA;
Query Match 100.0%; Score 40; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
Db 464 ALIAFLAFL 472
RESULT 17
ADQ39378 100.0%; Score 40; DB 8; Length 1192;
ID ADQ39378 standard; protein; 1219 AA.
XX ADQ39378;
AC
XX
DT 18-NOV-2004 (first entry)
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiac; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
XX
XX 10-MAR-2003; 2003US-0453135P.
XX
XX 30-APR-2003; 2003US-0466412P.
XX
XX 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JI, Iakubova O;
XX WPI; 2004-533949/51.
XX
XX N-PSDB; ADQ38550.
XX
XX Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1041; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's

CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiac activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

CC Sequence 1219 AA;

Query Match 100.0%; Score 40; DB 8; Length 1219;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
 |||||
 DB 491 ALIAFLAFL 499

RESULT 18
 ADM67187

ID ADM67187 standard; protein; 1256 AA.

AC ADM67187;

DT 03-JUN-2004 (first entry)

DE Human adipocyte specific PTPase receptor type C protein Segid 541.

XX human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group 1-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; PTPase receptor type C.

OS Homo sapiens.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMG-) HMG- INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66908.

XX Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.

PS Disclosure; SEQ ID NO 541; 91pp; English.

XX This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti
 CC -obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group 1-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.

XX Sequence 1256 AA;

Query Match 100.0%; Score 40; DB 8; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
 |||||
 DB 528 ALIAFLAFL 536

RESULT 19
 ADP12966

ID ADP12966 standard; protein; 1256 AA.

AC ADP12966;

DT 12-AUG-2004 (first entry)

DE Protein encoding reference mRNA sequence #51.

XX transplamt rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

OS Homo sapiens.

PN WO2004042346-A2.

PD 21-MAY-2004.

PF 24-APR-2003; 2003WO-US012946.

PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

DR WPI; 2004-400724/37.

XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.

PS Claim 65; SEQ ID NO 2975; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprising detecting the expression level of one or more genes. The

CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein encoded by an mRNA sequence of the invention which show altered
 CC expression in renal transplantation and expression.

CC Sequence 1256 AA;

CC Query Match 100.0%; Score 40; DB 8; Length 1256;

CC Best Local Similarity 100.0%; Pred. No. 47;

CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9

DB 528 ALIAFLAFL 536

RESULT 20

ADQ39376 standard; protein; 1258 AA.

ADQ39376;

18-NOV-2004 (first entry)

Human myocardial infarction-associated gene derived protein, SEQ ID 1039.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiant; gene therapy; human.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.

10-MAR-2003; 2003US-0453135P.

30-APR-2003; 2003US-0466412P.

23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Takoubova O;

WPI; 2004-533949/51.

myocardial infarction by detecting a single nucleotide polymorphism in

the individual's nucleic acids.

Claim 10; SEQ ID NO 1039; 145bp; English.

The invention relates to a novel method for identifying an individual who
 has an altered risk for developing myocardial infarction. The method
 comprises detecting a single nucleotide polymorphism (SNP) in any one of
 the nucleotide sequences given in the specification in the individual's
 nucleic acids, where the presence of the SNP is correlated with an
 altered risk for myocardial infarction in the individual. The invention
 further comprises: an isolated nucleic acid molecule comprising at least
 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 the specification or its complement and encoding any one of the amino
 acid sequences given in the specification; an isolated polypeptide
 comprising an amino acid sequence given in the specification; an antibody

CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

CC Sequence 1258 AA;

CC Query Match 100.0%; Score 40; DB 8; Length 1258;

CC Best Local Similarity 100.0%; Pred. No. 47;

CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9

DB 530 ALIAFLAFL 538

RESULT 21

ADQ39379 standard; protein; 1267 AA.

ADQ39379;

18-NOV-2004 (first entry)

Human myocardial infarction-associated gene derived protein, SEQ ID 1042.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiant; gene therapy; human.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.

10-MAR-2003; 2003US-0453135P.

30-APR-2003; 2003US-0466412P.

23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Takoubova O;

WPI; 2004-533949/51.

myocardial infarction by detecting a single nucleotide polymorphism in

the individual's nucleic acids.

Claim 10; SEQ ID NO 1042; 145bp; English.

The invention relates to a novel method for identifying an individual who
 has an altered risk for developing myocardial infarction. The method
 comprises detecting a single nucleotide polymorphism (SNP) in any one of
 the nucleotide sequences given in the specification in the individual's
 nucleic acids, where the presence of the SNP is correlated with an
 altered risk for myocardial infarction in the individual. The invention

CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction.
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

SQ Sequence 1267 AA;

Query Match 100.0%; Score 40; DB 8; Length 1267;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 539 ALIAFLAFL 547

RESULT 22

ABU05243 ID ABU05243 standard; protein; 1304 AA.

XX AC ABU05243;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1909.

XX DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX KW protease; protease inhibitor; transporter; cytoskeletal protein;

XX KW receptor; transcription factor; cancer; MHC; colon cancer; gastric cancer;

XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chiciz RM, Tomlinson AJ, Urban RG;

XX DR MPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PR leukemia.
XX Example 2; SEQ ID NO 1909; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1304 AA;

Query Match 100.0%; Score 40; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAFL 9
|||
DB 576 ALIAFLAFL 584

RESULT 23

ABU05241 ID ABU05241 standard; protein; 1304 AA.

XX AC ABU05241;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1907.

XX DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX KW protease; protease inhibitor; transporter; cytoskeletal protein;

XX KW receptor; transcription factor; cancer; MHC; colon cancer; gastric cancer;

XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chiciz RM, Tomlinson AJ, Urban RG;

XX DR MPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 40; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
Db 576 ALIAFLAFL 584
XX
RESULT 24
ABU05244
XX ID ABU05244 standard; protein; 1304 AA.
XX AC ABU05244;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1910.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.
XX
PS Example 2; SEQ ID NO 1910; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 40; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
Db 576 ALIAFLAFL 584
XX
RESULT 25
ADL16230
XX ID ADL16230 standard; protein; 1304 AA.
XX AC ADL16230;
XX DT 06-MAY-2004 (first entry)
XX DE Human protein tyrosine phosphatase #26.
XX KW cytostatic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX OS Homo sapiens.
XX PN WO2003068984-A2.
XX PD 21-AUG-2003.
XX PF 13-FEB-2003; 2003WO-EP001446.
XX PR 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-00366547.
XX PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTIR INC.
XX PI Tonks NK, Tzu-Ching M, Cool DE;
XX DR WPI; 2003-712572/67.
XX DR N-PDDB; ADL16229.
XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
XX cancer or autoimmune disease.
PS Disclosure; SEQ ID NO 79; 238pp; English.

XX The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (ii) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host diseases; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 40; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
DB 576 ALIAFLAFL 584
XX
RESULT 26
ADP65158
ID ADP65158 standard; protein; 1304 AA.
AC ADP65158;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
XX
KW autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
OS Homo sapiens.
XX
PN MO2003072827-A1.
XX
PD 04-SEP-2003.
XX
PF 31-OCT-2002; 2002WO-US035433.
XX
PR 31-OCT-2001; 2001US-0336220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thorton SL;
XX
DR MPI: 2003-712740/67.
XX
DR GENBANK; NP_002829.
XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
PS Disclosure; Page; 56pp; English.
XX
CC The invention relates to a novel method for diagnosing and analyzing

CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 40; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
DB 576 ALIAFLAFL 584
XX
RESULT 27
ADM67209
ID ADM67209 standard; protein; 1304 AA.
AC ADM67209;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human adipocyte specific leukocyte common antigen protein SegID 563.
XX
KW human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; leukocyte common antigen.
XX
OS Homo sapiens.
XX
PN MO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
XX
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMG-) HMG- INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR MPI: 2004-143846/14.
XX
DR N-PSDB; ADM66930.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of

PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 563; 91bp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin. Furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C^{-/-}, ob/ob, or HMGI-C^{-/-} ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 40; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ALIAPLAF 9
Db 576 ALIAPLAF 584
XX
RESULT 28
ABO84455
ID ABO84455 standard; protein; 1304 AA.
XX
AC ABO84455;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP13-011.2.
XX
KM Human: Cancer-associated protein; cytostatic; cancer; leukemia;
XX lymphoma; CAP.
XX
OS Homo sapiens.
XX
PN MO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
XX
PR 14-MAR-2003; 2003US-00388838.
XX
PR 15-APR-2003; 2003US-00417375.
XX
PR 13-JUN-2003; 2003US-00461862.
XX
PR 15-SEP-2003; 2003US-00663431.
XX
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
DR WPI; 2004-652914/63.
XX
DR N-PSDB; ABD32626.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.

PS claim 18; seqid 147; 310bp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acid encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 40; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ALIAPLAF 9
Db 576 ALIAPLAF 584
XX
RESULT 29
ADQ39380
ID ADQ39380 standard; protein; 1304 AA.
XX
AC ADQ39380;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiac; gene therapy; human.
XX
OS Homo sapiens.
XX
PN MO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US0040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
XX
PR 30-APR-2003; 2003US-0466412P.
XX
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.

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XX Cargill M, Devlin JJ, Iakubova O;
XX WPI; 2004-533949/51.
XX N-Psdb; ADQ38552.
XX
XX Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1043; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide
XX comprising an amino acid sequence given in the specification; an antibody
XX that specifically binds to the polypeptide or its antigen-binding
XX fragment; an amplified polynucleotide containing an SNP given in the
XX specification and which is between about 16 and 1000 nucleotides in
XX length; a kit for detecting an SNP in a nucleic acid, comprising the
XX polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX method for identifying an agent useful in treating or preventing
XX myocardial infarction. The novel detection method has cardiant activity.
XX The nucleic acids of the invention may be used in gene therapy. The
XX method is useful in identifying an individual who has an increased or
XX decreased risk for developing myocardial infarction and for preparing a
XX composition for treating or preventing myocardial infarction. This
XX sequence represents the protein of a human myocardial infarction-
XX associated gene containing one or more SNP's of the invention. Note: This
XX sequence was not shown in the specification. The sequence has come from
XX an electronic sequence listing downloaded from the WIPO website.
XX
XX SQ Sequence 1304 AA;
XX
XX Query Match 100.0%; Score 40; DB 8; Length 1304;
XX Best Local Similarity 100.0%; Pred. No. 48;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ALIAFLAFL 9
XX
XX Db 576 ALIAFLAFL 584
XX
XX RESULT 30
XX ADQ39375 100.0%; Score 40; DB 8; Length 1306 AA.
XX ID ADQ39375 standard; protein; 1306 AA.
XX
XX AC ADQ39375;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
XX
XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiac; gene therapy; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004058052-A2.
XX
XX PD 15-JUL-2004.
XX
XX PF 22-DEC-2003; 2003WO-US040978.
XX
XX PR 20-DEC-2002; 2002US-0434778P.

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PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
PR
PR (APPL-) APPLERA CORP.
PR
PR Cargill M, Devlin JJ, Iakubova O;
PR WPI; 2004-533949/51.
PR N-Psdb; ADQ38547.
PR
PR Identifying an individual who has an altered risk for developing
PR myocardial infarction by detecting a single nucleotide polymorphism in
PR the individual's nucleic acids.
PR
PR Claim 10; SEQ ID NO 1038; 145pp; English.
PR
PR The invention relates to a novel method for identifying an individual who
PR has an altered risk for developing myocardial infarction. The method
PR comprises detecting a single nucleotide polymorphism (SNP) in any one of
PR the nucleotide sequences given in the specification in the individual's
PR nucleic acids, where the presence of the SNP is correlated with an
PR altered risk for myocardial infarction in the individual. The invention
PR further comprises: an isolated nucleic acid molecule comprising at least
PR 8 contiguous nucleotides where one of the nucleotides is an SNP given in
PR the specification or its complement and encoding any one of the amino
PR acid sequences given in the specification; an isolated polypeptide
PR comprising an amino acid sequence given in the specification; an antibody
PR that specifically binds to the polypeptide or its antigen-binding
PR fragment; an amplified polynucleotide containing an SNP given in the
PR specification and which is between about 16 and 1000 nucleotides in
PR length; a kit for detecting an SNP in a nucleic acid, comprising the
PR polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
PR nucleic acid molecule; a method of detecting a variant polypeptide; and a
PR method for identifying an agent useful in treating or preventing
PR myocardial infarction. The novel detection method has cardiant activity.
PR The nucleic acids of the invention may be used in gene therapy. The
PR method is useful in identifying an individual who has an increased or
PR decreased risk for developing myocardial infarction and for preparing a
PR composition for treating or preventing myocardial infarction. This
PR sequence represents the protein of a human myocardial infarction-
PR associated gene containing one or more SNP's of the invention. Note: This
PR sequence was not shown in the specification. The sequence has come from
PR an electronic sequence listing downloaded from the WIPO website.
PR
PR SQ Sequence 1306 AA;
PR
PR Query Match 100.0%; Score 40; DB 8; Length 1306;
PR Best Local Similarity 100.0%; Pred. No. 48;
PR Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR
PR QY 1 ALIAFLAFL 9
PR
PR Db 578 ALIAFLAFL 586
PR
PR Search completed: May 3, 2005, 07:34:52
PR Job time : 71.6757 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-3

Perfect score: 43

Sequence: 1 KLFYAKLV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	1304	1 A46546	leukocyte common a
2	37	86.0	285	2 G90485	conserved hypochet
3	34	79.1	172	2 B96518	protein T26.12 [1
4	34	79.1	577	2 T30067	hypothetical prote
5	33	76.7	392	1 C69851	macrolide glycosyl
6	33	76.7	678	2 D82415	exoribonuclease II
7	32	74.4	205	2 I54685	pepa protein - Bsc
8	32	74.4	539	2 C91081	sulfite reductase
9	32	74.4	539	2 D85926	sulfite reductase
10	32	74.4	796	2 T20091	hypothetical prote
11	31	72.1	174	2 A71208	hypothetical prote
12	31	72.1	351	2 S52144	glycosyl transfera
13	31	72.1	680	2 T29871	hypothetical prote
14	30	69.8	174	2 T31133	biphenyl dioxygena
15	30	69.8	180	2 P70454	hypothetical prote
16	30	69.8	234	2 P90368	hypothetical prote
17	30	69.8	262	2 C84711	probable tropinone
18	30	69.8	338	2 T41448	hypothetical prote
19	30	69.8	510	2 C86209	protein P22G5.20 (
20	30	69.8	917	2 T05430	hypothetical prote
21	30	69.8	2278	1 S56274	FAB1 protein - yea
22	29	67.4	109	1 S55497	chlorodoxin - Salm
23	29	67.4	109	1 TXEC	chlorodoxin [valid
24	29	67.4	109	2 AF0922	chlorodoxin [impor
25	29	67.4	127	2 B91218	chlorodoxin I [imp
26	29	67.4	127	2 C86064	chlorodoxin I [imp
27	29	67.4	213	2 S73811	MG248 homolog H91
28	29	67.4	217	2 E81316	probable integral
29	29	67.4	223	2 D64613	cell division prot

30	29	67.4	236	2 E83879	hypothetical prote
31	29	67.4	250	1 Q0V2F2	F2 protein - vacci
32	29	67.4	250	2 H42512	23k myristylated I
33	29	67.4	250	2 G72159	NIR protein - vari
34	29	67.4	250	2 S33087	LIR protein - vari
35	29	67.4	250	2 T28511	hypothetical prote
36	29	67.4	256	2 S77176	cell-cell signalin
37	29	67.4	278	2 C70244	antigen, p35 homol
38	29	67.4	278	2 E70244	hypothetical prote
39	29	67.4	284	2 C64527	M protein - Helico
40	29	67.4	285	2 B90445	regucalcin homolog
41	29	67.4	330	2 T25940	hypothetical prote
42	29	67.4	358	2 S73776	MG269 homolog P11
43	29	67.4	360	2 AB3496	glucanate 2-dehydr
44	29	67.4	378	2 D70324	hypothetical prote
45	29	67.4	379	2 S55845	3-isopropylmalate

ALIGNMENTS

RESULT 1
A46546
Leukocyte common antigen long splice form precursor - human
N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote:
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A46546; B46546; C46546; A29449; B29449; I57658
R:Steuell, M.; Hall, L.R.; Saga, Y.; Schlozman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs encod
A:Reference number: A46546; MUID:88061067; PMID:2824653
A:Accession: A46546
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1304 <STR>
A:Cross-references: UNIPROT:P08575; GB:Y00638
A:Experimental source: clone LCA.111 and clone LCA.260
A:Accession: B46546
A:Molecule type: mRNA
A>Status: preliminary
A:Residues: 1-32,99-264 <ST2>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.111 and clone LCA.260
A:Accession: C46546
A:Molecule type: mRNA
A>Status: preliminary
A:Residues: 1-31,193-264 <ST3>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.1
A:Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A:Reference number: A91066; MUID:87275816; PMID:2956090
A:Accession: A29449
A:Molecule type: mRNA
A:Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
A:Cross-references: GB:Y00662; NID:934275; PIDN:CA68269.1; PID:G34276
A:Experimental source: clones pHLc-1 and lambdaHLG1
A:Accession: B29449
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 32-192 <RA2>
A:Experimental source: clone HLC-2
R:Tsal, A.Y.; Steuelli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative s
A:Reference number: I57658; MUID:90066468; PMID:2531281
A:Accession: I57658
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:g187020; PIDN:AA59497.1; PID:g553521
C:Genetics:
A:Gene: GDB:PTPRC; CD45
A:Cross-references: GDB:119768; OMIM:151460
A:Map position: 1q31-1q32
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:575-899/Domain: protein-tyrosine-phosphatase homology <PTP>
F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 43; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
|||||
Db 244 KLFYAKLV 252

RESULT 2
G90485
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90485
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Ueffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F
arrett, R.A.; Ragan, M.A.; Senese, C.W.; Van der Oost, J.
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90485
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-285 <KUR>
A:Cross-references: UNIPROT:Q97UH7; GB:AE006641; NID:g1816441; PIDN:AAK3142.1; GSPDB:G
C:Genetics:
A:Gene: SSO3041
C:Superfamily: senescence marker protein-30

Query Match 86.0%; Score 37; DB 2; Length 285;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
|||||
Db 267 RLFYAKLV 275

RESULT 3
E96518
protein T2E6.12 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96518
R:Rheologs, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, I.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96518
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-172 <STO>
A:Cross-references: UNIPROT:Q9FZF7; GB:AE005173; NID:g9802600; PIDN:AAF99802.1; GSPDB:GN

C:Genetics:
A:Gene: T2E6.12
A:Map position: 1

Query Match 79.1%; Score 34; DB 2; Length 172;
Best Local Similarity 77.8%; Pred. No. 5.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
|||||
Db 30 KLFYAKLV 38

RESULT 4
T30067
hypothetical protein Cl2D5.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T30067
R:Miller, N.; Stelly, L.; Bradshaw, H.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid Cl2D5.
A:Reference number: Z20729
A:Accession: T30067
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-577 <MLT>
A:Cross-references: EMBL:U53565; PIDN:AA98572.1; GSPDB:GN00023; CESP:Cl2D5.8
A:Experimental source: strain Bristol N2; clone Cl2D5
C:Genetics:
A:Gene: CESP:Cl2D5.8
A:Map position: 5
A:Introns: 11/1; 29/3; 77/3; 232/3; 260/2; 319/2; 371/1; 451/3; 523/3

Query Match 79.1%; Score 34; DB 2; Length 577;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
|||||
Db 378 KLFYAKLV 386

RESULT 5
C69851
macrolide glycosyltransferase homolog yj1c - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: C69851
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Gallizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koeber, P.; Koningsstein, G.; Krogan, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Manel
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetle
Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadde, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroefer, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunori, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dancho, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C69851
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-392 <KUN>
A:Cross-references: UNIPROT:Q34539; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CA813079.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yj1c

C:Superfamily: glycosyltransferase

Query Match 76.7%; Score 33; DB 1; Length 392;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
||| ||||
Db 113 KLFYAKLV 121

RESULT 6
D82415
exoribonuclease II VCA0805 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82415
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bae, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406: 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82415
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1678 <HEI>
A:Cross-references: UNIPROT:Q9KLE1; GB:AE004408; GB:AE003853; NID:9658225; PIDN:AAF9670
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0805
A:Map position: 2
C:Superfamily: exoribonuclease II

Query Match 76.7%; Score 33; DB 2; Length 678;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
||| ||||
Db 91 KLFYAKLV 99

RESULT 7

154685
Pera protein - Escherichia coli
C:Species: Escherichia coli
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 07-Jun-1996
C:Accession: 154685

R:Gomez-Duarte, O.G.; Kaper, J.B.
Infect. Immun. 63, 1767-1776, 1995
A>Title: A plasmid-encoded regulatory region activates chromosomal eaeA expression in enterobacteria.
A:Reference number: 154685; MUID:95247259; PMID:7729884
A:Accession: 154685
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1205 <RES>
A:Cross-references: EMBL:Z48561; NID:9695508; PID:9695509

Query Match 74.4%; Score 32; DB 2; Length 205;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLFYAKLV 8
||| ||||
Db 39 KLFYAKLV 46

RESULT 8

C91081
sulfite reductase (NADPH) beta subunit [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: C91081

R:Havashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91081
A:Status: Preliminary
A:Map position: 2
A:Molecule type: DNA
A:Residues: 1599 <HAY>
A:Cross-references: UNIPROT:Q8X7U1; GB:BA000007; PIDN:BA037042.1; PID:G13363090; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECG3619
C:Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferredoxin protein

C:Keywords: Flavoprotein

Query Match 74.4%; Score 32; DB 2; Length 599;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFTYAKLV 9
||| ||||
Db 86 LFTYAKLV 93

RESULT 9

D85926
sulfite reductase (NADPH) beta subunit [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85926

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Llim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85926
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1599 <STO>
A:Cross-references: UNIPROT:Q8X7U1; GB:AE005174; NID:G12517225; PIDN:AA057872.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: cysJ
C:Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH-ferredoxin protein

C:Keywords: Flavoprotein

Query Match 74.4%; Score 32; DB 2; Length 599;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFTYAKLV 9
||| ||||
Db 86 LFTYAKLV 93

RESULT 10

T20091
hypothetical protein C50B6.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20091

R:Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19222
A:Accession: T20091
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-796 <WIL>
A:Cross-references: UNIPROT:P91983; EMBL:Z81050; PIDN:CA02857.1; GSPDB:GN00023; CESP:C5
A:Experimental source: clone C50B6
C:Genetics:

A:Gene: CESP:C50B6.8
 A:Map position: 5
 A:Introns: 215/3; 316/2; 352/1; 430/3; 494/1; 587/3; 624/2; 664/1; 675/2; 711/1

Query Match
 Best Local Similarity 74.4%; Score 32; DB 2; Length 796;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

Query Match
 Best Local Similarity 75.0%; Score 31; DB 2; Length 680;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

RESULT 11

A71208
 hypothetical protein PH1929 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
 C:Accession: A71208

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic e
 A:Reference number: A71000; M01D:98344137; PMID:9679194
 A:Accession: A71208

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-174 <KAM>

A:Cross-references: UNIPROT:O59592; GB:AP000007; NID:G3236134; P1DN:BA31056.1; PID:G325
 A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1929

Query Match
 Best Local Similarity 72.1%; Score 31; DB 2; Length 174;
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

Query Match
 Best Local Similarity 66.7%; Score 24;
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

RESULT 12

S52144
 glycosyl transferase amed - Erwinia amylovora

C:Species: Erwinia amylovora
 C:Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S61897; S52144

R:Bugert, P.; Geider, K.
 Mol. Microbiol. 15, 917-933, 1995
 A:Title: Molecular analysis of the amc operon required for exopolysaccharide synthesis c
 A:Reference number: S61891; M01D:95319333; PMID:7596293
 A:Accession: S61897

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-351 <BU2>
 A:Cross-references: UNIPROT:Q46634; EMBL:X77921; NID:G600426; P1DN:CAA54885.1; PID:G6004

Query Match
 Best Local Similarity 72.1%; Score 31; DB 2; Length 351;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

Query Match
 Best Local Similarity 75.0%; Score 31; DB 2; Length 351;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

RESULT 13

T29871
 hypothetical protein F32B5.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29871

R:Ledwith, J.; Graves, T.; Biewald, T.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid F32B5.
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

Query Match
 Best Local Similarity 85.7%; Score 31; DB 2; Length 680;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

Query Match
 Best Local Similarity 85.7%; Score 31; DB 2; Length 680;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

Query Match
 Best Local Similarity 85.7%; Score 31; DB 2; Length 680;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

Query Match
 Best Local Similarity 85.7%; Score 31; DB 2; Length 680;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

Query Match
 Best Local Similarity 85.7%; Score 31; DB 2; Length 680;
 A:Reference number: Z20702
 A:Accession: T29871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <LED>
 A:Cross-references: UNIPROT:O01849; EMBL:AF003148; P1DN:AA54209.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone F32B5
 C:Genetics:
 A:Map position: 1
 A:Introns: 65/3; 102/3; 125/2; 175/3; 223/3; 493/2; 551/3; 633/1

RESULT 14

T31133
 biphenyl dioxygenase homolog - Sphingomonas aromaticivorans plasmid pNL1

C:Species: Sphingomonas aromaticivorans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T31133

R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
 submitted to the EMBL Data Library July 1998
 A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatic
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

Query Match
 Best Local Similarity 69.8%; Score 30; DB 2; Length 174;
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

Query Match
 Best Local Similarity 55.6%; Score 24;
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

Query Match
 Best Local Similarity 55.6%; Score 24;
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

Query Match
 Best Local Similarity 55.6%; Score 24;
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

RESULT 15

F70454
 hypothetical protein ag_1795 - Aquifex aeolicus

C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C:Accession: F70454

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; M01D:98196666; PMID:9537320
 A:Accession: F70454

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-180 <AGF>
 A:Cross-references: UNIPROT:O67664; GB:AE000756; NID:G2984076; P1DN:AA07626.1; PID:G298
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: ag_1795

Query Match
 Best Local Similarity 55.6%; Score 24;
 A:Reference number: Z20992
 A:Accession: T31133
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-174 <ROM>
 A:Cross-references: UNIPROT:O85842; EMBL:AF079317; NID:G3378261; PID:G3378274; P1DN:AA001
 C:Genetics:
 A:Genome: plasmid pNL1
 A:Note: bphA2f
 C:Superfamily: toluene dioxygenase terminal oxygenase component small chain

Query Match 69.8%; Score 30; DB 2; Length 180;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
|:| | | |
Db 71 KIFIKLV 79

Search completed: May 3, 2005, 06:14:57
Job time : 24.6892 secs

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DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	PTPRC protein (Fragment).
GN	Name=PTPRC;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Primary B-Cells;
RX	MEBLINR=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Groue L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner I., Shermen C.M., Schuler G.D.,
RA	Ahschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stepleman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshynki S., Carrinci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywnicki M.I., Skalske U., Smallus D.E., Schnerch A., Schein J.E.,
RA	James S.J., Maria M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RL	and mouse cDNA sequences."
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP	(2)
RP	SEQUENCE FROM N.A.
RC	TISSUE=Primary B-Cells;
RL	Submitted (SEP-2001) to the EMBL/genbank/DDST databases.
DR	EMBL; BC014238; AAH14238.1; ..
DR	HSSP; P18031; IAAX.
DR	GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR	InterPro; IPR003961; FN III.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR00242; Tyr_PP.
DR	Pfam; PF00041; fn3; 2.
DR	Pfam; PF00102; Y_phosphatase; 1.
DR	PRINTS; PR00700; PRTYPPHTASE.
DR	SMART; SM00194; PTPc; 1.
DR	PROSITE; PS00853; FN3; 2.
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
FT	NON TER
SQ	SEQUENCE 756 AA; 85430 MW; 8A9A863827BD69E6 CRC64;
QY	Query Match 100.0%; Score 48; DB 2; Length 756;
BT	Best Local Similarity 100.0%; Pred. No. 0.63;
Matches	%; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MIMBOKATV 9
	689 MIMBOKATV 697
RESULT 3	
ID	08CG07 PRELIMINARY; PRT; 878 AA.
AC	08CG07;
DT	01-MAR-2003 (TREMBlrel. 23, Created)
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-
DE	length enriched library, clone:E230015G23 product:protein tyrosine
DE	phosphatase, receptor type, C, full insert sequence. (fragment).
GN	Name=Ptpicc;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carminci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse expression transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=204939374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carminci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT "Normaliation and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20530933; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carminci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishige K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carminci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shingawa A., Shitaki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AK054056; BAC35538.1; --
DR HSSB, P18052; 1YFO.
DR MGD, MGI:97810; Ptpcr.
DR GO, GO:0009897; C:external side of plasma membrane; IDA.
DR GO, GO:0016021; C:integral to membrane; TAS.
DR GO, GO:0005515; F:protein binding; IPI.
DR GO, GO:0030183; P:B-cell differentiation; IMP.
DR GO, GO:0042100; P:B-cell proliferation; IMP.
DR GO, GO:0030217; P:T-cell differentiation; IMP.

DR GO:0042098; P-T-cell proliferation; IMP.
 DR GO:0046652; P-thymocyte differentiation; IMP.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00041; fn3; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRYPPHTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS50853; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase; Receptor.
 FT NON_TER 878 878
 SQ SEQUENCE 878 AA; 99891 MW; 19E5FCD7909D4CA6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 878;
 Best Local Similarity 100.0%; Pred. No. 0.73;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
 |||||
 DB 589 MIMOKATV 597

RESULT 4
 ID 06LDZ3 PRELIMINARY; PRT; 962 AA.
 AC 06LDZ3;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Leukocyte common antigen.
 GN Name=L-CA;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Spiguel-Davey;
 RX MEDLINE=85201691; PubMed=3158393; DOI=10.1016/0092-8674(85)90063-7;
 RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;
 RT "Evidence from cDNA clones that rat leukocyte-common antigen (T200)
 RT spans the lipid bilayer and contains a cytoplasmic domain of 80,000 M-
 RT r.";
 RL Cell 41:83-93(1985).
 DR EMBL: M10072; AAA1513.1; -.
 DR HSSP: P18031; 1A5Y.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR003595; PTPC motif.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRYPPHTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 2.
 DR SMART: SM00404; PTPC motif; 2.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolyase.
 SQ SEQUENCE 962 AA; 109934 MW; D2B6B7F23D29CC92 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 962;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
 |||||
 DB 397 MIMOKATV 405

RESULT 5
 ID CD45_MOUSE STANDARD; PRT; 1152 AA.
 AC P06800;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (BC 3.1.3.48) (L-CA) (lymphocyte
 DE common antigen Ly-5) (CD45) (T200).
 GN Name=Ptpcr; Synonyms=Ly-5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86313686; PubMed=2944116;
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RT "Sequences of Ly-5 cDNA: Isoform-related diversity of Ly-5 mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
 RN [2]
 RP REVISIONS.
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
 RN [3]
 RP SEQUENCE OF 10-124 FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=86042665; PubMed=3864163;
 RA Shen F.-W., Saga Y., Litman G., Freeman G., Tung J.-S., Cantor H.,
 RA Boyse E.A.;
 RT "Cloning of Ly-5 cDNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
 RN [4]
 RP SEQUENCE OF 822-1152 FROM N.A.
 RX MEDLINE=87092355; PubMed=2948186;
 RA Raschke W.C.;
 RT "Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B-
 RT and T-lymphocyte lineages.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
 RN [5]
 RP INTERACTIONS WITH GAMMA AND PRKCSH.
 RX MEDLINE=97294720; PubMed=9148925; DOI=10.1074/jbc.272.20.13117;
 RA Arendt C.W., Ostergaard H.L.;
 RT "Identification of the CD45-associated 116-kDa and 80-kDa proteins as
 RT the alpha- and beta-subunits of alpha-glucosidase II.";
 RL J. Biol. Chem. 272:13117-13125(1997).
 CC -!- FUNCTION: Required for T-cell activation through the antigen
 CC receptor. The first PTPase domain has enzymatic activity, while
 CC the second one seems to affect the substrate specificity of the
 CC first one.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBUNIT: Binds GAMMA and PRKCSH.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;
 CC IsoId=P06800-1; Sequence=Displayed;
 CC -!- DEVELOPMENTAL STAGE: Expression is restricted to the hematopoietic
 CC compartment of development.
 CC -!- PTM: Heavily N- and O-glycosylated.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 1/6 subfamily.

CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
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 CC -----
 CC EMBL; M14342; AAA39458.1; -
 CC EMBL; M11934; AAA39461.1; -
 CC EMBL; M15174; AAA40161.1; -
 CC PIR; A23329; A23329.
 CC PIR; A28334; A28334.
 CC HSSP; P18052; 1YFO.
 CC MGD; MG1:97810; PCPRC.
 CC GO; GO:0008997; C:external side of plasma membrane; IDA.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR000387; TYR_phosphatase.
 CC Pfam; PF00041; fn3; 3.
 CC Pfam; PF00102; Y_phosphatase; 2.
 CC PRINTS; PR00700; TRYPHPTASE.
 CC PROSITE; PS50853; FN3; 2.
 CC PROSITE; PS500383; TYR_PHOSPHATASE_1; 2.
 CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 CC KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;
 CC Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 CC Transmembrane.
 CC FT SIGNAL 1 23
 CC FT CHAIN 24 1152
 CC FT DOMAIN 24 425
 CC FT TRANSMEM 426 447
 CC FT DOMAIN 448 1152
 CC FT DOMAIN 232 328
 CC FT DOMAIN 333 420
 CC FT DOMAIN 520 769
 CC FT DOMAIN 811 1084
 CC FT ACT_SITE 701 701
 CC FT ACT_SITE 1016 1016
 CC FT ACT_SITE 1016 1016
 CC FT CARBOHYD 68 68
 CC FT CARBOHYD 72 72
 CC FT CARBOHYD 79 79
 CC FT CARBOHYD 114 114
 CC FT CARBOHYD 119 119
 CC FT CARBOHYD 151 151
 CC FT CARBOHYD 172 172
 CC FT CARBOHYD 183 183
 CC FT CARBOHYD 208 208
 CC FT CARBOHYD 277 277
 CC FT CARBOHYD 288 288
 CC FT CARBOHYD 318 318
 CC FT CARBOHYD 350 350
 CC FT CARBOHYD 379 379
 CC FT CARBOHYD 1152 1152
 CC FT SEQUENCE 1152 AA; 130421 MW; BAD956B4E32BA812 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIMBOKATV 9
 |||||
 DB 587 MIMBOKATV 595

RESULT 6

CC CD45_RAT
 ID CD45_RAT STANDARD; PRT; 1255 AA.
 AC P04157;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen variant 4 precursor (EC 3.1.3.48) (L-CN)
 DE (CD45) (T200) (Fragment).
 CN Name=Ppargc;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;
 RL Submitted (MAY-1987) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 190-1255 FROM N.A.
 RX MEDLINE=85201691; PubMed=3158393; DOI=10.1016/0092-8674(85)90063-7;
 RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;
 RT "Evidence from cDNA clones that the rat leukocyte-common antigen
 RT (T200) spans the lipid bilayer and contains a cytoplasmic domain of
 RT 80,000 Mr.";
 RL Cell 41:83-93 (1985).
 RN [3]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=87275817; PubMed=2440674;
 RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;
 RT "Lymphocyte specific heterogeneity in the rat leukocyte common antigen
 RT (T200) is due to differences in polypeptide sequences near the NH2-
 RT terminus.";
 RL EMBO J. 6:1259-1264 (1987).
 CC -1- FUNCTION: Required for T-cell activation through the antigen
 CC receptor. The first PTPase domain has enzymatic activity, while
 CC the second one seems to affect the substrate specificity of the
 CC first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2O) = protein
 CC tyrosine + phosphate.
 CC -1- SUBUNIT: Binds GNNAB and PRKSH (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P04157-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P04157-2; Sequence=VSP_005167;
 CC Name=3;
 CC IsoId=P04157-3; Sequence=VSP_005166;
 CC Name=4;
 CC IsoId=P04157-4; Sequence=VSP_005165, VSP_005168;
 CC -1- TISSUE SPECIFICITY: Variants 4 and 3 are found in the lymph node,
 CC variants 1 and 2 are found in thymocyte and lymph node.
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- PTM: The cytoplasmic domain contains potential phosphorylation
 CC sites.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 1/6 subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y00065; CAA68272.1; -
 CC EMBL; Y00065; CAA68273.1; -
 CC EMBL; Y00065; CAA68274.1; -

DR EMBL; Y00065; CAA68275.1; -
 DR EMBL; M25820; AAA41518.1; -
 DR EMBL; M25821; AAA41519.1; -
 DR EMBL; M25822; AAA41520.1; -
 DR EMBL; M25823; AAA41521.1; -
 DR HSSP; P18052; LYFO.
 DR RGD; 3451; Pcpic.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR00387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PSS0853; FN3_2.
 DR PROSITE; PSS0383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
 DR Alternative splicing; Antigen; Glycoprotein; Hydrolase;
 KM Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 KM Transmembrane.
 FT NON_TER 1 1
 FT SIGNAL <1 5
 FT CHAIN 6 1255
 FT DOMAIN 6 528
 FT TRANSMEM 529 550
 FT DOMAIN 551 1255
 FT DOMAIN 343 431
 FT DOMAIN 436 523
 FT DOMAIN 623 872
 FT DOMAIN 914 1187
 FT ACT_SITE 804 804
 FT ACT_SITE 1119 1119
 FT ACT_SITE 1119 1119
 FT CARBOHYD 44 44
 FT CARBOHYD 124 124
 FT CARBOHYD 135 135
 FT CARBOHYD 146 146
 FT CARBOHYD 160 160
 FT CARBOHYD 182 182
 FT CARBOHYD 227 227
 FT CARBOHYD 232 232
 FT CARBOHYD 253 253
 FT CARBOHYD 264 264
 FT CARBOHYD 309 309
 FT CARBOHYD 315 315
 FT CARBOHYD 353 353
 FT CARBOHYD 356 356
 FT CARBOHYD 453 453
 FT CARBOHYD 484 484
 FT VARSPPLIC 12 53
 FT VARSPPLIC 12 102
 FT VARSPPLIC 53 143
 FT VARSPPLIC 103 143
 FT CONFLICT 38 38
 FT CONFLICT 1255 AA; 141208 MM; C257CBD2A355BCEA CRC64;
 SQ SEQUENCE

Query Match 100.0%; Score 48; DB 1; Length 1255;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
 DB 690 MIMOKATV 698

RESULT 7
 Q6ED60

ID Q6ED60 PRELIMINARY; PRT; 1290 AA.
 AC Q6ED60;
 DT 25-OCT-2004 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE CD45.
 OS Actus vociferans (Spix's owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15245371;
 RA Montoya G.B., Vernot J.P., Patatroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human."
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL; AA445818; AAS06903.1; -
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003595; PTPc motif.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00194; PTPc; 2.
 DR SMART; SM00404; PTPc motif; 2.
 DR PROSITE; PSS0853; FN3_2.
 DR PROSITE; PSS0383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrolase.
 SQ SEQUENCE 1290 AA; 145616 MM; 99E810C75D932824 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 1290;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
 DB 723 MIMOKATV 731

RESULT 8
 Q61812 PRELIMINARY; PRT; 1291 AA.
 AC Q61812;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Lymphocyte common antigen precursor.
 GN Name=Pcpic; Synonyms=Lys;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALB/c;
 RX MEDLINE=92361152; PubMed=1822988;
 RA Zebende S.L., Barilt D.S., Raschke W.C.;
 RT "Comparison of mouse Lys A and Lys B leukocyte common antigen
 RT alleles."
 RL Dev. Immunol. 1:243-254(1991).
 DR EMBL; M92933; AAA59459.1; -
 DR HSSP; P18052; LYFO.
 DR MGD; MGI:97810; Pcpic.
 DR GO; GO:000897; C:external side of plasma membrane; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.

QY 1 MIMOKATV 9
 DB 723 MIMOKATV 731

RESULT 8
 Q61812 PRELIMINARY; PRT; 1291 AA.
 AC Q61812;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Lymphocyte common antigen precursor.
 GN Name=Pcpic; Synonyms=Lys;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALB/c;
 RX MEDLINE=92361152; PubMed=1822988;
 RA Zebende S.L., Barilt D.S., Raschke W.C.;
 RT "Comparison of mouse Lys A and Lys B leukocyte common antigen
 RT alleles."
 RL Dev. Immunol. 1:243-254(1991).
 DR EMBL; M92933; AAA59459.1; -
 DR HSSP; P18052; LYFO.
 DR MGD; MGI:97810; Pcpic.
 DR GO; GO:000897; C:external side of plasma membrane; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0030183; P:B-cell differentiation; IMP.
 DR GO; GO:0042100; P:B-cell proliferation; IMP.
 DR GO; GO:0030217; P:T-cell differentiation; IMP.
 DR GO; GO:0042098; P:T-cell proliferation; IMP.
 DR GO; GO:0046652; P:lymphocyte differentiation; IMP.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRYPHPHTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS50953; FN3; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrolyase; Signal.
 FT SIGNAL 1
 SQ SEQUENCE 1291 AA; 144559 MW; 25C3CB61AF4350CE CRC64;

Query Match 100.0%; Score 48; DB 2; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9
 DB 726 MIMBOKATV 734

RESULT 9
 06ED61 PRELIMINARY; PRT; 1303 AA.

AC 06ED61 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CD45.
 OS Aotus nancymae (Macaque night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human."
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL; AY445817; AAS06902.1; -;
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003595; PTPC motif.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRYPHPHTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC_motif; 2.
 DR PROSITE; PS50953; FN3; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolyase.
 SQ SEQUENCE 1303 AA; 146929 MW; DDBB0C640D1017B8 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 1303;
 Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMBOKATV 9
 DB 736 MIMBOKATV 744

RESULT 10
 06ED62 PRELIMINARY; PRT; 1303 AA.

AC 06ED62 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CD45.
 OS Aotus nigriceps (Black-headed owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human."
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL; AY445816; AAS06901.1; -;
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003595; PTPC motif.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRYPHPHTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC_motif; 2.
 DR PROSITE; PS50953; FN3; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolyase.
 SQ SEQUENCE 1303 AA; 146586 MW; 9BB023BEF4BC1165 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 1303;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9
 DB 736 MIMBOKATV 744

RESULT 11

ID CD45_HUMAN STANDARD; PRT; 1304 AA.
 AC P08575; Q1614; Q9H0Y6;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CAN) (CD45 antigen)
 DE (T200).
 GN Name=PTPRC; Synonyms=CD45;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOPFORM 1), AND ALTERNATIVE SPLICING.
 RC TISSUE=Lymphocytes;


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FT CARBOHYD 529 529 N-linked (GlcNAc... ) (Potential).
FT VARSPLIC 32 192 Missing (in isoform 2).
FT MUTAGEN 851 851 /Frid-VSP 007780.
FT CONFLICT 650 650 C->S: Loss of activity.
FT CONFLICT 1207 1207 L -> P (in Ref. 1).
SQ SEQUENCE 1304 AA; 147253 MW; A08FC22D06069BAF7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 1; Length 1304;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIMEXCATV 9
Db 737 MIMEXCATV 745

RESULT 12
O64730 PRELIMINARY; PRT; 1343 AA.
AC O64730;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE leucocyte common antigen (L-CAT) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=87260986; PubMed=2955416;
RA Thomas M.L., Reynolds P.J., Chain A., Ben-Neriah Y., Trowbridge I.S.;
RT "B-cell variant of mouse T200 (ly-5): evidence for alternative mRNA
RT splicing.";
RL J. Biol. Acad. Sci. U.S.A. 84:5360-5363(1987).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=89197920; PubMed=2522930;
RA Johnson N.A., Meyer C.M., Pingel J.T., Thomas M.L.;
RT "Sequence conservation in potential regulatory regions of the mouse
RT and human leukocyte-common antigen gene.";
RL J. Biol. Chem. 264:6220-6229(1989).
DR EMBL; M23148; AAA39418.1; JOINED.
DR EMBL; M23149; AAA39418.1; JOINED.
DR EMBL; M23150; AAA39418.1; JOINED.
DR EMBL; M23151; AAA39418.1; JOINED.
DR EMBL; M23153; AAA39418.1; JOINED.
DR EMBL; M23155; AAA39418.1; JOINED.
DR EMBL; M23157; AAA39418.1; JOINED.
DR EMBL; M23156; AAA39418.1; JOINED.
DR EMBL; M23154; AAA39418.1; JOINED.
DR EMBL; M23135; AAA39418.1; JOINED.
DR EMBL; M23134; AAA39418.1; JOINED.
DR EMBL; M23133; AAA39418.1; JOINED.
DR EMBL; M23132; AAA39418.1; JOINED.
DR EMBL; M23131; AAA39418.1; JOINED.
DR EMBL; M23130; AAA39418.1; JOINED.
DR EMBL; M23129; AAA39418.1; JOINED.
DR EMBL; M23128; AAA39418.1; JOINED.
DR EMBL; M23127; AAA39418.1; JOINED.
DR EMBL; M23144; AAA39418.1; JOINED.
DR EMBL; M23143; AAA39418.1; JOINED.
DR EMBL; M23142; AAA39418.1; JOINED.
DR EMBL; M23141; AAA39418.1; JOINED.
DR EMBL; M23140; AAA39418.1; JOINED.
DR EMBL; M23139; AAA39418.1; JOINED.
DR EMBL; M23138; AAA39418.1; JOINED.
DR EMBL; M23137; AAA39418.1; JOINED.
DR EMBL; M23136; AAA39418.1; JOINED.
DR EMBL; M23147; AAA39418.1; JOINED.
DR EMBL; M23146; AAA39418.1; JOINED.
DR EMBL; M23145; AAA39418.1; JOINED.

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DR EMBL; M23158; AAA39418.1; -.
DR EMBL; M23152; AAA39418.1; JOINED.
DR HSSP; P18052; 1YFO.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR00387; FN_III.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYHPHTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
FT NON_TER 1
SQ SEQUENCE 1343 AA; 150679 MW; 0DEBDEC97FC4C6A9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 1343;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIMEXCATV 9
Db 733 MIMEXCATV 741

RESULT 13
O91976 PRELIMINARY; PRT; 1237 AA.
AC O91976;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE protein tyrosine phosphatase lambda precursor (Protein tyrosine
DE phosphatase lambda precursor).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94245724; PubMed=8188686;
RA Fang K.S., Barker K., Sudol M., Hanafusa H.;
RT "A transmembrane protein-tyrosine-phosphatase contains spectrin-like
RT repeats in its extracellular domain.";
RL J. Biol. Chem. 269:14058-14063(1994).
RN (2)
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC TISSUE=Brain;
RA Fang K.S., Barker K., Sudol M., Hanafusa H.;
RT "A transmembrane protein-tyrosine-phosphatase contains spectrin-like
RT repeats in its extracellular domain.";
RL J. Biol. Chem. 269:14058-14063(1994).
DR EMBL; Z21960; CAA79972.1; -.
DR EMBL; L13285; AAZ0561.1; -.
DR PIR; A54080; A54080.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYHPHTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS00853; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

```

KW Hydrolyase; Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 1237 AA; 139319 MW; 0CDA3E84F5BDA0A8 CRC64;
Query Match 97.9%; Score 47; DB 2; Length 1237;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMOKATV 9
DB 672 MIMOKATV 680
RESULT 14
Q91054 PRELIMINARY; PRT; 1200 AA.
ID Q91054
AC Q91054;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CD45 homolog.
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_TaxID=7792;
RN [1]
RP SEQUENCE FROM N.A.
RA Okumura M., Matthews R.J., Robb B., Bork P., Thomas M.L.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34750; AAB01087.1; -.
DR PIR; T43148; T43148.
DR HSSP; P18052; LYFO.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid phosphorylation; IEA.
DR Pfam; PF00102; Y:phosphatase; 2.
DR PRINTS; PR00700; PRTYPHTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS00853; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolyase. 1200 AA; 135372 MW; EF6CB2B4DC028C2 CRC64;
SQ SEQUENCE 1200 AA; 135372 MW; EF6CB2B4DC028C2 CRC64;
Query Match 95.8%; Score 46; DB 2; Length 1200;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMOKATV 9
DB 637 MIMOKATV 645
RESULT 15
PRTD HUMAN STANDARD; PRT; 2485 AA.
ID PRTD HUMAN
AC Q12933; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q81WH7;
AC Q9NMY9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase 1E) (PTP-El) (hPTP-El)
DE (Protein-tyrosine phosphatase PTP1A) (Fas-associated protein-tyrosine
phosphatase 1) (FAP-1).
GN Name=PTP1A3; Synonyms=PNP1, PTP1E, PTP1J;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=Breast carcinoma;
RX MEDLINE=94350988; PubMed=8071359;
RA Banville D., Amad S., Scooco R., Shen S.-H.;
RT "A novel protein-tyrosine phosphatase with homology to both the
RT cytoskeletal proteins of the band 4.1 family and junction-associated
RT guanylate kinases.";
RL J. Biol. Chem. 269:22320-22327(1994).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemia;
RX MEDLINE=94116679; PubMed=8287977; DOI=10.1016/0014-5793(94)80273-4;
RA Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
RT "Molecular cloning of a novel protein-tyrosine phosphatase containing
RT a membrane-binding domain and GIGF repeats.";
RL FEBS Lett. 337:200-206(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=95014139; PubMed=7929060;
RA Saras J., Claesson-Welsh L., Heldin C.-H., Genez L.J.;
RT "Cloning and characterization of PTP1A, a protein tyrosine phosphatase
RT with similarities to cytoskeletal-associated proteins.";
RL J. Biol. Chem. 269:24082-24089(1994).
RN [4]
RP SEQUENCE OF 1216-2490 FROM N.A.
RC TISSUE=Pancreeas;
RA Wang H.Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4).
RC TISSUE=Brain;
RX MEDLINE=95232528; PubMed=7536343;
RA Sato T., Irie S., Kitada S., Reed J.C.;
RT "FAP-1: a protein tyrosine phosphatase that associates with Fas.";
RL Science 268:411-415(1995).
RN [6]
RP SEQUENCE OF 1323-1821 FROM N.A.
RA Irie S., Hachiyu T., Sato T.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 1323-1922 FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Uesdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson B.F.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP INTERACTION WITH TRIP6.
RX MEDLINE=99329089; PubMed=10400701; DOI=10.1074/jbc.274.29.20679;
RA Murphy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;
RT "ZRP-1, a tyrosine-related protein, interacts with the second puz domain
RT of the cytosolic protein tyrosine phosphatase hPTP1A.";
RL J. Biol. Chem. 274:20679-20687(1999).
RN [9]

RP INTERACTION WITH NGFR.
 RA MEDLINE=20012928; PubMed=10544233; DOI=10.1016/S0014-5793(99)01324-1;
 RX Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
 RA Reed J.C., Bredesen D.E., Sato T.A.;
 RT "Functional interaction of Fas-associated phosphatase-1 (FAP-1) with
 RT p75(NTR) and their effect on NF-kappaB activation.";
 RL FEBS Lett. 460:191-198(1999).
 (10)
 RP INTERACTION WITH PLEKHA1 AND PLEKHA2.
 RX PubMed=14516276; DOI=10.1042/BJO0031154;
 RA Kimber W.A., Deak M., Prescott A.R., Alessi D.R.;
 RT "Interaction of the protein tyrosine phosphatase PTPBL1 with the
 RT Ptdins(3,4)P2-binding adaptor protein TAPP1.";
 RL Biochem. J. 376:525-535(2003).
 (11)
 RP STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE
 RP C-TERMINUS OF TNFRSF6.
 RX MEDLINE=20170882; PubMed=10704206; DOI=10.1021/bi991913c;
 RA Kozlov G., Gehring K., Ekkel I.;
 RT "Solution structure of the PDZ2 domain from human phosphatase hPTPBL
 RT and its interactions with C-terminal peptides from the Fas receptor.";
 RL Biochemistry 39:2572-2580(2000).
 (12)
 RP STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE
 RP GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEF-2.
 RX MEDLINE=2090786; PubMed=12095257; DOI=10.1016/S0022-2836(02)00544-2;
 RA Kozlov G., Banville D., Gehring K., Ekkel I.;
 RT "Solution structure of the PDZ2 domain from cytosolic human
 RT phosphatase hPTPBL complexed with a peptide reveals contribution of
 RT the beta2-beta3 loop to PDZ domain-ligand interactions.";
 RL J. Mol. Biol. 320:813-820(2002).
 (13)
 RP VARIANTS PRO-1419 AND MET-1522.
 RX MEDLINE=22323362; PubMed=12436199; DOI=10.1007/s100380200094;
 RA Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., Emi M.;
 RT "Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1)
 RT and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and
 RT seven polymorphisms of the FAP-1 gene.";
 RL J. Hum. Genet. 47:614-619(2002).
 (14)
 RP FUNCTION: Regulates negatively Fas-induced apoptosis and NGFR-
 RP mediated pro-apoptotic signaling.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBUNIT: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through
 CC its second PDZ domain. Interacts with the C-terminal SVP motif of
 CC NGFR through its third PDZ domain. Interacts with the LIM domain
 CC of PDLIM4 through its second and fourth PDZ domains. Binds PLEKHA1
 CC and PLEKHA2 through its first PDZ domain.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q12923-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q12923-2; Sequence=VSP_000496;
 CC Name=3;
 CC IsoId=Q12923-3; Sequence=VSP_000497;
 CC Name=4;
 CC IsoId=Q12923-4; Sequence=VSP_007921;
 CC Note=May be due to a competing donor splice site;
 CC -1- TISSUE SPECIFICITY: Present in most tissues with the exception of
 CC the liver and skeletal muscle. Most abundant in lung, kidney and
 CC fetal brain.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -1- SIMILARITY: Contains 1 FERM domain.
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
 CC -----
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 CC -----
 DR EMBL; U12128; AAB60339.1; -
 DR EMBL; D21209; BAA04750.1; -
 DR EMBL; D21210; BAA04751.1; -
 DR EMBL; D21211; BAA04752.1; -
 DR EMBL; X80289; CAA56563.1; -
 DR EMBL; X79676; CAA56124.1; -
 DR EMBL; U34563; AAC41755.1; -
 DR EMBL; AF233323; AAF63474.1; -
 DR EMBL; BC039610; AAH39610.1; ALT_TERM.
 DR PIR; A54971; A54971.
 DR PIR; I67629; I67629.
 DR PIR; I67630; I67630.
 DR PDB; 1DSG; NMR; A=1361-1456.
 DR PDB; 1Q7X; NMR; A=1357-1459.
 DR PDB; 3PDZ; NMR; A=1361-1456.
 DR Genew; HGNC:9646; PTPN13.
 DR MIM; 600267; -
 DR GO; GO:0004725; P:protein-tyrosine-phosphatase activity; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro; IPR000299; Band_4.1.
 DR InterPro; IPR009065; FERM.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR011036; PH_related.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00373; Band_41; 1.
 DR Pfam; PF00595; PDZ; 5.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00935; BAND41.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR PROSITE; PS00660; FERM_1; FALSE_NEG.
 DR PROSITE; PS00661; FERM_2; FALSE_NEG.
 DR PROSITE; PS50057; FERM_3; 1.
 DR PROSITE; PS50106; PDZ; 5.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.

Query Match 93.8%; Score 45; DB 1; Length 2485;
 Best Local Similarity 88.9%; Pred. No. 8.9;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MIMEXATV 9
 Db 2296 MIMEXSTV 2304

Search completed: May 3, 2005, 05:58:58
 Job time : 41.1351 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:35:47 ; Search time 43 Seconds
(without alignments)
80.950 Million cell updates/sec

Title: US-10-003-983C-4

Perfect score: 48

Sequence: 1 MIWEQKATV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	48	100.0	9	ABG31974 Human CD4
2	48	100.0	235	Adj92680 Human leu
3	48	100.0	248	AdD22988 Human pro
4	48	100.0	253	AAB59374 Murine pr
5	48	100.0	309	AAg78272 Mouse CD4
6	48	100.0	641	AAm23689 Human EST
7	48	100.0	641	ABU07333 Human exp
8	48	100.0	664	AAm39262 Human pol
9	48	100.0	664	ABU07334 Human exp
10	48	100.0	764	ABO84454 Human can
11	48	100.0	960	ADQ39377 Human myo
12	48	100.0	962	ADL16236 Rat prote
13	48	100.0	1114	ABU05246 Human exp
14	48	100.0	1114	ABU05239 Human exp
15	48	100.0	1143	ABU05240 Human exp
16	48	100.0	1143	ABU05245 Human exp
17	48	100.0	1143	ADL16232 Human pro
18	48	100.0	1143	ADQ18845 Human sof
19	48	100.0	1149	AAm41048 Human pol
20	48	100.0	1149	ABU05242 Human exp
21	48	100.0	1157	ABO84453 Human can
22	48	100.0	1152	ADR39747 Human kin
23	48	100.0	1219	ADQ39378 Human myo
24	48	100.0	1256	ADMe7187 Human adi
25	48	100.0	1256	ADP12966 Protein e

26	48	100.0	1258	ADQ39376 Human myo
27	48	100.0	1267	ADQ39379 Human myo
28	48	100.0	1281	ADL16234 Mouse pro
29	48	100.0	1304	ABU05243 Human exp
30	48	100.0	1304	ABU05241 Human exp
31	48	100.0	1304	ABU05244 Human exp
32	48	100.0	1304	ADL16230 Human pro
33	48	100.0	1304	ADP65158 Human pro
34	48	100.0	1304	ADMe7209 Human adi
35	48	100.0	1304	ABO84455 Human can
36	48	100.0	1304	ADQ39380 Human myo
37	48	100.0	1306	ADQ39375 Human myo
38	48	100.0	1343	ADMe7208 Murine ad
39	47	97.9	1237	AAm44729 Chicken p
40	47	97.9	1237	AAm89347 Chicken t
41	45	93.8	766	ABU70688 Human adi
42	45	93.8	1267	AAg67637 Amino aci
43	45	93.8	1267	AAg67458 Amino aci
44	45	93.8	2466	AAr71498 Human pro
45	45	93.8	2466	AAw75999 Intracell

ALIGNMENTS

RESULT 1
ID ABG31974 standard; peptide; 9 AA.
XX
XX ABG31974;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CD45 HLA-binding peptide, hucD45/737.
XX
XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
XX antigen-presenting cell; APC; major histocompatibility complex; MHC;
XX antigen; allogenic; T cell receptor; TCR; cancer; tumour;
XX allogenic stem cell transplantation; CFU-GM; leukaemia;
XX colony forming unit-granulocyte macrophage; immunotherapeutic;
XX haematopoietic; malignant.
XX
OS Homo sapiens.
XX
XX PN MO200244207-A1.
XX
XX PD 06-JUN-2002.
XX
XX PF 30-NOV-2000; 2000MO-GB004566.
XX
XX PR 30-NOV-2000; 2000MO-GB004566.
XX
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX PI Staus HJ, Amrolia PJ;
XX WPI; 2002-599413/64.
XX
XX DR Novel peptide comprising leukocyte antigen binding peptide of human CD45 polypeptide, useful for producing activated cytotoxic T lymphocytes, for killing cancerous cells e.g. leukemia.
XX
XX PT Claim 2; Page 38; 56pp; English.
XX
XX PS The invention discloses a peptide comprising the human leukocyte antigen (HLA)-binding peptide of human CD45 polypeptide, its portion or variant, provided that the peptide is not the intact human CD45 polypeptide. The peptides are useful for producing activated cytotoxic T lymphocyte (CTL) in vitro which involves contacting the CTL with an antigen-presenting cell, where its major histocompatibility complex (MHC) class I molecules are loaded with the peptide, to activate, in an antigen specific manner, CC where the CTL and the antigen presenting cell are allogenic with respect to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animal models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/737,
CC comprising an HLA-binding peptide of human CD45
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMEDCATV 9
DB 1 MIMEDCATV 9
RESULT 2
ADJ92680
ID ADJ92680 standard; protein; 235 AA.
XX
AC ADJ92680;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human leukocyte common antigen (LCA) phosphatase domain (PD) 1.
XX
XX Receptor-type protein tyrosine phosphatase; RPTP;
XX phosphotyrosine phosphatase; cancer; diabetes; human;
XX leukocyte common antigen; LCA; phosphatase domain; PD.
OS Homo sapiens.
XX
PN US6682905-B1.
XX
XX 27-JAN-2004.
PD
PF 29-MAR-1999; 99US-00280597.
XX
XX 11-JUL-1990; 90US-00551270.
PR 26-FEB-1991; 91US-00654188.
PR 10-FEB-1993; 93US-00015985.
PR 23-MAY-1995; 95US-00448288.
XX
XX (UYNV) UNIV NEW YORK STATE.
PA
XX
XX Schlessinger J, Sap JM;
PI
XX
DR WPI; 2004-118574/12.
XX
PT Identifying a compound that modulates the phosphotyrosine phosphatase
XX activity of a polypeptide by incubating the compound with the
PT polypeptide, which is in pure form, in a membrane preparation or in a
XX whole cell.
XX
PS Example; SEQ ID NO 5; 52pp; English.
XX
XX The invention relates to receptor-type protein tyrosine phosphatase
CC (RPTP) and its corresponding nucleic acid. The invention also relates to
CC a method for identifying a compound that modulates the phosphotyrosine

CC phosphatase activity. The method is useful for identifying a compound
CC that modulates the phosphotyrosine phosphatase activity of a polypeptide
CC and for identifying susceptibility to cancer, diabetes or other diseases
CC associated with alterations in cellular phosphotyrosine metabolism. The
CC present sequence is human leukocyte common antigen (LCA) phosphatase
CC domain (PD) 1. This sequence is used to illustrate the method of the
CC invention.
XX
SQ Sequence 235 AA;
Query Match 100.0%; Score 48; DB 8; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMEDCATV 9
DB 63 MIMEDCATV 71
RESULT 3
ADD22988
ID ADD22988 standard; protein; 248 AA.
XX
AC ADD22988;
XX
XX 15-JAN-2004 (first entry)
DT
XX
DE Human protein tyrosine phosphatase, CD45-DL.
XX
XX Human; enzyme; protein tyrosine phosphatase; PTPH1; cytosolic;
XX gene therapy; retroviral vector; phosphotyrosine; pp60(V-src);
XX breast cancer; leukaemia; CD45-DL.
XX
OS Homo sapiens.
XX
PN US2003113294-A1.
XX
PD 19-JUN-2003.
XX
PF 12-NOV-2002; 2002US-00293231.
XX
XX 14-MAR-1990; 90US-00494036.
PR 01-MAR-1991; 91US-00663579.
PR 16-AUG-1993; 93US-00107420.
PR 04-DEC-1996; 96US-00759536.
PR 22-JAN-1999; 99US-00235251.
PR 03-MAY-2001; 2001US-00848294.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
PA
XX
XX Tonks NK;
PI
XX
DR WPI; 2003-810871/76.
XX
PT New isolated RNA encoding protein tyrosine phosphatase designated as
XX PTPH1 useful for treating malignancies such as breast cancer, leukemia.
XX
XX disclosure; Fig 4B; 12pp; English.
PS
XX
XX The invention relates to an isolated RNA encoding a protein tyrosine
CC phosphatase designated as PTPH1 appearing as ADD22988. Also included is a
CC retroviral vector comprising the RNA. The RNA is useful for treating or
CC preventing a condition in which abnormally high levels of phosphotyrosine
CC occur in a mammalian cell (which involves introducing into the mammalian
CC cell and agent which comprises DNA or RNA encoding all or a portion of a
CC PTPH1, under conditions sufficient to express PTPH1 where the polypeptide
CC can catalyze dephosphorylation of tyrosyl residues that are
CC phosphorylated through action of a protein tyrosine kinase. The RNA is
CC also useful for reversing a malignant phenotype of a mammalian cell which
CC is associated with tyrosyl phosphorylation catalysed by a protein
CC tyrosine kinase. The DNA or RNA is delivered via a recombinant retrovirus
CC or a recombinant vaccinia virus. At least one tyrosyl residue that is
CC dephosphorylated by the protein tyrosine phosphatase polypeptide can be

CC aberrantly phosphorylated by pp60(V-src). The RNA is useful for treating
CC or preventing malignancies such as breast cancer and leukaemia. The
CC present sequence is a PTP similar to PTPBL.

XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 48; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIMBQKATV 9
|||
DB 63 MIMBQKATV 71

RESULT 4
AAB59374
ID AAB59374 standard; protein; 253 AA.

XX
AC AAB59374;

XX
DT 21-MAR-2001 (first entry)

XX
DE Murine protein tyrosine phosphatase #1.

KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
XX substrate trapping.

XX
OS Mus sp.

XX
PN WO200075339-A1.

XX
PD 14-DEC-2000.

XX
PF 24-MAY-2000; 2000WO-US014211.

XX
PR 03-JUN-1999; 99US-0137219P.

XX
PR 16-JUN-1999; 99US-00334575.

XX
PA (COLD-) COLD SPRING HARBOR LAB.

XX
PI Tonks NK, Zhang S;

XX
DR WPI; 2001-080598/09.

PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
XX which the wild type PTP catalytic domain invariant aspartate is replaced
XX with an unphosphorylated amino acid, useful in gene therapy.

XX
PS Disclosure; Fig 1; 109pp; English.

CC The present invention provides substrate trapping mutant protein tyrosine
XX phosphatases (PTPs). They can be used to reduce the activity of tyrosine
XX phosphorylated proteins and to screen for modulators capable of altering
XX the binding of protein tyrosine phosphatases to their substrate. These
XX may be used in disease diagnosis and treatment

XX
SQ Sequence 253 AA;

Query Match 100.0%; Score 48; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIMBQKATV 9
|||
DB 74 MIMBQKATV 82

RESULT 5
AAG78272
ID AAG78272 standard; protein; 309 AA.
XX
AC AAG78272;

XX
DT 19-DEC-2001 (first entry)
XX
DE Mouse CD45-D1.

KM PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
XX dephosphorylation; phosphotyrosine; human; PTPB; mouse; fruit fly;
XX yeast.

XX
OS Mus sp.

XX
PN WO200161031-A2.

XX
PD 23-AUG-2001.

XX
PF 13-FEB-2001; 2001WO-US005180.

XX
PR 14-FEB-2000; 2000US-0181769P.

XX
PA (CEPT-) CEPTYR INC.

XX
PI Flint AJ, Cool DE;

XX
DR WPI; 2001-570570/64.

PT Screening assays to identify agents that alter protein tyrosine
XX phosphatase (PTP) binding to, and PTP-mediated catalytic
XX dephosphorylation of phosphotyrosine peptide substrates.

XX
PS Disclosure; Fig 1; 79pp; English.

CC The invention relates to identifying agents which alter the interaction
XX between a protein tyrosine phosphatase (PTP) and a tyrosine
XX phosphorylated polypeptide using fluorescence energy signals. The methods
XX are useful for performing screening assay to identify agents that alter
XX CPT binding to and PTP-mediated catalytic dephosphorylation of
XX CC phosphotyrosine peptide substrates. The present sequence is that of a
XX catalytic domain of a PTP for comparison with human PTPB (AAG78262)

XX
SQ Sequence 309 AA;

Query Match 100.0%; Score 48; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIMBQKATV 9
|||
DB 74 MIMBQKATV 82

RESULT 6
AAM23689
ID AAM23689 standard; protein; 641 AA.

XX
AC AAM23689;

XX
DT 12-OCT-2001 (first entry)

XX
DE Human EST encoded protein SEQ ID NO: 1214.

KM Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
XX gene therapy; nutrition.

XX
OS Homo sapiens.

XX
PN WO200154477-A2.

XX
PD 02-AUG-2001.

XX
PF 25-JAN-2001; 2001WO-US002687.

PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dmanac RA, Zhang J, Werhman T;
XX
XX WPI; 2001-476164/51.
DR N-PSDB; AAH98348.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
PS
XX Claim 20; Page 875-876; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 48; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMWOKATV 9
DB 578 MIMWOKATV 586

RESULT 7
ABU07333
ID ABU07333 standard; protein; 641 AA.
XX
XX AC ABU07333;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #2034.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX
XX PR 21-MAY-2001; 2001US-0292544P.
XX
XX PR 08-AUG-2001; 2001US-0310801P.
XX
XX PR 01-OCT-2001; 2001US-0326370P.
XX
XX PR 04-DEC-2001; 2001US-0336780P.
XX
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX

DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 2034; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 48; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMWOKATV 9
DB 578 MIMWOKATV 586

RESULT 8
AAM39262
ID AAM39262 standard; protein; 664 AA.
XX
XX AC AAM39262;
XX
XX DT 22-OCT-2001 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 2407.
XX
XX KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200153312-A1.
XX
XX PD 26-JUL-2001.
XX
XX PF 26-DEC-2000; 2000WO-US034263.
XX
XX PR 23-DEC-1999; 99US-00471275.
XX
XX PR 21-JAN-2000; 2000US-00488725.
XX
XX PR 25-APR-2000; 2000US-00552317.
XX
XX PR 20-JUN-2000; 2000US-00598042.
XX
XX PR 19-JUL-2000; 2000US-00620312.
XX
XX PR 03-AUG-2000; 2000US-00653450.
XX
XX PR 14-SEP-2000; 2000US-00662191.
XX
XX PR 19-OCT-2000; 2000US-00693036.
XX
XX PR 29-NOV-2000; 2000US-00727344.
XX

DR	MPI; 2004-652914/63.
DR	N-PSDB; ABDJ2625.
XX	
PT	New isolated cancer-associated polynucleotides and polypeptides useful
PT	for diagnosing, preventing or treating cancers, especially lymphoma and
PT	leukemia, or in screening for agents that modulate cancer.
XX	
XX	claim 18; seqid 145; 310pp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising at least 10
CC	contiguous nucleotides of any of the 233 polynucleotide sequences given
CC	in the specification, or its complement. The nucleic acids encode cancer-
CC	associated proteins. Also included are an expression vector comprising
CC	the isolated nucleic acid cited above, a host cell comprising the above
CC	recombinant nucleic acid or expression vector, a microarray for detecting
CC	a cancer-associated (CA) nucleic acid comprising at least one probe
CC	comprising at least 10 contiguous nucleotides of any of the above-
CC	mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC	an open reading frame of a CA sequence selected from any of the 95
CC	polynucleotide sequences as mentioned in the specification, or its
CC	complement), an isolated antibody, (or its antigen binding fragment) that
CC	binds to the above polypeptide, a hybridoma that produces the above
CC	monoclonal antibody, a pharmaceutical composition comprising the above
CC	antibody and a pharmaceutical excipient, a kit for detecting cancer
CC	cells (comprising the antibody cited above, methods for diagnosing cancer
CC	or for detecting the presence or absence of cancer cells in an
CC	individual, a method for inhibiting growth of cancer cells in an
CC	individual, a method for delivering a therapeutic agent to cancer cells
CC	in an individual, an electronic library comprising the above
CC	polynucleotide or polypeptide (or their fragments), methods of screening
CC	for anticancer activity or for a bioactive agent capable of modulating
CC	the activity of a CA protein (CAP), methods for detecting cancer
CC	associated with expression of a polypeptide in a test cell sample, a
CC	method for treating cancers and a method for inhibiting the expression of
CC	CA gene in a cell. The composition and methods are useful for detecting,
CC	diagnosing, preventing and treating cancers, especially lymphoma and
CC	leukemia. These may also be used in screening for agents that modulate
CC	cancer. The present sequence is a human CAP protein sequence. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 764 AA;
	Query Match 100.0%; Score 48; DB 8; Length 764;
	Best Local Similarity 100.0%; Pred. No. 5.7;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy	1 MIMKATY 9
Dd	197 MIMKATV 205
	RESULT 11
ID	ADQ39377 standard; protein; 960 AA.
XX	ADQ39377;
XX	
DT	18-NOV-2004 (first entry)
DE	Human myocardial infarction-associated gene derived protein, SEQ ID 1040.
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiac; gene therapy; human.
OS	Homo sapiens.
PM	MO2004058052-A2.
PD	15-JUL-2004.
PF	22-DEC-2003; 2003WO-US040978.

XX		20-DEC-2002; 2002US-0434778P.
PR	10-MAR-2003; 2003US-0453135P.	
PR	30-APR-2003; 2003US-0466412P.	
PR	23-SEP-2003; 2003US-0504955P.	
XX		
PA	(APPL-) APPLERA CORP.	
PI	Cargill M., Devlin JI, Yakubova O;	
DR	WPI; 2004-533949/51.	
DR	N-PSDB; ADO38549.	
PT	Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acid.	
PT		
XX		
PS	Claim 10; SEQ ID NO 1040; 145pp; English.	
CC	The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acid, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity.	
CC	The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.	
CC		
CC		
CC		
SQ	Sequence 960 AA;	
Query Match	100.0%; Score 48; DB 8; Length 960;	
Best Local Similarity	100.0%; Pred. No. 7.3;	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
QY	1 MIWEOKATV 9 	
Db	393 MIWEOKATV 401	
ID	ADL16236 standard; protein; 962 AA.	
XX		
AC	ADL16236;	
DT	06-MAY-2004 (first entry)	
DE	Rat protein tyrosine phosphatase #7.	
XX		
KM	cytosolic; immunosuppressive; antiallergic;	
KM	protein tyrosine phosphatase; reversible oxidation; dephosphorylation;	
KM	inducible signalling pathway; cell proliferation; cancer;	
KM	guet vs. host disease; autoimmune disease; allergy; metabolic disorder;	
KM	cell-cycle abnormality; enzyme.	

XX OS Rattus norvegicus.
 XX PN W02003068984-A2.
 XX PD 21-AUG-2003.
 XX PF 13-FEB-2003; 2003WO-EP001446.
 XX PR 13-FEB-2002; 2002US-0356810P.
 XX PR 12-FEB-2003; 2003US-00366547.
 XX PA (COLD-) GOLD SPRING HARBOR LAB.
 XX PA (CEPT-) CEPTVR INC.
 XX PI Tonks NK, Tzu-Ching M, Cool DE;
 XX DR WPI; 2003-712572/67.
 XX DR N-PSDB; ADL16235.
 XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX PS Disclosure; SEQ ID NO 85; 238bp; English.
 XX CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulphydryl-reactive agent (II) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host diseases; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 XX CC
 XX SQ Sequence 962 AA;
 Query Match 100.0%; Score 48; DB 7; Length 962;
 Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMBOKATV 9
 Db 397 MIMBOKATV 405
 RESULT 13
 AB005246 ID AB005246 standard; protein; 1114 AA.
 XX AC AB005246;
 XX AC
 XX DT 29-JAN-2003 (first entry)
 XX DE Human expressed protein tag (EPT) #1912.
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX OS Homo sapiens.

XX OS W0200278524-A2.
 XX PN 10-OCT-2002.
 XX PD 28-MAR-2002; 2002WO-US009671.
 XX PF 28-MAR-2001; 2001US-0279495P.
 XX PR 21-MAY-2001; 2001US-0292544P.
 XX PR 08-AUG-2001; 2001US-0310801P.
 XX PR 01-OCT-2001; 2001US-0326370P.
 XX PR 04-DEC-2001; 2001US-0336780P.
 XX PR 20-FEB-2002; 2002US-0358985P.
 XX PA (ZYCO-) ZYCOS INC.
 XX PA Chicz RM, Tomlinson AJ, Urban RG;
 XX PI WPI; 2003-040607/03.
 XX DR
 XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX PS Example 2; SEQ ID NO 1912; 134pp; English.
 XX CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_ptc_sequences
 XX CC
 XX SQ Sequence 1114 AA;
 Query Match 100.0%; Score 48; DB 6; Length 1114;
 Best Local Similarity 100.0%; Pred. No. 8.5; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMBOKATV 9
 Db 547 MIMBOKATV 555
 RESULT 14
 AB005239 ID AB005239 standard; protein; 1114 AA.
 XX AC AB005239;
 XX AC
 XX DT 29-JAN-2003 (first entry)
 XX DE Human expressed protein tag (EPT) #1905.
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX OS Homo sapiens.

```

XX  WO200278524-A2.
PN
XX
XX  10-OCT-2002.
PD
XX
XX  28-MAR-2002; 2002WO-US009671.
PF
XX
XX  28-MAR-2001; 2001US-0279495P.
PR
XX  21-MAY-2001; 2001US-0292544P.
PR
XX  08-AUG-2001; 2001US-0310801P.
PR
XX  01-OCT-2001; 2001US-0326370P.
PR
XX  04-DEC-2001; 2001US-036780P.
PR
XX  20-FEB-2002; 2002US-0358985P.
XX
XX  (ZYCO-) ZYCO INC.
PA
XX  Chicx RM, Tomlinson AJ, Urban RG;
PI
XX  WPI; 2003-040607/03.
DR
XX
XX  New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT  cytoskeletal proteins, receptors or transcription factors), useful for
PT  treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT  leukemia.
XX
XX  Example 2; SEQ ID NO 1905; 134pp; English.
PS
XX
CC  The invention describes a purified polypeptide, which comprises a
CC  fragment of a kinase, phosphatase, protease, protease inhibitor,
CC  transporter, cytoskeletal protein, receptor or transcription factor. The
CC  polypeptide is useful as an immunogenic composition for eliciting in a
CC  mammal an immunogenic response directed against any of the purified
CC  polypeptide. The purified polypeptide, or the antibody that binds to this
CC  polypeptide, is useful for treating cancer. The polypeptide is also
CC  useful for identifying compounds that binds to a naturally processed
CC  class I or class II MHC-binding polypeptide. The polypeptides and
CC  polynucleotides are particularly useful for treating or preventing
CC  myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC  lymphoma or leukemia. These are also useful for screening agents for
CC  treating the above mentioned diseases. This sequence represents an
CC  expressed protein tag (EPT) isolated from human tissue for translational
CC  profiling. Note: This sequence does not appear in the printed
CC  specification but was obtained in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 1114 AA;
SQ
XX
XX  Query Match          100.0%; Score 48; DB 6; Length 1114;
XX  Best Local Similarity 100.0%; Pred. No. 8.5;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 MIMEXKATV 9
XX  |||||
XX  547 MIMEXKATV 555
XX
XX  RESULT 15
XX  ID  ABU05240 standard; protein; 1143 AA.
XX  AC  ABU05240;
XX  DT  29-JAN-2003 (first entry)
XX
XX  Human expressed protein tag (EPT) #1906.
XX
XX  Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX  protease; protease inhibitor; transporter; cytoskeletal protein;
XX  receptor; transcription factor; cancer; MHC;
XX  major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX  adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX  Homo sapiens.
OS

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XX  WO200278524-A2.
PN
XX
XX  10-OCT-2002.
PD
XX
XX  28-MAR-2002; 2002WO-US009671.
PF
XX
XX  28-MAR-2001; 2001US-0279495P.
PR
XX  21-MAY-2001; 2001US-0292544P.
PR
XX  08-AUG-2001; 2001US-0310801P.
PR
XX  01-OCT-2001; 2001US-0326370P.
PR
XX  04-DEC-2001; 2001US-036780P.
PR
XX  20-FEB-2002; 2002US-0358985P.
XX
XX  (ZYCO-) ZYCO INC.
PA
XX  Chicx RM, Tomlinson AJ, Urban RG;
PI
XX  WPI; 2003-040607/03.
DR
XX
XX  New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT  cytoskeletal proteins, receptors or transcription factors), useful for
PT  treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT  leukemia.
XX
XX  Example 2; SEQ ID NO 1906; 134pp; English.
PS
XX
CC  The invention describes a purified polypeptide, which comprises a
CC  fragment of a kinase, phosphatase, protease, protease inhibitor,
CC  transporter, cytoskeletal protein, receptor or transcription factor. The
CC  polypeptide is useful as an immunogenic composition for eliciting in a
CC  mammal an immunogenic response directed against any of the purified
CC  polypeptide. The purified polypeptide, or the antibody that binds to this
CC  polypeptide, is useful for treating cancer. The polypeptide is also
CC  useful for identifying compounds that binds to a naturally processed
CC  class I or class II MHC-binding polypeptide. The polypeptides and
CC  polynucleotides are particularly useful for treating or preventing
CC  myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC  lymphoma or leukemia. These are also useful for screening agents for
CC  treating the above mentioned diseases. This sequence represents an
CC  expressed protein tag (EPT) isolated from human tissue for translational
CC  profiling. Note: This sequence does not appear in the printed
CC  specification but was obtained in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 1143 AA;
SQ
XX
XX  Query Match          100.0%; Score 48; DB 6; Length 1143;
XX  Best Local Similarity 100.0%; Pred. No. 8.7;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 MIMEXKATV 9
XX  |||||
XX  576 MIMEXKATV 584
XX
XX  RESULT 16
XX  ID  ABU05245 standard; protein; 1143 AA.
XX  AC  ABU05245;
XX  DT  29-JAN-2003 (first entry)
XX
XX  Human expressed protein tag (EPT) #1911.
XX
XX  Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX  protease; protease inhibitor; transporter; cytoskeletal protein;
XX  receptor; transcription factor; cancer; MHC;
XX  major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX  adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX  Homo sapiens.
OS

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XX WO200278524-A2.
PN
XX 10-OCT-2002.
PD
XX
XX 28-MAR-2002; 2002WO-US009671.
PF
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCO INC.
PA
XX Chicx RM, Tomlinson AJ, Urban RG;
PI
XX WPI; 2003-040607/03.
DR
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 191; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1143 AA;
SQ
Query Match 100.0%; Score 48; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMWQKATV 9
DB 576 MIMWQKATV 584

RESULT 17
ADL16232
ID ADL16232 standard; protein; 1143 AA.
XX
XX ADL16232;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human protein tyrosine phosphatase #27.
DE
XX cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
XX Homo sapiens.
OS

XX WO2003068984-A2.
PN
XX 21-AUG-2003.
PD
XX
XX 13-FEB-2003; 2003WO-EP001446.
PF
XX 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-00366547.
PR
XX (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
XX
XX Tonke NK, Tzu-Ching M, Cool DE;
PI
XX WPI; 2003-712572/67.
DR N-PSDB; ADL16231.
DR
XX
XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 81; 238pp; English.
PS
XX The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulphydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
XX Sequence 1143 AA;
SQ
Query Match 100.0%; Score 48; DB 7; Length 1143;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIMWQKATV 9
DB 576 MIMWQKATV 584

RESULT 18
ADQ18845
ID ADQ18845 standard; protein; 1143 AA.
XX
XX ADQ18845;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
DE
XX soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human.
KW
XX Homo sapiens.
OS
XX WO2004048938-A2.
PN
XX 10-JUN-2004.
PD
XX
XX 26-NOV-2003; 2003WO-US038193.
PF

PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1908; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1149 AA;

Query Match 100.0%; Score 48; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9
|||||
581 MIMBOKATV 589

RESULT 21

AB084453 standard; protein; 1157 AA.

XX AB084453;

XX 18-NOV-2004 (first entry)

XX Mouse cancer-associated protein MP13-011.1.

XX Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;

KM lymphoma; CAP.

XX Mus musculus.

XX WO2004074320-A2.

XX 02-SEP-2004.

XX 17-FEB-2004; 2004WO-US004730.

XX 14-FEB-2003; 2003US-00367094.

XX 14-MAR-2003; 2003US-0038838.

XX 15-APR-2003; 2003US-00417375.

XX 13-JUN-2003; 2003US-00461862.

XX 15-SEP-2003; 2003US-00663431.

XX 15-DEC-2003; 2003US-00737318.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Morris DW, Malandro MS;
PI
XX WPI; 2004-652914/63.
XX
XX N-PSDB; ABD32623.
XX

PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.

XX disclosure; seqid 142; 310pp; English.

XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1157 AA;

Query Match 100.0%; Score 48; DB 8; Length 1157;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9
|||||
592 MIMBOKATV 600

RESULT 22

ADR39747 standard; protein; 1192 AA.

XX ADR39747;

XX 18-NOV-2004 (first entry)

XX Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.

XX human; kinase and phosphatase protein; KPP; enzyme; cytoprotective;

KM antitumor; kinase; antitumor; neurotrophic; neuroprotective;

KM ceramide; ceramide; anti-HIV; antiallergic; anti-inflammatory;

KM thymol; thymol; gene therapy; cell proliferative disorder; cancer;

KM atherosclerosis; neurological disorder; epilepsy; Huntington's disease;

KM stroke; immune disorder; inflammatory disorder; AIDS; allergy;

KM developmental disorder; Hypothyroidism; Cushing's syndrome; infection;

DE	Human adipocyte specific PRPase receptor type C protein Segid 541.
XX	
KM	human; adipocyte specific; adipose tissue; anti-obesity;
XX	
KM	high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
XX	
KW	adipogenesis; hypertension; cardiovascular disease; anorectic;
XX	
KV	antidiabetic; hypotensive; PRPase receptor type C.
XX	
OS	Homo sapiens.
XX	
PN	WO2004011618-A2.
XX	
PD	05-FEB-2004.
XX	
PR	29-JUL-2003; 2003WO-US023684.
XX	
PF	29-JUN-2002; 2002US-0398785P.
XX	
PR	12-JUN-2003; 2003US-0478206P.
XX	
PA	(HMGE-) HMGE INC.
XX	
PI	Chada K, Chouinard R, Ashar H, Sayed AMD;
DR	WPI; 2004-143846/14.
XX	
DR	N-PSTDB; ADM66908.
XX	
PT	Identifying adipocyte specific genes, useful for treating obesity or
XX	
PT	diabetes, and for identifying drug targets, by differential gene
XX	
PT	expression analysis between adipose tissue or stromal vascular tissue of
XX	
PS	mice of different genotypes.
XX	
PS	Disclosure; SEQ ID NO 541; 91pp; English.
XX	
CC	This invention relates to a novel method for identifying genes that are
XX	
CC	over-expressed in adipose tissue and as such it provides targets for anti-
XX	
CC	-obesity pharmaceutical compositions. Specifically, it refers to a high
XX	
CC	mobility group I-C protein (HMG1-C) that is associated with obesity and
XX	
CC	is epistatic to leptin, furthermore, it refers to the ob gene where an
XX	
CC	autosomal recessive trait is linked to obesity and diabetes. The present
XX	
CC	invention describes performing differential gene expression analysis
XX	
CC	between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
XX	
CC	of any two different mice selected from a group consisting of wild-type,
XX	
CC	HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
XX	
CC	this method novel nucleotides and the encoded proteins thereof were
XX	
CC	identified that are adipocyte specific, and as such can be used for
XX	
CC	preventing adipogenesis, diagnosing and treating diabetes, obesity,
XX	
CC	hypertension and cardiovascular disease, as well as screening for
XX	
CC	compounds that can modulate or prevent adipogenesis and treat diabetes or
XX	
CC	obesity. These compositions exhibit anorectic, antidiabetic and
XX	
CC	hypotensive activities. This polypeptide sequence is a human homologue of
XX	
CC	a murine adipocyte specific protein sequence of the invention.
XX	
SQ	Sequence 1256 AA;
XX	
Query Match	100.0%; Score 48; DB 8; Length 1256;
Best Local Ssimilarity	100.0%; Pred. No. 9.6;
Matches 9; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MIMBOKATV 9
Db	689 MIMBOKATV 697
RESULT 25	
ID	ADP12966
XX	ADP12966 standard; protein; 1256 AA.
AC	ADP12966;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Protein encoding reference mRNA sequence #51.
XX	
XX	transplant rejection; immune system; rheumatoid arthritis; lupus;

KW		inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX		
OS	Homo sapiens.	
XX		
FN	WO2004042346-A2.	
XX		
PD	21-MAY-2004.	
XX		
PF	24-APR-2003; 2003WO-US012946.	
XX		
PR	24-APR-2002; 2002US-00131831.	
XX		
PR	20-DEC-2002; 2002US-00325899.	
XX		
PA	(EXPR-) EXPRESSION DIAGNOSTICS INC.	
XX		
PI	Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;	
XX	Rosenberg S;	
XX		
DR	WPI; 2004-400724/37.	
XX		
XX		
PT	Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,	
XX	pancreas, pancreatic islet, lung, bone marrow or stem cell transplant	
PT	rejection, in an individual, comprises detecting the expression level of	
XX	the genes.	
XX		
PS	Claim 65; SEQ ID NO 2975; 1762pp; English.	
XX		
CC	The present invention relates to diagnosing or monitoring transplant	
CC	rejection, e.g. cardiac or kidney transplant rejection, in an individual	
CC	comprises detecting the expression level of one or more genes. The	
CC	methods, system and kits are useful in diagnosing or monitoring	
CC	transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic	
CC	islet, lung, bone marrow or stem cell transplant rejection,	
CC	xenotransplant rejection or mechanical organ replacement rejection, in an	
CC	individual. The method is also useful in assessing the immune status of	
CC	an individual. The methods are also useful in diagnosing and monitoring	
CC	diseases that involve the immune system, e.g. rheumatoid arthritis,	
CC	lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or	
CC	viral, bacterial or fungal infection. The present sequence represents a	
CC	protein encoded by an mRNA sequence of the invention which show altered	
CC	expression in renal transplantation and expression.	
XX		
SQ	Sequence 1256 AA:	
	Query Match	100.0%; Score 48; DB 8; Length 1256;
	Best Local Similarity	100.0%; Pred. No. 9.6;
	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MIMEXKATV 9	
Db	689 MIMEXKATV 697	
RESULT 26		
ADQ39376		
ID	ADQ39376 standard; protein; 1258 AA.	
XX		
AC	ADQ39376;	
XX		
DT	18-NOV-2004 (first entry)	
XX		
DE	Human myocardial infarction-associated gene derived protein, SEQ ID 1039.	
XX		
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;	
XX	cardiant; gene therapy; human.	
OS	Homo sapiens.	
XX		
PN	WO2004058052-A2.	
XX		
PD	15-JUL-2004.	
XX		
PF	22-DEC-2003; 2003WO-US040978.	

XX 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin JT, Iakubova O;
 XX
 DR MPI; 2004-533949/51.
 DR N-PSDB; ADQ38548.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1039; 145pp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 XX
 SQ Sequence 1258 AA;
 Query Match 100.0%; Score 48; DB 8; Length 1258;
 Best Local Similarity 100.0%; Pred. No. 9.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXKATV 9
 Db 691 MIMEXKATV 699
 XX
 AC ADQ39379;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 XX cardiant; gene therapy; human.
 XX
 OS Homo sapiens.
 XX

PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin JT, Iakubova O;
 XX
 DR MPI; 2004-533949/51.
 DR N-PSDB; ADQ38551.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1042; 145pp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 XX
 SQ Sequence 1267 AA;
 Query Match 100.0%; Score 48; DB 8; Length 1267;
 Best Local Similarity 100.0%; Pred. No. 9.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXKATV 9
 Db 700 MIMEXKATV 708
 XX
 AC ADL16234;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Mouse protein tyrosine phosphatase #7.
 XX

KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1907; 134pp; English.
 XX
 SS The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 1304 AA;
 XX
 SO
 Query Match 100.0%; Score 48; DB 6; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MIMEXKATV 9
 DB 737 MIMEXKATV 745

KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1910; 134pp; English.
 XX
 SS The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 1304 AA;
 XX
 SO
 Query Match 100.0%; Score 48; DB 6; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MIMEXKATV 9
 DB 737 MIMEXKATV 745

RESULT 32
 ADL16230
 ID ADL16230 standard; protein; 1304 AA.
 XX
 AC ADL16230;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human protein tyrosine phosphatase #26.
 XX
 KW cytosolic; immunosuppressive; antiallergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW

KV		inducible signalling pathway; cell proliferation; cancer;
KW		guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KM		cell-cycle abnormality; enzyme.
XX		
OS	Homo sapiens.	
PX	WO2003068984-A2.	
PN		
XX		
PD	21-AUG-2003.	
XX		
PF	13-FEB-2003; 2003WO-EP001446.	
XX		
PR	13-FEB-2002; 2002US-0356810P.	
XX		
PA	12-FEB-2003; 2003US-0036547.	
PP	(COLD-) COLD SPRING HARBOR LAB.	
PT	(CEPT-) CEPTYR INC.	
PI	Tonks NK, Tzu-Ching M, Cool DE;	
DR	WPI; 2003-712572/67.	
DR	N-PSDB; ADL16229.	
PT	Identifying reversibly oxidized protein tyrosine phosphatase, useful in screening for specific modulators, potential agents for treating e.g. cancer or autoimmune disease.	
XX		
PS	Disclosure; SEQ ID NO 79; 238pp; English.	
CC		
CC	The invention relates to a method for identifying a protein tyrosine phosphatase (PTP) that is reversibly oxidized in a cell by:	(1)
CC	subjecting a sample, including a cell that contains at least one PTP, to conditions that cause reversible oxidation of PTP; (ii) isolating PTP anaerobically, in presence of a sulfhydryl-reactive agent (II) that irreversibly modifies the thiol group of an invariant Cys in the active site of PTP; and (iii) determining, under reducing conditions, the level of dephosphorylation, caused by PTP, of a labelled substrate (III), where dephosphorylation indicates that an active PTP is present. . No details of tests for these activities are given. The method is used to identify CC reversibly oxidized PTP, also to identify agents that: (a) reversibly modify such PTP; or (b) alter inducible signalling pathways in which PTP are involved. These agents are potentially useful, in human or veterinary medicine, for treating abnormal cell proliferation or growth (cancer); CC guest vs. host disease; autoimmune diseases; allergy or other CC immunosuppressed states; metabolic disorders and cell-cycle CC abnormalities. This sequence represents one of the PTP enzyme of the invention.	
XX		
SQ	Sequence 1304 AA;	
	Query Match	100.0%; Score 48; DB 7; Length 1304;
	Best Local Similarity	100.0%; Pred. No. 10;
	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MIWEOKATV 9 	
Db	737 MIWEOKATV 745	
RESULT 33		
ID	ADP65158	
AD	ADP65158 standard; protein; 1304 AA.	
XX		
AC	ADP65158;	
DT	12-AUG-2004 (first entry)	
DE	Human protein tyrosine phosphatase, receptor type, C, isoform 1.	
KM	autoimmune disease; arthritis; gene expression analysis;	
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;	
KM	antiarthritic; osteopathic; antigenic; antiinflammatory; dermatological;	
KW	immunomodulatory; lupus; ankylosing spondylitis; fibrosis;	

KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KX	immune; human.
XX	
OS	Homo sapiens.
XX	
PN	MO2003072827-AL.
XX	
XX	04-SEP-2003.
PD	
XX	
PF	31-OCT-2002; 2002WO-US035433.
PR	
XX	31-OCT-2001; 2001US-0336220P.
XX	
PA	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX	
P1	Hirsch R, Thornton SL;
XX	
DR	WPI; 2003-712740/67.
DR	GENBANK; NP_002829.
PT	
PT	Diagnosing and analyzing autoimmune disease using gene expression
PT	profiles and microarray technology, useful for diagnosing and treating
PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
XX	gout.
XX	
PS	Disclosure; Page; 56pp; English.
XX	
CC	The invention relates to a novel method for diagnosing and analysing
CC	autoimmune disease or arthritides. The method comprises obtaining a
CC	patient sample containing mRNA, analysing gene expression using the mRNA
CC	that results in a gene expression signature of the mRNA, and using that
CC	gene expression signature to diagnose or analyse the autoimmune disease
CC	or arthritides in the patient, where gene expression of at least 60% of
CC	the genes correlates with that of the gene signature. The invention
CC	further comprises: a treatment of rheumatoid arthritis; identification of
CC	genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC	other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC	analyses of autoimmune disease or rheumatoid arthritis; screening the
CC	efficacy of a candidate drug in vitro for the treatment of collagen-
CC	induced arthritis; and reducing the symptoms associated with collagen-
CC	induced arthritis. The compositions of the invention have the following
CC	activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC	antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC	methods and compositions of the present invention are useful for
CC	diagnosing and treating autoimmune disease or arthritides, such as
CC	rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC	fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC	immune disease caused by an infectious agent. This sequence represents a
CC	protein sequence relating to the genes used in the analysis and treatment
CC	of autoimmune diseases or arthritides. Note: This sequence is not shown
CC	in the specification. It has been supplied in an electronic format from
CC	WIPO.
XX	
SQ	Sequence 1304 AA;
QY	
QY	Query Match 100.0%; Score 48; DB 7; Length 1304;
QY	Best Local Similarity 100.0%; Pred. No. 10;
QY	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY	1 MIWEOKATV 9
QY	
QY	
QY	737 MIWEOKATV 745
Db	
Db	737 MIWEOKATV 745
XX	
RESULT 34	
ID	ADM67209
XX	ADM67209 standard; protein; 1304 AA.
XX	
AC	ADM67209;
XX	
DT	03-JUN-2004 (first entry)
XX	

DE Human adipocyte specific leukocyte common antigen protein Segid 563.
 XX
 KW human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; leukocyte common antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011618-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-US023684.
 XX
 PR 29-JUL-2002; 2002US-0398785P.
 XX
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMGE-) HMGCE INC.
 XX
 PI Chada K, Choulhard R, Ashar H, Sayed AMD;
 XX
 DR WPI; 2004-143846/14.
 DR N-PSDB; ADM66930.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 PS Disclosure; SEQ ID NO 563; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC -obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C-/-, ob/ob, or HMGI-C-/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 XX
 SQ Sequence 1304 AA;
 XX
 Query Match 100.0%; Score 48; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXKATV 9
 DB 737 MIMEXKATV 745
 XX
 AC ABO84455; standard; protein; 1304 AA.
 XX
 DT 18-NOV-2004 (first entry)
 DE Human cancer-associated protein HP13-011.2.
 XX
 KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;

KW Lymphoma; CAP.
 XX
 OS Homo sapiens.
 XX
 PN WO2004074320-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 XX
 PR 14-MAR-2003; 2003US-00388838.
 XX
 PR 15-APR-2003; 2003US-00417375.
 XX
 PR 13-JUN-2003; 2003US-00461862.
 XX
 PR 15-SEP-2003; 2003US-00663431.
 XX
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABD32626.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS claim 18; seqid 147; 310pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1304 AA;
 XX
 Query Match 100.0%; Score 48; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMEXKATV 9
 DB 737 MIMEXKATV 745

RESULT 36
ADQ39380
ID ADQ39380 standard; protein; 1304 AA.
XX
AC ADQ39380;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiact; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003MO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
PI Cargill M, Devlin JJ, Iakubova O;
XX
DR WPI; 2004-533949/51.
DR N-PSTB; ADQ38552.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1043; 145bp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SO Sequence 1304 AA;
XX
Query Match 100.0%; Score 48; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMOKATV 9
|||
Db 737 MIMOKATV 745
XX
RESULT 37
ADQ39375
ID ADQ39375 standard; protein; 1306 AA.
XX
AC ADQ39375;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiact; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003MO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
PI Cargill M, Devlin JJ, Iakubova O;
XX
DR WPI; 2004-533949/51.
DR N-PSTB; ADQ38547.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1038; 145bp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX

SQ Sequence 1306 AA;

Query Match 100.0%; Score 48; DB 8; Length 1306;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9

DB 739 MIMBOKATV 747

RESULT 38

ADM67208

ID ADM67208 standard; protein; 1343 AA.

AC ADM67208;

DT 03-JUN-2004 (first entry)

DE Murine adipocyte specific leukocyte common antigen protein SegID 562.

KW murine; mouse; adipocyte specific; adipose tissue; anti-obesity;

KW high mobility group 1-C protein; HMGI-C; obesity; leptin; ob; diabetes;

KW adipogenesis; hypertension; cardiovascular disease; anorectic;

KW antidiabetic; hypotensive; leukocyte common antigen.

OS Mus musculus.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMGCR-) HMGCR INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66929.

Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue of mice of different genotypes.

PS Disclosure; SEQ ID NO 562; 91pp; English.

This invention relates to a novel method for identifying genes that are over-expressed in adipose tissue and as such it provides targets for anti-obesity pharmaceutical compositions. Specifically, it refers to a high mobility group 1-C protein (HMGI-C) that is associated with obesity and is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were identified that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, hypertension and cardiovascular disease, as well as screening for compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, antidiabetic and hypotensive activities. This polypeptide sequence is a murine adipocyte specific protein sequence of the invention.

SQ Sequence 1343 AA;

Query Match 100.0%; Score 48; DB 8; Length 1343;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMBOKATV 9

DB 733 MIMBOKATV 741

Search completed: May 3, 2005, 07:41:44
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds
(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-5

Perfect score: 49

Sequence: 1 NLSELHPYL 9

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	49	100.0	1304	1	A46546	leukocyte common a
2	38	77.6	579	2	S11027	L-ascorbate oxidase
3	38	77.6	794	2	T39171	probable peroxidase
4	37	77.6	905	2	S29329	hypothetical prote
5	37	75.5	327	1	S76143	probable aldehyde
6	36	73.5	587	1	KSKVAO	L-ascorbate oxidase
7	36	73.5	1237	2	A54080	protein-tyrosine-p
8	36	73.5	1493	2	S49777	probable membrane
9	35	71.4	101	2	C75074	periplasmic di
10	35	71.4	224	2	T04246	hypothetical prote
11	35	71.4	244	2	T40881	hypothetical prote
12	35	71.4	325	2	T39169	probable oxidoredu
13	35	71.4	452	2	G83713	magnesium (Mg2+) c
14	35	71.4	552	2	A51027	L-ascorbate oxidase
15	35	71.4	590	2	S40707	hypothetical prote
16	35	71.4	1190	2	T38636	cat binding homolo
17	35	71.4	1286	2	B71413	hypothetical prote
18	34	69.4	223	2	H69118	probable phosphos
19	34	69.4	273	2	T05454	hypothetical prote
20	34	69.4	280	2	C86780	oxidoreductase ymg
21	34	69.4	316	2	A59021	aldenylase
22	34	69.4	352	2	E90416	hypothetical prote
23	34	69.4	481	2	T32260	hypothetical prote
24	34	69.4	493	2	H72011	hypothetical prote
25	34	69.4	493	2	A86613	hypothetical prote
26	34	69.4	525	2	C64313	conserved hypothet
27	34	69.4	551	2	T39092	hypothetical ser-p
28	34	69.4	581	2	S09140	coiled intron protei
29	34	69.4	633	2	T06703	hypothetical prote

30	34	69.4	779	2	S57805	aconitate hydratase
31	34	69.4	797	2	A71267	hypothetical prote
32	34	69.4	824	2	AD3098	periplasmic nitrat
33	34	69.4	828	2	A10788	probable nitrate r
34	34	69.4	828	2	G91015	probable nitrate r
35	34	69.4	828	2	D64990	probable nitrate r
36	34	69.4	828	2	A85860	probable nitrate r
37	34	69.4	829	2	F83499	periplasmic nitrat
38	34	69.4	829	2	D82430	periplasmic nitrat
39	34	69.4	830	2	AE0369	nitrate reductase
40	34	69.4	831	2	S50163	nitrate reductase
41	34	69.4	831	2	A48489	nitrate reductase
42	34	69.4	834	2	E98188	periplasmic nitrat
43	34	69.4	834	2	B95346	NapA periplasmic n
44	34	69.4	924	2	D81349	nitrate reductase
45	34	69.4	1061	2	C88690	protein FAI110.4 [

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N/Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 09-Jul-2004
C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A/Reference number: A46546; MUID:88061067; PMID:2824653
A/Accession: A46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.6/2
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-31,193-264 <ST3>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.111 and clone LCA.260
A/Accession: C46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-31,193-264 <ST3>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.1
R/Ralph, S.U.; Thomas, M.W.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A/Reference number: A91066; MUID:87275816; PMID:2956090
A/Accession: A29449
A/Molecule type: mRNA
A/Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
A/Cross-references: GB:Y00662; NID:934275; PIDN:CA68269.1; PID:934276
A/Experimental source: clones pHLC-1 and lambdaHLG1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Itai, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative t
A/Reference number: I57658; MUID:9006468; PMID:2531281
A/Accession: I57658
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:G187020; PIDN:AA59497.1; PID:G553521
 C:Genetics:
 A:Gene: GDB:PTPRC; CD45
 A:Cross-references: GDB:119768; OMIM:151460
 A:Map position: 1q31-1q32
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoster hyd
 F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 49; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NUSELHPYL 9
 |||||
 Db 919 NUSELHPYL 927

RESULT 2
 S11027
 L-ascorbate oxidase (EC 1.10.3.3) precursor - Cucurbita cv. Eblisu Nankin
 C:Species: Cucurbita cv. Eblisu Nankin
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S11027; S36936
 R:Esaka, M.; Hattori, T.; Fujisawa, K.; Sakajo, S.; Asahi, T.
 Eur. J. Biochem. 191, 537-541, 1990
 A:Title: Molecular cloning and nucleotide sequence of full-length cDNA for ascorbate oxi
 A:Reference number: S11027; MUID:90361033; PMID:2143984
 A:Accession: S11027
 A:Molecule type: mRNA
 A:Residues: 1-579 <EUR>
 A:Cross-references: UNIPROT:P24792; EMBL:X55779; NID:G18251; PIDN:CAA39300.1; PID:G18252
 A:Accession: S36936
 A:Molecule type: protein
 A:Residues: 31-48 <RSA>
 C:Superfamily: laccase
 C:Keywords: oxidoreductase
 F:375-568/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
 F:49-231/Disulfide bonds: #status predicted
 F:90,478/Binding site: copper (His) (type 2) #status predicted
 F:92,134,136,480,536,538/Binding site: 2Cu-O cluster (His) (copper type 3) #status predi
 F:111-568/Disulfide bonds: #status predicted
 F:193,392,473,542/Binding site: substrate (Trp, Trp, Glu, His) #status predicted
 F:210-223/Disulfide bonds: #status predicted

Query Match 77.6%; Score 38; DB 2; Length 579;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NUSELHPY 8
 |||||
 Db 470 NUSELHPW 477

RESULT 3
 T33171
 probable peroxisomal copper amine oxidase [imported] - fission yeast (Schizosaccharomyce
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T50376; T33171
 R:Connor, R.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, February 1998
 A:Reference number: Z21832
 A:Accession: T50376
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-794 <CO2>
 A:Cross-references: UNIPROT:O42890; EMBL:AL021815; PIDN:CAA16999.1; GSPDB:GNO0067; SPDB:
 A:Experimental source: strain 972h-; cosmid c8B4
 C:Genetics:

A:Gene: SPDB:SPAC8E4.06
 A:Map position: 2
 C:Keywords: peroxisome

Query Match 77.6%; Score 38; DB 2; Length 794;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NUSELHPY 8
 |||||
 Db 506 NMLKLHPY 513

RESULT 4
 S29329
 hypothetical protein 1 - maize transposon En-1
 C:Species: Zea mays (maize)
 C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C:Accession: S29329
 R:Pereira, A.; Cuypers, H.; Gierl, A.; Schwarz-Sommer, Z.; Saedler, H.
 EMBO J. 5, 835-841, 1986
 A:Title: Molecular analysis of the En/Spm transposable element system of Zea mays.
 A:Reference number: S28365
 A:Accession: S29329
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-905 <PER>
 A:Cross-references: UNIPROT:O41865; EMBL:M25427
 C:Genetics:
 A:Mobile element: transposon En-1

Query Match 77.6%; Score 38; DB 2; Length 905;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NUSELHPY 8
 |||||
 Db 841 NMPELHPY 848

RESULT 5
 S76143
 probable aldehyde reductase (EC 1.1.1.-) - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C:Accession: S76143
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76143
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-327 <KAN>

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 A:Start codon: GTG
 C:Superfamily: Aldehyde reductase
 C:Keywords: oxidoreductase

Query Match 75.5%; Score 37; DB 1; Length 327;
 Best Local Similarity 77.8%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NUSELHPYL 9
 |||||
 Db 188 NUSELHPYL 196

RESULT 6
KSKXAO
L-ascorbate oxidase (EC 1.10.3.3) precursor - cucumber
N/Alternate names: ascorbate
C/Species: Cucumis sativus (cucumber)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: A30094
R/Ohkawa, J.; Okada, N.; Shimizu, A.; Takano, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1239-1243, 1989
A/Title: Primary structure of cucumber (Cucumis sativus) ascorbate oxidase deduced from
A/Reference number: A30094; MIMD:89145218; PMID:2919172
A/Accession: A30094
A/Molecule type: mRNA
A/Residues: 1-587 <OHK>
A/Cross-references: UNIPROT:P14133; GB:J04494; NID:g167512; PID:AAA3119.1; PID:g167513
C/Comment: This enzyme, which catalyzes the oxidation of L-ascorbate to dehydroascorbate
C/Superfamily: lactase
C/Keywords: copper; glycoprotein; oxidoreductase
F/1-33/Domain: signal sequence #status predicted <SIG>
F/34-587/Product: L-ascorbate oxidase #status predicted <MAT>
F/38-168/Domain: amino-terminal beta-barrel #status predicted <BB1>
F/169-346/Domain: middle beta-barrel #status predicted <BB2>
F/379-574/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F/54-236,116-574,215-228/Disulfide bonds: #status predicted
F/95,483/Binding site: copper (His) (type 2) #status predicted
F/97,139,141,485,542,544/Binding site: 2Cu-O cluster (His) (copper type 3) #status predicted
F/360,401,475/Binding site: carbohydrate (asn) (covalent) #status predicted
F/480,543,548,553/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 73.5%; Score 36; DB 1; Length 587;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NUSELHPY 8
DB 475 NMSSEHPW 482

RESULT 7
A54080
Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C/Accession: A54080; 150592
R/Pang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
J. Biol. Chem. 269, 14056-14063, 1994
A/Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in
A/Reference number: A54080; MIMD:94245724; PMID:8188686
A/Accession: A54080
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1237 <PAN>
A/Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:g510510; PID:CAA79972.1; PID:g5105
C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C/Keywords: phosphoprotein; phosphoric monoster hydrolase; tyrosine-specific phosphatase
F/528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F/610-834/Domain: protein-tyrosine-phosphatase homology <PT>
F/86/Active site: Cys (phosphoserine intermediate) #status predicted
F/792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 73.5%; Score 36; DB 2; Length 1237;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NUSELHPY 9
DB 854 SLSEHSHYL 862

RESULT 8
S49777
probable membrane protein YDR180w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YD9395.14

C/Species: Saccharomyces cerevisiae
C/Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C/Accession: S49777
R/Murphy, L.; Harris, D.E.
Submitted to the EMBL Data Library, November 1994
A/Reference number: S49764
A/Accession: S49777
A/Molecule type: DNA
A/Residues: 1-1493 <MB>
A/Cross-references: UNIPROT:Q04002; EMBL:Z46727; NID:g1289283; PID:e223645; PID:g128929
C/Genetics:
A/Gene: SGD:SCC2; MIPS:YDR180w
A/Cross-references: SGD:S0002588
A/Map position: 4R
C/Keywords: transmembrane protein
F/279-295/Domain: transmembrane #status predicted <TM>

Query Match 73.5%; Score 36; DB 2; Length 1493;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSELHPY 9
DB 1038 LSELHPY 1045

RESULT 9
C75074
periplasmic divalent cation tolerance protein PAB1717 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: C75074
R/anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A/Reference number: A75001
A/Accession: C75074
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-101 <KAM>
A/Cross-references: UNIPROT:Q9V010; GB:AJ248286; GB:AL096836; NID:g5458366; PID:CAM498;
A/Experimental source: strain Orsay
C/Genetics:
A/Gene: PAB1717
C/Superfamily: divalent cation tolerance protein CUK1

Query Match 71.4%; Score 35; DB 2; Length 101;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSELHPY 8
DB 69 LSELHPY 75

RESULT 10
T04246
hypothetical protein F20B18.20 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C/Accession: T04246
R/Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohneisel, J.; Mewes, H.W.; Mayer, K.F.X
Submitted to the Protein Sequence Database, March 1999
A/Reference number: Z15263
A/Accession: T04246
A/Molecule type: DNA
A/Residues: 1-224 <BEV>
A/Cross-references: UNIPROT:Q9S7G6; EMBL:AL049483
A/Experimental source: cultivar Columbia; BAC clone F20B18
C/Genetics:
A/Map position: 4
A/Introns: 22/3; 62/1; 161/3
A/Note: F20B18.20

Query Match 71.4%; Score 35; DB 2; Length 224;
 Best Local Similarity 87.5%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSELHPYL 9
 |||||
 Db 163 LSELHPYL 170

RESULT 11

T40881

hypothetical protein SPCC1235.07 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T40881

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21954

A:Accession: T40881

A:Status: preliminary; translated from GB/EMBL/DDBL

A:Molecule type: DNA

A:Residues: 1-244 <WOO>

A:Cross-references: UNIPROT:O74844; EMBL:AL031764; PDB:CAA2111.1; GSPDB:GN00068; SPDB:

A:Experimental source: strain 972h-; cosmid c1235

C:Genetics:

A:Gene: SPDB:SPCC1235.07

A:Map position: 3 91/3; 146/3

A:introns: 39/2; 91/3; 146/3

Query Match 71.4%; Score 35; DB 2; Length 244;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SELHPYL 9
 |::|||
 Db 145 SKLHPYL 151

RESULT 12

T39169

probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T50378; T39169

R:Connor, R.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, February 1998

A:Reference number: Z21832

A:Accession: T50378

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-325 <CO2>

A:Cross-references: UNIPROT:O42888; EMBL:AL021815; PDB:1A021815; GSPDB:GN00067; SPDB:

A:Experimental source: strain 972h-; cosmid c8E4

C:Genetics:

A:Gene: SPDB:SPAC8E4.04

A:Map position: 2

C:Superfamily: aldehyde reductase

Query Match 71.4%; Score 35; DB 2; Length 325;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELHPYL 9
 |||||
 Db 190 ELHPYL 195

RESULT 13

G83713 magnesium (Mg2+) transporter BH0511 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: G83713
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: G83713

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-452 <STO>

A:Cross-references: UNIPROT:Q9KFG8; GB:AP001508; GB:BA000004; NID:g10172890; PDB:BAB042

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0511

C:Superfamily: magnesium transport protein mgTE

Query Match 71.4%; Score 35; DB 2; Length 452;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSELHPY 8
 |||||
 Db 29 LDELHPY 35

RESULT 14

A51027

L-ascorbate oxidase (EC 1.10.3.3) [validated] - zucchini

N:Alternate names: ascorbate

C:Species: Cucurbita pepo var. melopepo (zucchini)

C>Date: 08-Nov-1989 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004

C:Accession: A51027; A30066

R:Messerschmidt, A.; Ladenstein, R.; Huber, R.

submitted to the Brookhaven Protein Data Bank, January 1992

A:Reference number: A51027; PDB:1AOZ

A:Accession: A51027

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA; protein

A:Residues: 1-552 <MES>

A:Cross-references: UNIPROT:P37064

R:Rossi, A.; Petruzzelli, R.

unpublished results, cited by Messerschmidt, A., Rossi, A., Ladenstein, R., Huber, R., B

A:Reference number: A30066

A:Contents: sequence; X-ray crystallography, 2.5 angstroms

A:Accession: A30066

A:Molecule type: protein

A:Residues: 52-67;100-108,'H';445-454;498-517 <ROS>

R:Messerschmidt, A.; Ladenstein, R.; Huber, R.; Bolongesi, M.; Avigliano, L.; Petruzzelli

J. Mol. Biol. 224, 179-205, 1992

A:Title: Refined crystal structure of ascorbate oxidase at 1.9 Angstroms resolution.

A:Reference number: A58657; MUID:92194315; PMID:1548698

A:Contents: annotation; X-ray crystallography, 1.9 angstroms

A>Note: the sequence reported in A51027 is attributed to R. Petruzzelli and A. Rossi

R:Messerschmidt, A.; Luecke, H.; Huber, R.

submitted to the Brookhaven Protein Data Bank, November 1992

A:Reference number: A51619; PDB:1A50

A:Contents: annotation; X-ray crystallography, 2.2 angstroms, reduced form, residues 1-5

R:Messerschmidt, A.; Luecke, H.; Huber, R.

submitted to the Brookhaven Protein Data Bank, November 1992

A:Reference number: A51620; PDB:1A5P

A:Contents: annotation; X-ray crystallography, 2.59 angstroms, peroxide form, residues 1

R:Messerschmidt, A.; Luecke, H.; Huber, R.

submitted to the Brookhaven Protein Data Bank, November 1992

A:Reference number: A51621; PDB:1A5Q

A:Contents: annotation; X-ray crystallography, 2.32 angstroms, azide form, residues 1-55

R:Messerschmidt, A.; Rossi, A.; Ladenstein, R.; Huber, R.; Bolongesi, M.; Gatti, G.; Mar

J. Mol. Biol. 206, 513-529, 1989

A:Title: X-ray crystal structure of the blue oxidase ascorbate oxidase from zucchini. An

A:Reference number: A30633; MUID:89236417; PMID:2716059

A:Contents: annotation; X-ray crystallography, 2.5 angstroms

C:Complex: homotetramer

A:Description: catalyses the oxidation of L-ascorbate to dehydroascorbate by dioxygen

C:Superfamily: laccase
 C:Keywords: copper; glycoprotein; homotetramer; metalloprotein; oxidoreductase
 F:1-133/Domain: amino-terminal beta-barrel #status experimental <BB1>
 F:134-311/Domain: middle beta-barrel #status experimental <BB2>
 F:345-538/Domain: carboxyl-terminal beta-barrel #status experimental <BB3>
 F:19-201,81-538,180-193/Disulfide bonds: #status experimental
 F:60,448/Binding site: copper (His) (type 2) #status experimental
 F:62,104,106,450,506,508/Binding site: 2Cu-0 cluster (His) (copper type 3) #status experimental
 F:92/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:163,362,443,512/Binding site: substrate (Trp, Trp, Glu, His) #status predicted
 F:325,440/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:445,507,512,517/Binding site: copper (His, Cys, His, Met) (type 1) #status experimental

Query Match 71.4%; Score 35; DB 2; Length 552;
 Best Local Similarity 75.0%; Pred. No. 95;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLSLHPY 8
 ||| |||
 ||| |||
 Db 440 NLSLHPW 447

RESULT 15

S40707
 hypothetical protein C07A9.11 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S40707
 R/Smith, M.
 submitted to the EMBL Data Library, December 1993
 A:Reference number: S40701
 A:Accession: S40707
 A:Molecule type: DNA
 A:Residues: 1-590 <SMI>
 A:Cross-references: UNIPROT:P34322; EMBL:Z29094; NID:G436440; PID:G436447
 C:Genetics:
 A:introns: 5/3; 49/3; 144/1; 209/1; 271/1; 387/1; 428/3; 508/1; 528/3; 552/1

Query Match 71.4%; Score 35; DB 2; Length 590;
 Best Local Similarity 75.0%; Pred. NO. 1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLSLHPY 8
 ||| |||
 ||| |||
 Db 252 NLSLHPY 259

Search completed: May 3, 2005, 06:15:20
 Job time : 21.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-5

Perfect score: 49

Sequence: 1 NLSLHPYL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	1290	2 Q6ED60	Q6ED60 actus vocif
2	49	100.0	1303	2 Q6ED61	Q6ED61 actus nancy
3	49	100.0	1303	2 Q6ED62	Q6ED62 actus nigri
4	49	100.0	1304	1 CD45_HUMAN	P08575 homo sapien
5	40	81.6	1541	2 Q81UF6	Q81JF6 plasmodium
6	39	79.6	283	2 Q6C804	Q6C804 yarrowia li
7	39	79.6	747	2 Q8RP87	Q8RP87 bacteroides
8	39	79.6	747	2 Q64PT4	Q64PT4 bacteroides
9	39	79.6	757	2 Q75FE5	Q75FE5 leptospira
10	39	79.6	757	2 Q8EX87	Q8EX87 leptospira
11	39	79.6	822	2 Q64TX8	Q64TX8 bacteroides
12	39	79.6	1338	2 Q8A3N1	Q8A3N1 bacteroides
13	38	77.6	390	2 Q6CS19	Q6CS19 kluveromyc
14	38	77.6	579	1 ASO_CUCMA	P24792 cucurbita m
15	38	77.6	706	2 Q89E60	Q89E60 clostridium
16	38	77.6	794	1 AMO_SCHPO	Q42890 schizosacch
17	38	77.6	897	2 Q41865	Q41865 zea mays (m
18	37	75.5	101	2 Q971X4	Q971X4 sulfolobus
19	37	75.5	178	2 Q7XWV8	Q7XWV8 cryza sativ
20	37	75.5	193	1 ASC_MOUSE	Q9EPH4 mus musculu
21	37	75.5	220	2 Q96SU1	Q96SU1 homo sapien
22	37	75.5	277	2 Q96ID9	Q96ID9 homo sapien
23	37	75.5	280	2 Q68SU0	Q68SU0 pleurotus d
24	37	75.5	283	2 Q8Y090	Q8Y090 ralestonia s
25	37	75.5	289	2 Q7ZWA4	Q7ZWA4 brachydanio
26	37	75.5	314	2 Q6BVX2	Q6BVX2 debaryomyc
27	37	75.5	327	2 P74308	P74308 synechocyst
28	37	75.5	352	2 Q8T2C7	Q8T2C7 methanopyru
29	37	75.5	352	2 Q9BYE7	Q9BYE7 homo sapien
30	37	75.5	517	2 Q9XYS3	Q9XYS3 dictyostell
31	37	75.5	1539	2 Q68UT1	Q68UT1 pan troglod

32	37	75.5	2248	1 Y539_HUMAN	Q60287 homo sapien
33	37	75.5	2605	2 Q8IDB8	Q8IDB8 plasmodium
34	36	73.5	269	2 Q8ICQ4	Q8ICQ4 cryza sativ
35	36	73.5	279	2 Q6AT73	Q6AT73 cryza sativ
36	36	73.5	330	2 Q68E89	Q68E89 aeromonas p
37	36	73.5	562	2 Q67PM2	Q67PM2 symbiodacte
38	36	73.5	587	1 ASO_CUCSA	P14133 cucumis sat
39	36	73.5	761	2 Q7MTC3	Q7MTC3 porphyromon
40	36	73.5	798	2 Q7Q3P9	Q7Q3P9 anopheles g
41	36	73.5	963	2 Q9L730	Q9L730 arabidopsis
42	36	73.5	1237	2 Q91976	Q91976 gallus gall
43	36	73.5	1493	1 SCC2_YEAST	Q04002 saccharomyc
44	36	73.5	2033	2 Q7RQ61	Q7RQ61 plasmodium
45	36	73.5	2280	2 Q67211	Q67211 sapovirus h

ALIGNMENTS

RESULT 1					
ID	Q6ED60	PRELIMINARY;	PRT;	1290 AA.	
AC	Q6ED60;				
DT	25-OCT-2004 (TREMBLrel. 28, Created)				
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)				
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)				
DE	CD45.				
OS	Actus vociferans (Spix's owl monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.				
OX	NCBI_TaxID=57176;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	PubMed=15245371;				
RA	Montoya G.E., Vernot J.P., Patarroyo M.E.;				
RT	"Comparative analysis of CD45 protein in primate context: owl monkeys				
RT	vs. human."				
RL	Tissue Antigens 64:165-172(2004).				
DR	EMBL: AY445818; FAS06903.1; -.				
DR	GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.				
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.				
DR	InterPro; IPR003961; FN III.				
DR	InterPro; IPR008957; FN III-like.				
DR	InterPro; IPR003595; PTPc motif.				
DR	InterPro; IPR000387; TYR_phosphatase.				
DR	InterPro; IPR00242; TYR_PP.				
DR	Pfam; PF00041; fn3; 2.				
DR	Pfam; PF00102; Y_phosphatase; 2.				
DR	PRINTS; PR00700; PRTYPHPTASE.				
DR	SMART; SM00060; FN3; 2.				
DR	SMART; SM00194; PTPc; 2.				
DR	SMART; SM00404; PTPc_motif; 2.				
DR	PROSITE; PS00853; FN3; 2.				
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.				
DR	PROSITE; PS0056; TYR_PHOSPHATASE_2; 2.				
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.				
KW	Hydrolase.				
SQ	SEQUENCE 1290 AA; 145616 MW; 99E810C75D932824 CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 49; DB 2; Length 1290;					
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 NLSLHPYL 9				
DB	905 NLSLHPYL 913				
RESULT 2					
ID	Q6ED61	PRELIMINARY;	PRT;	1303 AA.	
AC	Q6ED61;				
DT	25-OCT-2004 (TREMBLrel. 28, Created)				

DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE CD45
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human."
RT Tissue Antigens 64:165-172(2004).
DR EMBL; AY445817; AAS06902.1; -.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; FN3; 2.
DR SMART; SM00404; PTPC_motif; 2.
DR PROSITE; PS00853; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolase. 1303 AA; 146929 MW; DDB00640D1D178B CRC64;
SQ

Query Match 100.0%; Score 49; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLSLHPYL 9
DB 918 NLSLHPYL 926

RESULT 3
Q6ED62 PRELIMINARY; PRT; 1303 AA.
AC Q6ED62;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE CD45.
OS Aotus nigriceps (Black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human."
RT Tissue Antigens 64:165-172(2004).
DR EMBL; AY445816; AAS06901.1; -.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; FN3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.

DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC_motif; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolase. 1303 AA; 146586 MW; 9BB023BEF4BC1165 CRC64;
SQ

Query Match 100.0%; Score 49; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLSLHPYL 9
DB 918 NLSLHPYL 926

RESULT 4
CD45_HUMAN STANDARD; PRT; 1304 AA.
ID CD45_HUMAN
AC P08575; Q1614; Q9H0Y6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)
DE (T200).
DE Name=PTPRC; Synonyms=CD45;
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RX MEDLINE=88061067; PubMed=2824653;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different
mRNAs encoding human leukocyte common antigens.";
RT J. Exp. Med. 166:1548-1566(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RX MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common
antigen).";
RT EMBO J. 6:1251-1257(1987).
RN [3]
RP SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89009812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
antigen (CD45) gene.";
RT J. Immunol. 141:2781-2787(1988).
RN [4]
RP FUNCTION.
RX MEDLINE=89017162; PubMed=2845400;
RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
protein tyrosine phosphatase.";
RT Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
RN [5]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
domains of the receptor-linked protein tyrosine phosphatases LCA and
LAR.";
RT EMBO J. 9:2399-2407(1990).
RC -1- FUNCTION: Required for T-cell activation through the antigen

receptor. The first PRPase domain has enzymatic activity, while the second one seems to affect the substrate specificity of the first one.

-1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.

-1- SUBUNIT: Binds GANAB and PRKCSH (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Comment=At least 8 isoforms are produced;

Name=1;

isoId=P08575-1; Sequence=Displayed;

Name=2;

isoId=P08575-2; Sequence=VSP_007780;

-1- PTM: Heavily N- and O-glycosylated.

-1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 1/6 subfamily.

-1- SIMILARITY: Contains 2 fibronectin type III domains.

-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

-1- DATABASE: NAME=PROW; NOTE=CD guide CD45 entry;

WWW=http://www.ncbi.nlm.nih.gov/prow/cd/cd45.htm".

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DR EMBL; Y00638; CA66869.1; -

DR EMBL; Y00662; CA66869.1; -

DR EMBL; M23492; AAD15273.2; -

DR EMBL; M23496; AAD15273.2; JOINED.

DR EMBL; M23466; AAD15273.2; JOINED.

DR EMBL; M23467; AAD15273.2; JOINED.

DR EMBL; M23468; AAD15273.2; JOINED.

DR EMBL; M23469; AAD15273.2; JOINED.

DR EMBL; M23470; AAD15273.2; JOINED.

DR EMBL; M23471; AAD15273.2; JOINED.

DR EMBL; M23472; AAD15273.2; JOINED.

DR EMBL; M23473; AAD15273.2; JOINED.

DR EMBL; M23474; AAD15273.2; JOINED.

DR EMBL; M23475; AAD15273.2; JOINED.

DR EMBL; M23476; AAD15273.2; JOINED.

DR EMBL; M23477; AAD15273.2; JOINED.

DR EMBL; M23478; AAD15273.2; JOINED.

DR EMBL; M23479; AAD15273.2; JOINED.

DR EMBL; M23480; AAD15273.2; JOINED.

DR EMBL; M23481; AAD15273.2; JOINED.

DR EMBL; M23482; AAD15273.2; JOINED.

DR EMBL; M23483; AAD15273.2; JOINED.

DR EMBL; M23484; AAD15273.2; JOINED.

DR EMBL; M23485; AAD15273.2; JOINED.

DR EMBL; M23486; AAD15273.2; JOINED.

DR EMBL; M23487; AAD15273.2; JOINED.

DR EMBL; M23488; AAD15273.2; JOINED.

DR EMBL; M23489; AAD15273.2; JOINED.

DR EMBL; M23490; AAD15273.2; JOINED.

DR EMBL; M23491; AAD15273.2; JOINED.

DR PIR; A46546; A46546.

DR HSSP; P18031; 1C88.

DR Inactive; P08575; -

DR GlycoSuiteDB; P08575; -

DR Gene; HGNC:9666; PTPRC.

DR MIM; 151460; -

DR CO; GO:0005887; C:integral to plasma membrane; TAS.

DR CO; GO:0005001; F:transmembrane receptor protein tyrosine phosphatase; TAS.

DR CO; GO:0007166; P:cell surface receptor linked signal transduction; TAS.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR008957; FN_III-like.

DR InterPro; IPR000387; TYR_phosphatase.

DR InterPro; IPR000242; Tyr_PP.

DR Pfam; PF00041; fn3; 2.

DR Pfam; PF0102; Y_phosphatase; 2.

DR PRINTS; P00700; PRTYDPHTASE.

DR PROSITE; PSS0853; FN3; 2.

DR PROSITE; PSS0083; TYR_PHOSPHATASE_1; 2.

DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.

KM Alternative splicing; Antigen; Glycoprotein; Hydrolase;

KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;

KW Transmembrane.

FT SIGNAL 1 23

FT CHAIN 24 1304

FT DOMAIN 24 575

FT TRANSMEM 576 597

FT DOMAIN 598 1304

FT DOMAIN 390 478

FT DOMAIN 482 570

FT DOMAIN 670 919

FT DOMAIN 961 1235

FT ACT_SITE 851 851

FT ACT_SITE 1167 1167

FT CARBOHYD 78 78

FT CARBOHYD 90 90

FT CARBOHYD 95 95

FT CARBOHYD 184 184

FT CARBOHYD 190 190

FT CARBOHYD 197 197

FT CARBOHYD 232 232

FT CARBOHYD 260 260

FT CARBOHYD 270 270

FT CARBOHYD 276 276

FT CARBOHYD 335 335

FT CARBOHYD 378 378

FT CARBOHYD 419 419

FT CARBOHYD 468 468

FT CARBOHYD 488 488

FT CARBOHYD 529 529

FT VARSPIC 32 192

FT MUTAGEN 851 851

FT CONFLICT 650 650

FT CONFLICT 1207 1207

SO SEQUENCE 1304 AA; 147253 MW; A08FC22D6069BA7 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 1304;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NISELHPYL 9

Db 919 NISELHPYL 927

RESULT 5

08LJF6 PRELIMINARY; PRT; 1541 AA.

AC 08LJF6;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN ORFNames=PF10_0242;

OS Plasmodium falciparum (Isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OC NCBI_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2225705; PubMed=12368864; DOI=10.1038/nature01097;

RA Gardiner M.J., Hall N., Fung B., Bertram M., Hyman R.W.,

RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,

RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M., Fairclamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carnuci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Frazer C.M., Bartell B.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum";
 RL Nature 419:498-511(2002).
 DR EMBL; AE014833; AAN35439.1; -.
 KW Hypothetical protein. 180939 MW; B060D6567D5C9816 CRC64;
 SQ SEQUENCE 1541 AA; 180939 MW;

Query Match 81.6%; Score 40; DB 2; Length 1541;
 Best local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NUSELHPYL 9
 DB 1106 NMLDHPYL 1114

RESULT 6
 Q6C804 PRELIMINARY; PRT; 283 AA.
 AC Q6C804;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Yarrowia lipolytica chromosome D of strain C11899 of Yarrowia
 DE lipolytica.
 GN ORFNames=YAL10D23859g;
 OS Yarrowia lipolytica C11899.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetaceae; Dipodascaceae; Yarrowia.
 NC NCB1_TaxID=284591;
 RX NCB1_TaxID=284591;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C11899;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anichouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boistrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropfi A.,
 RA Hantaye F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Niclaud J.M., Nikolski M., Oltas S., Oster-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weisenbach J.,
 RA Wincker P., Souciet J.L.,
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C11899;
 RA Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382130; CAG81408.1; -.
 DR InterPro; IPR007109; Brix.
 DR Pfam; PF04427; Brix; 1.
 DR PROSITE; PS50833; Brix; 1.
 SQ SEQUENCE 283 AA; 32225 MW; 9EAB02EE1E281C7 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 283;
 Best local Similarity 66.7%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NUSELHPYL 9
 DB 174 NMSEVPHYL 182

RESULT 7
 Q8RP87 PRELIMINARY; PRT; 747 AA.
 AC Q8RP87;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Aconitase protein.
 GN Name=acna;
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 NC NCB1_TaxID=817;
 RX NCB1_TaxID=817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TM400;
 RX MEDLINE=21927545; PubMed=11880608; DOI=10.1073/pnas.052710199;
 RA Baughn A.D., Malamy M.H.,
 RT "A mitochondrial-like aconitase in the bacterium Bacteroides fragilis:
 RT implications for the evolution of the mitochondrial Krebs cycle.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4662-4667(2002).
 DR EMBL; AF434843; AAM10631.1; -.
 DR HSSP; P20004; 1AMJ.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0003994; F:aconitate hydratase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0006152; F:metabolism; IEA.
 DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
 DR InterPro; IPR000573; Aconitase_C.
 DR InterPro; IPR006248; Aconitase_mito.
 DR InterPro; IPR010130; Aconitase_N.
 DR Pfam; PR00330; Aconitase; 1.
 DR Pfam; PR00694; Aconitase_C; 1.
 DR PRINTS; PR00415; ACONITASE_N.
 DR ProDom; PD000511; Aconitase_N; 1.
 DR TIGRFAMs; TIGR01340; aconitase_mito; 1.
 DR PROSITE; PS00450; ACONITASE_1; 1.
 DR PROSITE; PS01244; ACONITASE_2; 1.
 SQ SEQUENCE 747 AA; 81930 MW; 11B3392621615127 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 747;
 Best local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NUSELHPYL 9
 DB 315 NMSELEPYI 323

RESULT 8
 Q64PT4 PRELIMINARY; PRT; 747 AA.
 AC Q64PT4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Aconitase protein.
 GN ORFNames=BF3755;
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 NC NCB1_TaxID=817;
 RX NCB1_TaxID=817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YCH46;
 RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
 RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.,
 RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
 RT Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
 DR EMBL; AP006841; BAD50497.1; -.

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SQ SEQUENCE 747 AA; 81903 MW; A149C273DC49744A CRC64;
Query Match 79.6%; Score 39; DB 2; Length 747;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NUSELHPYL 9
    |||||
    315 NUSELHPYL 323

Db 315 NUSELHPYL 323

RESULT 9
Q75FE5 PRELIMINARY; PRT; 757 AA.
ID 075FE5;
AC 075FE5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Aconitase hydratase.
DE Aconitase hydratase.
GN Name=acn; OrderedlocusNames=LI020249;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OC Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F100027; DOI=10.1128/JB.186.7.2164-2172.2004;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascentino A.L.T.O., Ko A.I., Martins E.A.L., Montelero-Vitorcello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeel R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carier H.,
RA Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furian L.R., Gambertini M., Gigliotti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakura R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.B., Lemos E.G.M., Lemos M.V.F., Martino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schrieffer A.,
RA Siqueira M.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Slyke M.A.,
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE016824; AAS72270.1; -.
DR HSSP; P16276; 1B0J
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0003994; F:aconitase hydratase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR006248; Aconitase_mito.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; Aconitase_C; 1.
DR Pfam; PF00694; Aconitase_C; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; ACONITASE_N; 1.
DR TIGRAME; TIGR01340; aconitase_mito; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Complete proteome.
KW SEQUENCE 757 AA; 81983 MW; E0D29E079F21D1A4 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 757;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NUSELHPYL 9
    |||||
    315 NUSELHPYL 323

Db 315 NUSELHPYL 323

RESULT 10
Q8EX87

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ID 08EX87 PRELIMINARY; PRT; 757 AA.
AC 08EX87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Aconitase hydratase (BC 4.2.1.3).
GN Name=acn; OrderedlocusNames=LB327;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-O., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-O., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Glrons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011619; AAN51886.1; -.
DR HSSP; P20004; 1C96.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0003994; F:aconitase hydratase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR006248; Aconitase_mito.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; Aconitase_C; 1.
DR Pfam; PF00694; Aconitase_C; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; ACONITASE_N; 1.
DR TIGRAME; TIGR01340; aconitase_mito; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Complete proteome.
KW SEQUENCE 757 AA; 81953 MW; 40D92AE7697CF878 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 757;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NUSELHPYL 9
    |||||
    315 NUSELHPYL 323

Db 315 NUSELHPYL 323

RESULT 11
Q64TX8 PRELIMINARY; PRT; 822 AA.
ID 064TX8;
AC 064TX8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATP-dependent protease.
GN ORFNames=BF2304;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwaha S., Hattori M., Hayashi T., Ohnishi Y.,
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";

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RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
 DR EMBL; AP006841; BAD49051.1; -.
 KW: Protease.
 SQ SEQUENCE 822 AA; 92674 MW; 32AF703F08834041 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 822;
 Best Local Similarity 66.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLSLHPYL 9
 DB 131 NITETHPYL 139

RESULT 12

O6A3N1 PRELIMINARY; PRT; 1338 AA.
 ID O6A3N1
 AC O6A3N1
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Two-component system sensor histidine kinase/response regulator,
 GN hybrid ('one-component system').
 OS OrderedLocustNames=BT923;
 OC Bacteroides thetaiotaomicron.
 CC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OK NCBI_TaxID=816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=2250858; PubMed=1263928; DOI=10.1126/science.1080029;
 RA Xu J., Bursell M.K., Himrod J., Beng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 CC -1- SIMILARITY: Contains 1 histidine kinase domain.
 DR EMBL; AE016938; AA078029.1; -.
 DR HSSP; P06143; JMBE.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0001600; P:two-component signal transduction system (p. . .); IEA.
 DR InterPro; IPR003594; ATPbind ATPase.
 DR InterPro; IPR004358; Bact_sens_pr_C.
 DR InterPro; IPR011006; CheY_like.
 DR InterPro; IPR005467; His_Kinase.
 DR InterPro; IPR003661; His_KinA_N.
 DR InterPro; IPR000005; HTHARAC.
 DR InterPro; IPR011110; Reg_prop.
 DR InterPro; IPR001789; Response_reg.
 DR InterPro; IPR01046; Wpd0_like.
 DR InterPro; IPR011123; Y_Y_Y.
 DR Pfam; PF02518; HATPase_c1.
 DR Pfam; PF00512; HisKA_1.
 DR Pfam; PF00165; HTH_ARAC_2.
 DR Pfam; PF07494; Reg_prop; 14.
 DR Pfam; PF00072; Response_reg; 1.
 DR Pfam; PF07495; Y_Y_Y_1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR PRINTS; PR00032; HTHARAC.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HisKA_1.
 DR SMART; SM00342; HTH_ARAC; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50109; His_Kin; 1.

DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
 DR PROSITE; PS01110; RESPONSE_REGULATOR; 1.
 KW Complete proteome; DNA-binding; kinase; phosphorylation;
 KW Sensory transduction; Transcription; Transcription regulation;
 KW Transferase.
 SQ SEQUENCE 1338 AA; 153289 MW; B20E8D763809D808 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 1338;
 Best Local Similarity 77.8%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLSLHPYL 9
 DB 204 NLKTLHPYL 212

RESULT 13

O6CSL9 PRELIMINARY; PRT; 390 AA.
 ID O6CSL9
 AC O6CSL9;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Similar to ca|CA3241|IPF7493 Candida albicans putative permease.
 GN ORFNames=KLAC019481g;
 OS Kluyveromyces fragilis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OK NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marcq C., Neveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Baray S., Blanchin S., Beckerich J.M., Beyne E., Bleykaen C.,
 RA Boisarme A., Boyer J., Catolico L., Confanieri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Niclaud J.M., Nikolaki M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pelland S., Pottier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic I., Bolotin-Pukhaz M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Winkler P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; CR382123; CAH01921.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub_transporter.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF00083; Sugar_tr; 1.
 DR PROSITE; PS50850; MFS; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 KW Transmembrane.
 SQ SEQUENCE 390 AA; 43768 MW; A7522C7557CB5640 CRC64;

Query Match 77.6%; Score 38; DB 2; Length 390;
 Best Local Similarity 66.7%; Pred. No. 88;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NLSLHPYL 9
 |||||
 Db 69 NLSLHPYL 77

RESULT 14
 ID ASO CUCMA STANDARD; PRT; 579 AA.
 AC P24792; 039539;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbace) (ASO).
 OS Name=AOO;
 OS Cucurbita maxima (Pumpkin) (Winter squash).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Erosoids 1; Cucurbitales; Cucurbitaceae; Cucurbita.
 OC NCB1_TaxID=3661;
 [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 31-48.
 RC STRAIN=Cv. Edisu Nankin;
 RX MEDLINE=90361033; PubMed=2143984;
 RA Esaka M., Hattori T., Fujisawa K., Sakajo S., Asahi T.;
 RT "Molecular cloning and nucleotide sequence of full-length cDNA for
 RT ascorbate oxidase from cultured pumpkin cells.";
 RL Eur. J. Biochem. 191:537-541(1990).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97354114; PubMed=9210335;
 RA Kisu Y., Harada Y., Goto M., Esaka M.;
 RT "Cloning of the pumpkin ascorbate oxidase gene and analysis of a cis-
 RT acting region involved in induction by auxin.";
 RL Plant Cell Physiol. 38:631-637(1997).
 CC -1- FUNCTION: May be involved in a redox system involving ascorbic
 CC acid.
 CC -1- CATALYTIC ACTIVITY: 2 L-ascorbate + O(2) = 2 dehydroascorbate + 2
 CC H(2)O.
 CC -1- COFACTOR: This protein belongs to the multicopper oxidases which
 CC contain three distinct Cu centers known as type 1 or blue, type 2
 CC or normal, and type 3 or coupled binuclear.
 CC -1- SIMILARITY: Belongs to the multicopper oxidase family.
 CC -1- SIMILARITY: Contains 3 plastocyanin-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X55779; CAA39300.1; -;
 DR EMBL; D55677; BAA09528.1; -;
 DR PIR; S11027; S11027.
 DR HSSP; P37064; 1A0Z.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR002355; Cu-ox_copper_BS.
 DR InterPro; IPR008972; Cupredoxin.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR PROSITE; PS00079; MULTICOPPER OXIDASE1; 1.
 DR PROSITE; PS00080; MULTICOPPER OXIDASE2; 1.
 KW Copper; Direct protein sequencing; Glycoprotein; Metal-binding;
 KW Oxidoreductase; Repeat; Signal.
 FT CHAIN 1 30
 FT SIGNAL 1 30
 FT CHAIN 31 579
 FT DOMAIN 33 152 L-ascorbate oxidase.
 FT DOMAIN 164 330 Plastocyanin-like 1.
 FT DOMAIN 374 553 Plastocyanin-like 2.
 FT DISULFID 49 231 Plastocyanin-like 3.
 FT DISULFID 111 568 By similarity.
 FT DISULFID 210 223 By similarity.
 FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 470 470 N-linked (GlcNAc...) (Potential).
 FT METAL 90 90 Copper (type 2) (Probable).
 FT METAL 92 92 Copper (type 2) (Probable).
 FT METAL 134 134 Copper (type 3) (Probable).
 FT METAL 136 136 Copper (type 3) (Probable).
 FT METAL 475 475 Copper (type 1) (Probable).
 FT METAL 478 478 Copper (type 2) (Probable).
 FT METAL 480 480 Copper (type 2) (Probable).
 FT METAL 536 536 Copper (type 3) (Probable).
 FT METAL 537 537 Copper (type 3) (Probable).
 FT METAL 538 538 Copper (type 3) (Probable).
 FT METAL 542 542 Copper (type 1) (Probable).
 FT METAL 547 547 Copper (type 1) (Probable).
 FT METAL 547 547 Copper (type 1) (Probable).
 FT CONFLICT 175 175 W-C (in Ref. 1).
 SQ SEQUENCE 579 AA; 64667 MW; 8F5AF4CB07B276B9 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 579;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLSLHPYL 8
 |||||
 Db 470 NLSLHPYL 477

RESULT 15
 Q89860
 ID Q89860 PRELIMINARY; PRT; 706 AA.
 AC Q89860;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Internalin A-like protein/putative S-layer protein.
 GN OrderedocumenNames=CTC00494;
 OS Clostridium tetani.
 OS Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCB1_TaxID=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Massachusetts / B88;
 RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.033853100;
 RA Bruggemann H., Bauner S., Fricke W.F., Wierer A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gotschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 RT tetanus disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
 DR EMBL; AB015937; AAO35121.1; -;
 DR HSSP; P25146; 106V.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007092; LRR_SD522.
 DR Pfam; PF00560; LRR 1; 19.
 DR PRINTS; PR00019; LEURICHRPT.
 KW Complete proteome.
 SO SEQUENCE 706 AA; 80455 MW; F84607EDB53CEN39 CRC64;

Query Match 77.6%; Score 38; DB 2; Length 706;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLSLHPYL 7
 |||||
 Db 424 NLSLHPYL 430

Search completed: May 3, 2005, 05:59:13
 Job time : 46.1351 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 06:25:02 ; Search time 44 Seconds
(without alignments)
79.110 Million cell updates/sec

Title: US-10-003-983C-5

Perfect score: 49

Sequence: 1 NLSLHPYL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	5	ABG31975 Human CD4
2	49	100.0	10	5	ABG31976 Human CD4
3	49	100.0	764	8	ABO84454 Human can
4	49	100.0	960	8	ADQ39377 Human myo
5	49	100.0	1114	6	ABU05246 Human exp
6	49	100.0	1114	6	ABU05239 Human exp
7	49	100.0	1143	6	ABU05240 Human exp
8	49	100.0	1143	6	ABU05245 Human exp
9	49	100.0	1143	7	ADL16232 Human pro
10	49	100.0	1143	8	ADQ18845 Human pol
11	49	100.0	1149	4	AA441048 Human pol
12	49	100.0	1149	6	ABU05242 Human exp
13	49	100.0	1192	8	ADQ39376 Human myo
14	49	100.0	1219	8	ADQ39378 Human myo
15	49	100.0	1256	8	ADQ67187 Human adi
16	49	100.0	1256	8	ADP12966 Protein e
17	49	100.0	1258	8	ADQ39376 Human myo
18	49	100.0	1267	8	ADQ39379 Human myo
19	49	100.0	1304	6	ABU05243 Human exp
20	49	100.0	1304	6	ABU05241 Human exp
21	49	100.0	1304	6	ABU05244 Human exp
22	49	100.0	1304	7	ADL16230 Human pro
23	49	100.0	1304	7	ADP65158 Human pro
24	49	100.0	1304	8	ADM67209 Human adi
25	49	100.0	1304	8	ABO84455 Human can

26	49	100.0	1304	8	ADQ39380 Human myo
27	49	100.0	1306	8	ADQ39375 Human myo
28	39	79.6	273	8	ADN21825 Bacterial
29	39	79.6	273	8	ADN24584 Bacterial
30	39	79.6	322	6	ABU21347 Protein e
31	39	79.6	813	6	ABU20999 Protein e
32	38	77.5	579	2	AA14306 Acorbate
33	37	75.5	103	7	ADQ31123 Human nov
34	37	75.5	168	4	AA012232 Human pol
35	37	75.5	168	7	ADC32832 Human nov
36	37	75.5	193	4	AA820086 Mouse CAR
37	37	75.5	193	4	AA800592 Mouse car
38	37	75.5	193	5	AAU99352 Mouse cas
39	37	75.5	194	7	ADQ43845 Mouse pro
40	37	75.5	220	4	AA894801 Human pro
41	37	75.5	220	5	AAU80360 Human cel
42	37	75.5	267	8	AD524989 Bacterial
43	37	75.5	327	8	ADN20106 Bacterial
44	37	75.5	352	5	AAU80358 Human cel
45	37	75.5	352	7	ADM25397 Hyperther

ALIGNMENTS

RESULT 1
ABG31975
ID ABG31975 standard; peptide; 9 AA.

AC ABG31975;

DT 05-NOV-2002 (first entry)

DE Human CD45 HLA-binding peptide, huCD45/919.

XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;

XX antigen-presenting cell; APC; major histocompatibility complex; MHC;

XX antigen; allogenic; T cell receptor; TCR; cancer; tumour;

XX allogenic stem cell transplantation; CFU-GM; leukaemia;

XX colony forming unit-granulocyte macrophage; immunotherapeutic;

XX haematopoietic; malignant.

XX Homo sapiens.

OS MO200244207-A1.

PN 06-JUN-2002.

PD 30-NOV-2000, 2000MO-GB004566.

PF 30-NOV-2000, 2000MO-GB004566.

PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PA Staus HJ, Amrolia PJ;

XX MPI, 2002-599413/64.

XX Claim 2, Page 38, 56pp; English.

XX The invention discloses a peptide comprising the human leukocyte antigen

XX (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,

XX provided that the peptide is not the intact human CD45 polypeptide. The

XX peptides are useful for producing activated cytotoxic T lymphocyte (CTL)

XX in vitro which involves contacting the CTL with an antigen-presenting

XX cell, where its major histocompatibility complex (MHC) class I molecules

XX are loaded with the peptide, to activate, in an antigen specific manner,

XX where the CTL and the antigen presenting cell are allogenic with respect

XX to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animals models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/919,
CC comprising an HLA-binding peptide of human CD45

SQ Sequence 9 AA;
Query Match 100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLSLHPYL 9
DB 1 NLSLHPYL 9

RESULT 2
ABG31976
ID ABG31976 standard; peptide; 10 AA.
XX
AC ABG31976;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CD45 HLA-binding peptide, huCD45/918.
XX
XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
XX antigen-presenting cell; APC; major histocompatibility complex; MHC;
XX antigen; allogenic; T cell receptor; TCR; cancer; tumour;
XX allogenic stem cell transplantation; CFU-GM; leukaemia;
XX colony forming unit-granulocyte macrophage; immunotherapeutic;
XX haematopoietic; malignant.
XX
XX Homo sapiens.
XX
XX WO200244207-A1.
XX
XX 06-JUN-2002.
XX
XX 30-NOV-2000; 2000WO-GB004566.
XX
XX 30-NOV-2000; 2000WO-GB004566.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Steaus HJ, Amrolia PJ;
XX
XX WPI; 2002-599413/64.
XX
XX
XX Novel peptide comprising leukocyte antigen binding peptide of human CD45
XX polypeptide, useful for producing activated cytotoxic T lymphocytes, for
XX killing cancerous cells e.g. leukemia.
XX
XX Claim 2; Page 38; 56pp; English.
XX
XX The invention discloses a peptide comprising the human leukocyte antigen
XX (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,
XX provided that the peptide is not the intact human CD45 polypeptide. The
XX peptides are useful for producing activated cytotoxic T lymphocyte (CTL)

CC in vitro which involves contacting the CTL with an antigen-presenting
CC cell, where its major histocompatibility complex (MHC) class I molecules
CC are loaded with the peptide, to activate, in an antigen specific manner,
CC where the CTL and the antigen presenting cell are allogenic with respect
CC to the class I MHC molecule that is presenting peptides of CD45. The
CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animals models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/918,
CC comprising an HLA-binding peptide of human CD45

SQ Sequence 10 AA;
Query Match 100.0%; Score 49; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLSLHPYL 9
DB 2 NLSLHPYL 10

RESULT 3
ABO84454
ID ABO84454 standard; protein; 764 AA.
XX
AC ABO84454;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP13-011.1.
XX
XX Human; cancer-associated protein; cytosolic; cancer; leukaemia;
XX lymphoma; CAP.
XX
XX Homo sapiens.
XX
XX OS
XX
XX PN WO2004074320-A2.
XX
XX 02-SEP-2004.
XX
XX 17-FEB-2004; 2004WO-US004730.
XX
XX 14-FEB-2003; 2003US-00367094.
XX
XX 14-MAR-2003; 2003US-0038838.
XX
XX 15-APR-2003; 2003US-00417375.
XX
XX 13-JUN-2003; 2003US-00461862.
XX
XX 15-SEP-2003; 2003US-00663431.
XX
XX 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
XX
XX WPI; 2004-652914/63.
XX
XX N-PSDB; ABD32625.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.

XX claim 18; seqid 145; 310pp; English.

CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 23 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX Sequence 764 AA;

Query Match 100.0%; Score 49; DB 8; Length 764;

Best Local Similarity 100.0%; Pred. No. 0.75; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLSLHPYL 9
DB 379 NLSLHPYL 387

RESULT 4
ADQ39377 standard; protein; 960 AA.

XX ADQ39377;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1040.

KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
cardiac; gene therapy; human.

OS Homo sapiens.

PN MO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin JT, Iakubova O;

DR WPI; 2004-533949/51.

DR N-PDB; ADQ38549.

PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.

PS Claim 10; SEQ ID NO 1040; 145pp; English.

CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 960 AA;

Query Match 100.0%; Score 49; DB 8; Length 960;

Best Local Similarity 100.0%; Pred. No. 0.97; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLSLHPYL 9
DB 575 NLSLHPYL 583

RESULT 5
ABU05246 standard; protein; 1114 AA.

XX ABU05246;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1912.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

```
XX 28-MAR-2002; 2002MO-US009671.
PF 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1912; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1114 AA;
XX
XX Query Match 100.0%; Score 49; DB 6; Length 1114;
XX Best Local Similarity 100.0%; Pred. No. 1.1; 0; Indels 0; Gaps 0;
XX Matches 9; Conservative 0; Mismatches 0;
XX
XX QY 1 NLSLHPYL 9
XX |||||
XX 729 NLSLHPYL 737
XX
XX Db
XX
XX RESULT 6
XX ABU05239
XX ID ABU05239 standard; protein; 1114 AA.
XX
XX AC ABU05239;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1905.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
```

```
XX 28-MAR-2002; 2002MO-US009671.
PF 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1905; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1114 AA;
XX
XX Query Match 100.0%; Score 49; DB 6; Length 1114;
XX Best Local Similarity 100.0%; Pred. No. 1.1; 0; Indels 0; Gaps 0;
XX Matches 9; Conservative 0; Mismatches 0;
XX
XX QY 1 NLSLHPYL 9
XX |||||
XX 729 NLSLHPYL 737
XX
XX Db
XX
XX RESULT 7
XX ABU05240
XX ID ABU05240 standard; protein; 1143 AA.
XX
XX AC ABU05240;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1906.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
```

```
XX 28-MAR-2002; 2002MO-US009671.
PF
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX
PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1143 AA;
SQ
Query Match 100.0%; Score 49; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLSLHPYL 9
Db 758 NLSLHPYL 766
RESULT 8
ABU05245
ID ABU05245 standard; protein; 1143 AA.
XX
AC ABU05245;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1911.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
XX WO200278524-A2.
XX
PD 10-OCT-2002.
```

```
XX 28-MAR-2002; 2002MO-US009671.
PF
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX
PS Example 2; SEQ ID NO 1911; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1143 AA;
SQ
Query Match 100.0%; Score 49; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLSLHPYL 9
Db 758 NLSLHPYL 766
RESULT 9
ADL16232
ID ADL16232 standard; protein; 1143 AA.
XX
AC ADL16232;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #27.
XX
KW cytostatic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.
XX
XX WO2003068984-A2.
XX
XX 21-AUG-2003.
```

XX PF 13-FEB-2003; 2003WO-BE001446.
XX PR 13-FEB-2002; 2002US-0356810P.
XX PR 12-FEB-2003; 2003US-00366547.
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PA (CEPT-) CEPTYR INC.
XX PI Tonks NK, Tzu-Ching M, Cool DE;
XX DR WPI; 2003-712572/67.
XX DR N-PSDB; ADL16231.
XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX PT screening for specific modulators, potential agents for treating e.g.
XX PT cancer or autoimmune disease.
XX PS Disclosure; SEQ ID NO 81; 238bp; English.
XX CC The invention relates to a method for identifying a protein tyrosine
XX CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX CC subjecting a sample, including a cell that contains at least one PTP, to
XX CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX CC anaerobically, in presence of a sulfhydryl-reactive agent (iii) that
XX CC irreversibly modifies the thiol group of an invariant Cys in the active
XX CC site of PTP; and (iii) determining, under reducing conditions, the level
XX CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
XX CC dephosphorylation indicates that an active PTP is present. . No details
XX CC of tests for these activities are given. The method is used to identify
XX CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX CC are involved. These agents are potentially useful, in human or veterinary
XX CC medicine, for treating abnormal cell proliferation or growth (cancer);
XX CC guest vs. host disease; autoimmune diseases; allergy or other
XX CC immunosuppressed states; metabolic disorders and cell-cycle
XX CC abnormalities. This sequence represents one of the PTP enzyme of the
XX CC invention.
XX SQ Sequence 1143 AA;
XX
XX Query Match 100.0%; Score 49; DB 7; Length 1143;
XX Best Local Similarity 100.0%; Pred. No. 1.2;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NISELHPYL 9
XX DB 758 NISELHPYL 766
XX
XX RESULT 10
XX ID ADQ18845 standard; protein; 1143 AA.
XX AC ADQ18845;
XX XX
XX DT 26-AUG-2004 (first entry)
XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX OS Homo sapiens.
XX XX
XX PN WO2004048938-A2.
XX PD 10-JUN-2004.
XX PF 26-NOV-2003; 2003WO-US038193.
XX PR 26-NOV-2002; 2002US-0429739P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX XX
XX PI Aziz N, Gineburg WM, Zlotnik A;
XX DR WPI; 2004-441208/41.
XX PT Early detection of soft tissue sarcoma comprises determining expression
XX PT of a gene in a first soft tissue sample and a normal soft tissue sample
XX PT and comparing the gene expression, also useful in treating soft tissue
XX PT sarcoma.
XX PS Example 2; SEQ ID NO 1664; 210bp; English.
XX CC The invention relates to a novel method for detecting soft tissue sarcoma
XX CC which comprises obtaining a first soft tissue sample from an individual
XX CC and a normal soft tissue sample from the same or different individual,
XX CC determining the expression of a gene in both samples and comparing the
XX CC expression of the gene in both soft tissue samples, where a higher level
XX CC of protein expression in the first soft tissue sample indicates the
XX CC presence of soft tissue sarcoma. The method of the invention has
XX CC cyrostatic applications and may be useful for detecting soft tissue
XX CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX CC acid sequences may be useful in diagnostic and screening applications.
XX CC The current sequence is that of a human soft tissue sarcoma-upregulated
XX CC protein of the invention. The current sequence is not shown within the
XX CC specification per se but was submitted in CD format by the inventor.
XX SQ Sequence 1143 AA;
XX
XX Query Match 100.0%; Score 49; DB 8; Length 1143;
XX Best Local Similarity 100.0%; Pred. No. 1.2;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NISELHPYL 9
XX DB 758 NISELHPYL 766
XX
XX RESULT 11
XX ID AAM41048 standard; protein; 1149 AA.
XX AC AAM41048;
XX XX
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 5979.
XX XX
XX KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX KW leukaemia.
XX OS Homo sapiens.
XX XX
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US034263.
XX XX
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00468725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AAI60204.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 2; SEQ ID NO 5979; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA038642-AA042213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1149 AA;
XX
Query Match 100.0%; Score 49; DB 4; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLSLHPYL 9
DB 764 NLSLHPYL 772
XX
RESULT 12
ABU05242
ID ABU05242 standard; protein; 1149 AA.
XX
AC ABU05242;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1908.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCO INC.
XX

PI Chicz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
DR
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1908; 134pp; English.
PS
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1149 AA;
XX
Query Match 100.0%; Score 49; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLSLHPYL 9
DB 764 NLSLHPYL 772
XX
RESULT 13
ADR39747
ID ADR39747 standard; protein; 1192 AA.
XX
AC ADR39747;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human kinase and phosphatase KRP-20 protein SEQ ID NO:20.
XX
XX human, kinase and phosphatase protein; KRP; enzyme; cytostatic;
KW antiarteriosclerotic; anticoagulant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; anti-allergic; anti-inflammatory;
KW chymotryptic; gene therapy; cell proliferative disorder; cancer;
KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KW KRP-20.
XX
OS Homo sapiens.
XX
PN WO2004074453-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005092.
XX
XX 20-FEB-2003; 2003US-0449059P.
PR 19-MAR-2003; 2003US-0458932P.
PR 28-MAR-2003; 2003US-0458844P.
PR 09-APR-2003; 2003US-0461678P.
PR 17-APR-2003; 2003US-0463937P.
XX
XX

PA (INCY-) INCYTE CORP.
 XX Rankumar J, Margulis JP, Swarnakar A, Chawla NK, Tran UK,
 PI Becha SD, Lee ST, Hafalia AJA, Richardson TW, Khare R, Jiang X,
 PI Jackson AA, Yang J, Gorvad AE;
 XX MPI; 2004-635568/61.
 DR N-PSDB; ADR39793.
 XX
 PT New human kinases and phosphatases (KPP) for diagnosing, treating and
 PT preventing diseases or conditions associated with aberrant KPP expression
 PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
 PS
 XX Claim 1, SEQ ID NO 20; 299pp; English.
 XX
 CC The present sequence represents the human kinase and phosphatase protein
 CC (KPP), designated KPP-20. The human KPP sequences from the present
 CC invention have cytosolic, antiarteriosclerotic, anticonvulsant,
 CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, anti-allergic,
 CC antiinflammatory and thymometric activities, and can be used in gene
 CC therapy. The human KPP proteins and polynucleotides can be used in
 CC diagnosing, treating and preventing diseases or conditions associated
 CC with the decreased expression or overexpression of KPP, such as cell
 CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g. AIDS,
 CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
 CC allergies), and developmental (e.g. Hypothyroidism, Cushing's syndrome)
 CC disorders, or infections. They can also be used in assessing the effects
 CC of exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of KPP. The KPP or its fragments are useful in screening
 CC compounds for effectiveness as agonist or antagonist of the polypeptides,
 CC or in altering the expression of the target polynucleotide and compounds
 CC that specifically bind to or modulate the activity of the polypeptide.
 XX
 SQ Sequence 1192 AA;
 Query Match 100.0%; Score 49; DB 8; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NUSELHPYL 9
 Db 807 NUSELHPYL 815
 RESULT 14
 ADO39378
 ID ADO39378 standard; protein; 1219 AA.
 XX
 AC ADO39378;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JD, Iakoubova O;

XX
 DR MPI; 2004-533949/51.
 DR N-PSDB; ADO38550.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1041; 145pp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1219 AA;
 Query Match 100.0%; Score 49; DB 8; Length 1219;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NUSELHPYL 9
 Db 834 NUSELHPYL 842
 RESULT 15
 ADM67187
 ID ADM67187 standard; protein; 1256 AA.
 XX
 AC ADM67187;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human adipocyte specific PRPase receptor type C protein SeqID 541.
 XX
 KW human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
 KW antidiabetic; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; PRPase receptor type C.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011618-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-US023684.
 XX
 PR 29-JUL-2002; 2002US-0398785P.
 XX
 PI

PR 12-JUN-2003; 2003US-0478206P.
XX
XX (HMGCE-) HMGCE INC.
PA
XX
XX Chada K, Chouinard R, Ashar H, Sayed AMD;
PI
XX WPI; 2004-143846/14.
DR
XX N-PSDB; ADM66908.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 541; 91pp; English.
XX
XX This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti-
CC obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMG1-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
XX
SQ Sequence 1256 AA;
XX
Query Match 100.0%; Score 49; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLSLHPYL 9
DB 871 NLSLHPYL 879
XX
RESULT 16
ADP12966
ID ADP12966 standard; protein; 1256 AA.
XX
XX ADP12966;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
XX Protein encoding reference mRNA sequence #51.
DE
XX
XX transplacental rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
XX Homo sapiens.
OS
XX
XX WO2004042346-A2.
PN
XX
XX 21-MAY-2004.
PD
XX
XX 24-APR-2003; 2003WO-US012946.
PF
XX
XX 24-APR-2002; 2002US-00113831.
PR
XX 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI

PI Rosenberg S;
XX
XX WPI; 2004-400724/37.
DR
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 65; SEQ ID NO 2975; 1762pp; English.
PS
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprising detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein encoded by an mRNA sequence of the invention which show altered
CC expression in renal transplantation and expression.
XX
SQ Sequence 1256 AA;
XX
Query Match 100.0%; Score 49; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLSLHPYL 9
DB 871 NLSLHPYL 879
XX
RESULT 17
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.
XX
XX ADQ39376;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
DE
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiac; gene therapy; human.
XX
XX Homo sapiens.
OS
XX
XX WO2004058052-A2.
PN
XX
XX 15-JUL-2004.
PD
XX
XX 22-DEC-2003; 2003WO-US040978.
PF
XX
XX 20-DEC-2002; 2002US-0434778P.
PR
XX 10-MAR-2003; 2003US-0453135P.
PR
XX 30-APR-2003; 2003US-0466412P.
PR
XX 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
PA
XX
XX Cargill M, Devlin J, Iakubova O;
PI
XX
XX WPI; 2004-533949/51.
DR
XX N-PSDB; ADQ38548.
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
PI

XX PS Claim 10; SEQ ID NO 1039; 145bp; English.
 XX CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 CC SQ Sequence 1258 AA;
 CC
 CC Query Match 100.0%; Score 49; DB 8; Length 1258;
 CC Best Local Similarity 100.0%; Pred. No. 1.3;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 NLSLHPYL 9
 CC DB 873 NLSLHPYL 881
 CC
 CC RESULT 18
 CC ADQ39379
 CC ID ADQ39379 standard; protein; 1267 AA.
 CC XX ADQ39379;
 CC DT 18-NOV-2004 (first entry)
 CC XX
 CC DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
 CC XX
 CC KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 CC KW cardiant; gene therapy; human.
 CC XX
 CC OS Homo sapiens.
 CC XX
 CC PN MO2004058052-A2.
 CC PD 15-JUL-2004.
 CC XX
 CC PF 22-DEC-2003; 2003WO-US040978.
 CC XX
 CC PR 20-DEC-2002; 2002US-0434778P.
 CC PR 10-MAR-2003; 2003US-0453135P.
 CC PR 30-APR-2003; 2003US-0466412P.
 CC PR 23-SEP-2003; 2003US-0504955P.
 CC XX
 CC PA (APPL-) APPLERA CORP.
 CC XX
 CC PI Cargill M, Devlin JT, Jakubova O,
 CC XX
 CC DR WPI; 2004-533949/51.

DR N-PSDB; ADQ38551.
 XX PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 XX PS Claim 10; SEQ ID NO 1042; 145bp; English.
 XX CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 CC SQ Sequence 1267 AA;
 CC
 CC Query Match 100.0%; Score 49; DB 8; Length 1267;
 CC Best Local Similarity 100.0%; Pred. No. 1.3;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 NLSLHPYL 9
 CC DB 882 NLSLHPYL 890
 CC
 CC RESULT 19
 CC ABU05243
 CC ID ABU05243 standard; protein; 1304 AA.
 CC XX ABU05243;
 CC DT 29-JAN-2003 (first entry)
 CC XX
 CC DE Human expressed protein tag (EPT) #1909.
 CC XX
 CC KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 CC XX
 CC OS Homo sapiens.
 CC XX
 CC PN WO200278524-A2.
 CC PD 10-OCT-2002.
 CC XX
 CC PF 28-MAR-2002; 2002WO-US009671.
 CC XX
 CC PR 28-MAR-2001; 2001US-0279495P.
 CC PR 21-MAY-2001; 2001US-0292544P.

XX Hirsch R, Thornton SL;
 PI WPI; 2003-712740/67.
 DR GENBANK; NP_002829.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 gout.
 XX
 PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC anti-gout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 XX
 SQ Sequence 1304 AA;
 Query Match 100.0%; Score 49; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NLSLHPYL 9
 Db 919 NLSLHPYL 927
 RESULT 24
 ADM67209
 ID ADM67209 standard; protein; 1304 AA.
 XX
 AC ADM67209;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human adipocyte specific leukocyte common antigen protein SegID 563.
 XX
 KW human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; leukocyte common antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011618-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-US023684.

XX 29-JUL-2002; 2002US-0398785P.
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMG1-) HMG1 INC.
 XX
 PI Chada K, Chouinard R, Ashar H, Sayed AMD;
 XX WPI; 2004-143846/14.
 DR N-PSDB; ADM66930.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 PS Disclosure; SEQ ID NO 563; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC -obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMG1-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMG1-C-/-, ob/ob, or HMG1-C-/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 XX
 SQ Sequence 1304 AA;
 Query Match 100.0%; Score 49; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NLSLHPYL 9
 Db 919 NLSLHPYL 927
 RESULT 25
 AB084455
 ID AB084455 standard; protein; 1304 AA.
 XX
 AC AB084455;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human cancer-associated protein HPI3-011.2.
 XX
 KW Human; cancer-associated protein; cytosolic; cancer; leukaemia;
 KW lymphoma; CAP.
 XX
 OS Homo sapiens.
 XX
 PN WO2004074320-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
 XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KM cardiant; gene therapy; human.
 XX Homo sapiens.
 OS
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JJ, Takubova O,
 XX
 DR WPI; 2004-533949/51.
 DR N-PSDB; ADQ38547.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 PS Claim 10; SEQ ID NO 1038; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1306 AA;

Query Match 100.0%; Score 49; DB 8; Length 1306;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NISELAPYL 9
 DB 921 NISELAPYL 929

Search completed: May 3, 2005, 07:29:32
 Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 7.43243 Seconds
(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-6

Perfect score: 53

Sequence: 1 VNLSHLHPYL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	1304	1	A46546	leukocyte common a
2	42	79.2	905	2	S29329	hypothetical prote
3	41	77.4	327	1	S76143	probable aldehyde
4	40	75.5	1237	2	A54080	protein-tyrosine-P
5	38	71.7	316	2	A59021	aldehyde reductase
6	38	71.7	579	2	S11027	L-ascorbate oxidas
7	38	71.7	794	2	T39171	probable peroxisom
8	37	69.8	277	1	A45961	2,5-diketo-D-gluc
9	37	69.8	280	2	C86780	oxidoreductase ymg
10	37	69.8	289	2	AE0660	probable oxidoredu
11	37	69.8	289	2	B90671	probable reductase
12	37	69.8	294	2	P85521	probable dehydrog
13	37	69.8	295	1	S30383	morphine 6-dehydro
14	37	69.8	779	2	S57805	aconitine hydratase
15	37	69.8	2910	2	T42214	otogelin - mouse
16	36	67.9	277	2	T34993	probable oxidoredu
17	36	67.9	302	2	A34406	aldehyde reductase
18	36	67.9	315	1	A35452	aldehyde reductase
19	36	67.9	316	1	A39763	aldehyde reductase
20	36	67.9	316	1	A60603	aldehyde reductase
21	36	67.9	316	2	T49484	aldehyde reductase
22	36	67.9	322	2	T49435	aldo-keto reductas
23	36	67.9	325	2	T39169	probable oxidoredu
24	36	67.9	587	1	KSKYAO	L-ascorbate oxidas
25	36	67.9	620	2	S55086	probable membrane
26	36	67.9	780	2	T52543	aconitine hydratase
27	36	67.9	781	2	A35544	aconitine hydratase
28	36	67.9	781	2	S57528	aconitine hydratase
29	36	67.9	1273	1	TDRILT	leukocyte common a

30	36	67.9	1291	1	A28334	protein-tyrosine-P
31	36	67.9	1493	2	S49777	probable membrane
32	35	66.0	101	2	C75074	periplasmic divale
33	35	66.0	224	2	T04246	hypothetical prote
34	35	66.0	244	2	T40881	hypothetical prote
35	35	66.0	277	2	D89964	hypothetical prote
36	35	66.0	335	2	S64421	hypothetical prote
37	35	66.0	452	2	G83713	magnesium (Mg2+) t
38	35	66.0	552	2	A51027	L-ascorbate oxidas
39	35	66.0	581	2	S09140	coll intron protei
40	35	66.0	590	2	S40707	hypothetical prote
41	35	66.0	633	2	T06703	hypothetical prote
42	35	66.0	833	2	S50225	potassium transpor
43	35	66.0	841	2	T38703	hypothetical prote
44	35	66.0	1190	2	T38636	cat binding homolo
45	35	66.0	1286	2	B71413	hypothetical prote

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C:Species: Homo sapiens (nan)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 09-Jul-2004
C/Accession: A46546; B46546; A29449; B29449; I57658
R:Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A:Reference number: A46546; MUID:88061067; PMID:2824653
A:Accession: A46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1304 <STR>
A:Cross-references: UNIPROT:P08575; GB:Y00638
A:Experimental source: clone LCA.6/2
A:Accession: B46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-32,99-264 <ST2>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.111 and clone LCA.260
A:Accession: C46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-31,193-264 <ST3>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.1
A:Experimental source: clone LCA.1
R:Ralph, S.U.; Thomas, W.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A:Reference number: A91066; MUID:87275816; PMID:2956090
A:Accession: A29449
A:Molecule type: mRNA
A:Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
A:Cross-references: GB:Y00662; NID:934275; PIDN:CA68269.1; PID:934276
A:Experimental source: clones pHLC-1 and lambdaHLG1
A:Accession: B29449
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 32-192 <RA2>
A:Experimental source: clone HLC-2
R:Tsal, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative ;
A:Reference number: I57658; MUID:90066468; PMID:2531281
A:Accession: I57658
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 146-192 <RBS>

A/Cross-references: GB:M29253; NID:G187020; PIDN:AAA59497.1; PID:G553521

C/Genetics:

A/Gene: GDB:PTPRC; CD45

A/Cross-references: GDB:119768; OMIM:151460

A/Map position: 1q31-1q32

C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>

F:851/Active site: Cys (phosphocysteine intermediate) #status predicted

F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match

100.0%; Score 53; DB 1; Length 1304;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNLSLHAPYL 10

Db 918 VNLSLHAPYL 927

RESULT 2

S29329
hypothetical protein 1 - maize transposon En-1

C/Species: Zea mays (maize)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004

C/Accession: S29329

R:Peretira, A.; Clypers, H.; Gierl, A.; Schwarz-Sommer, Z.; Saedler, H.

EMBO J. 5, 835-941, 1986

A/Title: Molecular analysis of the En/Spm transposable element system of Zea mays.

A/Reference number: S28365

A/Accession: S29329

A/Status: preliminary; translation not shown

A/Molecule type: DNA

A/Residues: 1-905 <PER>

A/Cross-references: UNIPROT:Q41865; EMBL:M25427

C/Genetics:

A/Mobile element: transposon En-1

Query Match

79.2%; Score 42; DB 2; Length 905;

Best Local Similarity 77.8%; Pred. No. 9.9;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VNLSLHAPYL 9

Db 840 VNMLHAPYL 848

RESULT 3

S76143
probable aldehyde reductase (EC 1.1.1.-) - Synecchocystis sp. (strain PCC 6803)

C/Species: Synecchocystis sp.

A/Variety: PCC 6803

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004

C/Accession: S76143

R:Tanaka, T.; Sato, S.; Kozami, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis

S.

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S76143

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-327 <FAN>

A/Cross-references: UNIPROT:P74308; EMBL:D90914; GB:AB001339; NID:G1653477; PIDN:BA1840

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Genetics:

A/Start codon: GNG

C/Superfamily: Aldehyde reductase

C/Keywords: oxidoreductase

Query Match

77.4%; Score 41; DB 1; Length 327;

Best Local Similarity 80.0%; Pred. No. 5;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLSLHAPYL 10

Db 187 VNQVELHAPYL 196

RESULT 4

A54080
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken

C/Species: Gallus gallus (chicken)

C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C/Accession: A54080; 150592

R:Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.

J. Biol. Chem. 269, 14056-14063, 1994

A/Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in

A/Reference number: A54080; MUID:94245724; PMID:8188686

A/Accession: A54080

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1237 <FAN>

A/Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:G510510; PIDN:CAA79972.1; PID:G5105

C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol

C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:610-834/Domain: protein-tyrosine-phosphatase homology <PTP>

F:786/Active site: Cys (phosphocysteine intermediate) #status predicted

F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match

75.5%; Score 40; DB 2; Length 1237;

Best Local Similarity 80.0%; Pred. No. 34;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VNLSLHAPYL 10

Db 853 VLSLSHAPYL 862

RESULT 5

A59021
aldehyde reductase (EC 1.1.1.21) [validated] - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 16-Aug-2004

C/Accession: A59021; A59019; S43018

R:Kubisecki, T.; Green, N.C.; Flynn, T.G.

Adv. Exp. Med. Biol. 328, 259-265, 1993

A/Title: Location of an essential arginine residue in the primary structure of pig aldol

A/Reference number: A59021; MUID:93263021; PMID:8493902

A/Accession: A59021

A/Molecule type: mRNA

A/Residues: 1-316 <KUB>

A/Cross-references: UNIPROT:P80276; GB:U46065; NID:G1184819; PIDN:AAC48515.1; PID:G11848

A/Experimental source: adult brain

A/Note: submitted to Genbank January 1996

R:Daquinod, M.; Potier, N.; Klagskov, K.; Reymann, J.M.; Sorokine, O.; Kieffer, S.; Bart

Eur. J. Biochem. 218, 893-903, 1993

A/Title: Sequence of pig lens aldose reductase and electrospray mass spectrometry of non

A/Reference number: S43018; MUID:94109388; PMID:8281941

A/Accession: A59019

A/Molecule type: protein

A/Residues: 2-98, 'D', '100-316 <JAO1>

A/Experimental source: eye lens

A/Note: the authors found that a disulfide bond between residues 299-304 which they thou

A/Accession: S43018

A/Molecule type: protein

A/Residues: 2-12 <JAO2>

R:Moras, D.; Podjarny, A.

submitted to the Brookhaven Protein Data Bank, April 1997

A/Reference number: A69051; PDB:1IA4

A/Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 2-98, 'D', '100-316

R:Rondeau, J.M.; Tete-Favre, F.; Podjarny, A.; Reymann, J.M.; Barth, P.; Biellmann, J.F

submitted to the Brookhaven Protein Data Bank, February 1993

A:Reference number: A52185; PDB:1DLA
A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 2-98, 'D', 100-316
C:Genetics:
A:Gene: AUR2
C:Superfamily: Aldehyde reductase
C:Keywords: acetylated amino end; oxidoreductase
F:2-316/Product: aldehyde reductase #status experimental <MAT>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 71.7%; Score 38; DB 2; Length 316;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
DB 182 VNQIEVHPYL 191

RESULT 6
S11027
L-ascorbate oxidase (EC 1.10.3.3) precursor - Cucurbita cv. Edisau Nankin
C:Species: Cucurbita cv. Edisau Nankin
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S11027; S36936
R:Esaka, M.; Hattori, T.; Fujisawa, K.; Sakajo, S.; Asahi, T.
Eur. J. Biochem. 191, 537-541, 1990
A:Title: Molecular cloning and nucleotide sequence of full-length cDNA for ascorbate oxi
A:Reference number: S11027; MIMD:90361033; PMID:2143964
A:Molecule type: mRNA
A:Residues: 1-579 <EUR>
A:Cross-references: UNIPROT:P24792; EMBL:X55779; NID:g18251; PIDN:CAA9300.1; PID:g18252
A:Accession: S36936
A:Molecule type: protein
A:Residues: 31-48 <ESA>
C:Superfamily: Laccase
C:Keywords: oxidoreductase
F:375-568/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F:49-231/Disulfide bonds: #status predicted
F:90-478/Binding site: copper (His) (type 2) #status predicted
F:92-134, 136, 480, 536, 538/Binding site: 2Cu-O cluster (His) (copper type 3) #status predi
F:111-568/Disulfide bonds: #status predicted
F:193-392, 472, 542/Binding site: substrate (Trp, Trp, Glu, His) #status predicted
F:210-223/Disulfide bonds: #status predicted

Query Match 71.7%; Score 38; DB 2; Length 579;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLSLHPY 9
DB 470 NLSLHPW 477

RESULT 7
T39171
Probable peroxisomal copper amine oxidase [imported] - fission yeast (Schizosaccharomyce
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T50376; T39171
R:Connor, R.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21832
A:Accession: T50376
A:Molecule type: DNA
A:Status: preliminary
A:Cross-references: UNIPROT:O42890; EMBL:AL021815; PIDN:CAA16999.1; GSPDB:GN00067; SPDB:
A:Experimental source: strain 972h-; cosmid c884
C:Genetics:
A:Gene: SPDB:SPAC8E4.06
A:Map position: 2
C:Keywords: peroxisome

Query Match 71.7%; Score 38; DB 2; Length 794;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NLSLHPY 9
DB 506 NLSLHPY 513

RESULT 8
A45961
2,5-diketo-D-glucuronate reductase (EC 1.1.1.-) - Corynebacterium sp. (strain SH5752001)
C:Species: Corynebacterium sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jul-2004
C:Accession: A45961
R:Grindley, J.F.; Payton, M.A.; van de Pol, H.; Hardy, K.G.
Appl. Environ. Microbiol. 54, 1770-1775, 1988
A:Title: Conversion of glucose to 2-keto-L-gulonate, an intermediate in L-ascorbate syn
A:Reference number: A45961
A:Accession: A45961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-277 <GRI>
A:Cross-references: UNIPROT:P15339; GB:M21193; NID:g144962; PIDN:AAA23291.1; PID:g144963
C:Keywords: oxidoreductase

Query Match 69.8%; Score 37; DB 1; Length 277;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLSLHPY 9
DB 160 VNQIEVHPY 168

RESULT 9
C86780
Oxidoreductase ymgK [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 16-Aug-2004
C:Accession: C86780
R:Bolotin, A.; Winker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weisenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MIMD:21235186; PMID:11337471
A:Accession: C86780
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <STO>
A:Cross-references: UNIPROT:Q9CG67; GB:AE005176; PID:g12724215; PIDN:AAK05341.1; GSPDB:
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ymgK
C:Superfamily: Aldehyde reductase

Query Match 69.8%; Score 37; DB 2; Length 280;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNLSLHPY 9
DB 160 VNQIEVHPY 168

RESULT 10
AE0660
Probable oxidoreductase SYR1388 [imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
C:Accession: AE0660
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0660
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01654.1; PID:g16502506; GSPDB:GN00176
C:Genetics:
A:Gene: STY1388
C:Superfamily: Aldehyde reductase

Query Match 69.8%; Score 37; DB 2; Length 289;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLSLHPY 9
DB 160 VNQVELHPY 168

RESULT 11
B90671
probable reductase [imported] - *Escherichia coli* (strain O157:H7, substrain RMD 0509952
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C:Accession: B90671
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11238796
A:Accession: B90671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <HAY>
A:Cross-references: UNIPROT:Q8X6G0; GB:BA000007; PIDN:BA833761.1; PID:g13359795; GSPDB:G
C:Genetics:
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Superfamily: Aldehyde reductase

Query Match 69.8%; Score 37; DB 2; Length 289;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLSLHPY 9
DB 160 VNQVELHPY 168

RESULT 12
F85521
probable dehydrogenase Z0377 [imported] - *Escherichia coli* (strain O157:H7, substrain ED
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C:Accession: F85521
R:Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.D.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: F85521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-294 <STO>
A:Cross-references: UNIPROT:Q8X6G0; GB:AE005174; NID:g12513101; PIDN:AA654634.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain ED1933
C:Genetics:
A:Gene: Z0377

C:Superfamily: Aldehyde reductase

Query Match 69.8%; Score 37; DB 2; Length 294;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLSLHPY 9
DB 165 VNQVELHPY 173

RESULT 13
S30383
morphine 6-dehydrogenase (EC 1.1.1.218) - *Pseudomonas putida* plasmid pmh7.2
C:Species: *Pseudomonas putida*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: S30383; S14366
R:Willey, D.L.; Caswell, D.A.; Lowe, C.R.; Bruce, N.C.
Biochem. J. 290, 539-544, 1993
A:Title: Nucleotide sequence and over-expression of morphine dehydrogenase, a plasmid-en
A:Reference number: S30383; MUID:93199531; PMID:8452544
A:Accession: S30383
A:Molecule type: DNA
A:Residues: 1-295 <WIL>
A:Cross-references: EMBL:M94775
A:Experimental source: strain M10
R:Bruce, N.C.; Wilnot, C.J.; Jordan, K.N.; Stephens, L.D.G.; Lowe, C.R.
Biochem. J. 274, 875-880, 1991
A:Title: Microbial degradation of the morphine alkaloids. Purification and characterizat
A:Reference number: S14366; MUID:91190106; PMID:2012614
A:Accession: S14366
A:Molecule type: protein
A:Residues: 2-26 <BRU>
A:Experimental source: M10
C:Genetics:
A:Gene: mora
A:Genome: plasmid pmh7.2
C:Function:
A:Description: catalyses the oxidation of morphine to morphinone
C:Superfamily: Aldehyde reductase
C:Keywords: alkaloid degradation; monomer; NADP; oxidoreductase

Query Match 69.8%; Score 37; DB 1; Length 295;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNLSLHPY 9
DB 160 VNQIELHPY 168

RESULT 14
S57805
aconitate hydratase (EC 4.2.1.3) precursor - red alga (*Gracilaria verrucosa*)
N:Alternate names: aconitase
C:Species: *Gracilaria verrucosa*
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57805
R:Zhong, Y.H.; Kagan, M.A.
Plant Mol. Biol. 28, 635-646, 1995
A:Title: Characterization of the nuclear gene encoding mitochondrial aconitase in the ma
A:Reference number: S57805; MUID:95375228; PMID:7647296
A:Accession: S57805
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-779 <ZHO>
A:Cross-references: UNIPROT:P49609; EMBL:U17709; NID:g600170; PIDN:AAA80494.1; PID:g6001
C:Genetics:
A:Genome: nuclear
A:Introns: 57/2
C:Superfamily: Iron-responsive element-binding protein
C:Keywords: carbon-oxygen lyase; hydro-lyase; mitochondrion; tricarboxylic acid cycle

Query Match 69.8%; Score 37; DB 2; Length 779;
 Best Local Similarity 60.0%; Pred. No. 74;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
 :|||||:::
 Db 338 INLSLEPHI 347

RESULT 15

T42214
 otogelin - mouse
 N;Alternate names: mucin-like extracellular matrix protein
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
 C;Accession: T42214
 R;Cohen-Salmon, M.; El-Amraoui, A.; Leibovici, M.; Petit, C.
 Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
 A;Title: Otogelin: A glycoprotein specific to the acellular membranes of the inner ear.
 A;Reference number: Z22079; MUID:98070772; PMID:9405633
 A;Accession: T42214
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2910 <COH>
 A;Cross-references: UNIPROT:O55225; EMBL:U96411; NID:G2760883; PID:G2760884; PIDN:AAB965
 A;Experimental source: strain BALB/c
 A;Note: component of all the acellular membranes of the inner ear
 C;Superfamily: von Willebrand factor type A repeat homology; von Willebrand factor type

Query Match 69.8%; Score 37; DB 2; Length 2910;
 Best Local Similarity 87.5%; Pred. No. 3.2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNLSLHP 8
 :|||||
 Db 878 VNCSELHP 885

Search completed: May 3, 2005, 06:15:24
 Job time : 11.4324 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 34.5946 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-6

Perfect score: 53

Sequence: 1 VNLSLHPTL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	100.0	1290	2	Q6ED60	Q6ED60 actus vocif
2	53	100.0	1303	2	Q6ED61	Q6ED61 actus nancy
3	53	100.0	1303	2	Q6ED62	Q6ED62 actus nigri
4	53	100.0	1304	1	CD45_HUMAN	P08575 homo sapien
5	42	79.2	747	2	Q8RP87	Q8RP87 bacteroides
6	42	79.2	747	2	Q64PT4	Q64PT4 bacteroides
7	42	79.2	757	2	Q75FES	Q75FES leptospira
8	42	79.2	757	2	Q8EX87	Q8EX87 leptospira
9	42	79.2	897	2	Q41865	Q41865 zea mays (m
10	41	77.4	280	2	Q68SU0	Q68SU0 pleurotus d
11	41	77.4	289	2	Q7ZWA4	Q7ZWA4 brachydanio
12	41	77.4	314	2	Q6BVX2	Q6BVX2 debaryomyce
13	41	77.4	327	2	P74308	P74308 synochocyst
14	41	77.4	1541	2	Q81UP6	Q81UP6 plasmodium
15	40	75.5	220	2	Q96SU1	Q96SU1 homo sapien
16	40	75.5	277	2	Q96ID9	Q96ID9 homo sapien
17	40	75.5	352	2	Q9BYE7	Q9BYE7 homo sapien
18	40	75.5	1237	2	Q91976	Q91976 gallus gall
19	39	73.6	194	2	Q88XR5	Q88XR5 lactobacilli
20	39	73.6	283	2	Q6C804	Q6C804 yarrowia ii
21	39	73.6	324	2	Q6C2L0	Q6C2L0 yarrowia ii
22	39	73.6	452	2	Q8A1V1	Q8A1V1 bacteroides
23	39	73.6	822	2	Q64TX8	Q64TX8 bacteroides
24	39	73.6	1019	2	Q9FVE7	Q9FVE7 glycine max
25	39	73.6	1338	2	Q8A3N1	Q8A3N1 bacteroides
26	38	71.7	101	2	Q971X4	Q971X4 sulfolobus
27	38	71.7	315	1	ALDR_PIG	P80276 sus scrofa
28	38	71.7	390	2	Q6CS19	Q6CS19 kluyveromyc
29	38	71.7	579	1	ASO_CUCWA	P24792 cucurbita m
30	38	71.7	706	2	Q898G0	Q898G0 clostridium
31	38	71.7	794	1	AMO_SCHPO	Q42890 schizosacch

32	37	69.8	113	2	Q7NDP4	Q7NDP4 gloeobacter
33	37	69.8	178	2	Q7XWV8	Q7XWV8 oryza sativ
34	37	69.8	193	1	ASC_MOUSE	Q9EPB4 mus musculu
35	37	69.8	246	2	Q8FS67	Q8FS67 corynebacte
36	37	69.8	269	2	Q8NSZ0	Q8NSZ0 corynebacte
37	37	69.8	276	1	DKGB_CORSS	P15339 corynebacte
38	37	69.8	279	2	Q8CO19	Q8CO19 staphylococ
39	37	69.8	280	2	Q9CG67	Q9CG67 lactococcus
40	37	69.8	282	2	Q9XBS1	Q9XBS1 zymomonas m
41	37	69.8	283	2	Q9C1X5	Q9C1X5 schizosacch
42	37	69.8	283	2	Q8Y090	Q8Y090 ralstonia s
43	37	69.8	289	2	Q7AHAS	Q7AHAS escherichia
44	37	69.8	289	2	Q8Z7A2	Q8Z7A2 salmonella
45	37	69.8	289	2	Q8ZP71	Q8ZP71 salmonella

ALIGNMENTS

RESULT 1						
ID	Q6ED60	PRELIMINARY;	PRT,	1290	AA.	
AC	Q6ED60;					
DT	25-OCT-2004 (TREMBLrel. 28, Created)					
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)					
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)					
DE	CD45.					
OS	Actus vociferans (Spix's owl monkey).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.					
OX	NCBI_Taxid=57176;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	PubMed=15245371;					
RA	Montoya G.E., Vernot J.P., Patarroyo M.E.;					
RT	"Comparative analysis of CD45 protein in primate context: owl monkeys vs. human.";					
RT						
RL	Tissue Antigens 64:165-172(2004).					
DR	EMBL; AY445818; AAS06903.1; -					
DR	GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.					
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.					
DR	InterPro; IPR003961; FN III.					
DR	InterPro; IPR003595; PTPc motif-like.					
DR	InterPro; IPR000387; TYR_phosphatase.					
DR	InterPro; IPR000242; TYR_PP.					
DR	Pfam; PF00041; fn3; 2.					
DR	Pfam; PF00102; Y_phosphatase; 2.					
DR	PRINTS; PR00700; PRTYPHPTASE.					
DR	SMART; SM00060; FN3; 2.					
DR	SMART; SM00194; PTPc; 2.					
DR	SMART; SM00404; PTPc motif; 2.					
DR	PROSITE; PS00383; FN3; 2.					
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.					
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.					
DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.					
KW	Hydrolase.					
SQ	SEQUENCE 1290 AA; 145616 MW; 99EB10C75D932824 CRC64;					
Query Match						
Best local Similarity 100.0%; Score 53; DB 2; Length 1290;						
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1 VNLSLHPTL 10					
Db	904 VNLSLHPTL 913					
RESULT 2						
ID	Q6ED61	PRELIMINARY;	PRT,	1303	AA.	
AC	Q6ED61;					
DT	25-OCT-2004 (TREMBLrel. 28, Created)					

DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE CD45
OS Aotus nancyrae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_Taxid=37293;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004770; F:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PRO0700; PRTYPHTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1303 AA; 146929 MW; DOBBOC640DD1D17E8 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPTL 10
DB 917 VNLSLHPTL 926

RESULT 3
Q6ED62 PRELIMINARY; PRT; 1303 AA.
AC Q6ED62;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE CD45.
OS Aotus nigriceps (Black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_Taxid=57175;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL; AY445816; AAS06901.1; -.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004770; F:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.

DR PRINTS; PRO0700; PRTYPHTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1303 AA; 146586 MW; 9BB023BFA4C1165 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPTL 10
DB 917 VNLSLHPTL 926

RESULT 4
CD45_HUMAN STANDARD; PRT; 1304 AA.
ID CD45_HUMAN
AC P08575; Q16614; Q9H0Y6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CAN) (CD45 antigen)
(T200).
GN Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RA MEDLINE=86061067; PubMed=2824653;
RX Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different
mRNAs encoding human leukocyte common antigens.";
RT J. Exp. Med. 166:1548-1566(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RX MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common
antigen).";
RT EMBO J. 6:1251-1257(1987).
RN [3]
RP SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89009812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
antigen (CD45) gene.";
RT J. Immunol. 141:2781-2787(1988).
RN [4]
RP FUNCTION.
RX MEDLINE=89017162; PubMed=2845400;
RA Chabouneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
protein tyrosine phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
RN [5]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Kruenger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
domains of the receptor-linked protein tyrosine phosphatases LCA and
LAR.";
RL EMBO J. 9:2399-2407(1990).
CC -!- FUNCTION: Required for T-cell activation through the antigen

receptor. The first PRPase domain has enzymatic activity, while the second one seems to affect the substrate specificity of the first one.

-1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.

-1- SUBUNIT: Binds GANAB and PRKCSH (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Comment=At least 8 isoforms are produced;

Name=1;

Isoid=P08575-1; Sequence=Displayed;

Name=2;

Isoid=P08575-2; Sequence=VSP_007780;

-1- PTM: Heavily N- and O-glycosylated.

-1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class I/6 subfamily.

-1- SIMILARITY: Contains 2 fibronectin type III domains.

-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

-1- DATABASE: NAME=PROM; NOTE=CD guide CD45 entry;

WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm.

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DR EMBL; Y00638; CAA68669.1; -

DR EMBL; Y00662; CAA68269.1; -

DR EMBL; M23497; AAD15273.2; -

DR EMBL; M23496; AAD15273.2; JOINED.

DR EMBL; M23466; AAD15273.2; JOINED.

DR EMBL; M23467; AAD15273.2; JOINED.

DR EMBL; M23468; AAD15273.2; JOINED.

DR EMBL; M23469; AAD15273.2; JOINED.

DR EMBL; M23470; AAD15273.2; JOINED.

DR EMBL; M23471; AAD15273.2; JOINED.

DR EMBL; M23472; AAD15273.2; JOINED.

DR EMBL; M23473; AAD15273.2; JOINED.

DR EMBL; M23474; AAD15273.2; JOINED.

DR EMBL; M23475; AAD15273.2; JOINED.

DR EMBL; M23476; AAD15273.2; JOINED.

DR EMBL; M23477; AAD15273.2; JOINED.

DR EMBL; M23478; AAD15273.2; JOINED.

DR EMBL; M23479; AAD15273.2; JOINED.

DR EMBL; M23480; AAD15273.2; JOINED.

DR EMBL; M23481; AAD15273.2; JOINED.

DR EMBL; M23482; AAD15273.2; JOINED.

DR EMBL; M23483; AAD15273.2; JOINED.

DR EMBL; M23484; AAD15273.2; JOINED.

DR EMBL; M23485; AAD15273.2; JOINED.

DR EMBL; M23486; AAD15273.2; JOINED.

DR EMBL; M23487; AAD15273.2; JOINED.

DR EMBL; M23488; AAD15273.2; JOINED.

DR EMBL; M23489; AAD15273.2; JOINED.

DR EMBL; M23490; AAD15273.2; JOINED.

DR EMBL; M23491; AAD15273.2; JOINED.

DR PIR; A46546; A46546.

DR HSSP; P18031; 1C86.

DR Intract; P08575; -

DR GlycosultedB; P08575; -

DR Genew; HGNC:9666; PTPRC.

DR MIM; 151460; -

DR GO; GO:0005887; C:Integral to plasma membrane; TAS.

DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR008957; FN_III-like.

DR InterPro; IPR000387; TYR_phosphatase.

DR InterPro; IPR000242; Tyr_PP.

DR Pfam; PF00041; fn3; 2.

DR Pfam; PF00102; Y_phosphatase; 2.

DR PRINTS; PR00700; PRTYPHTASE.

DR PROSITE; PS00853; FN3; 2.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.

KM Alternative splicing; Antigen; Glycoprotein; Hydrolase;

KM Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;

KW Transmembrane.

FT SIGNAL 1 23

FT CHAIN 24 1304

FT DOMAIN 24 575

FT TRANSMEM 576 597

FT DOMAIN 598 1304

FT DOMAIN 390 478

FT DOMAIN 482 570

FT DOMAIN 670 919

FT DOMAIN 961 1235

FT ACT_SITE 851 851

FT ACT_SITE 1167 1167

FT CARBOHYD 78 78

FT CARBOHYD 90 90

FT CARBOHYD 95 95

FT CARBOHYD 184 184

FT CARBOHYD 190 190

FT CARBOHYD 197 197

FT CARBOHYD 232 232

FT CARBOHYD 260 260

FT CARBOHYD 270 270

FT CARBOHYD 276 276

FT CARBOHYD 335 335

FT CARBOHYD 378 378

FT CARBOHYD 419 419

FT CARBOHYD 468 468

FT CARBOHYD 529 529

FT VARSPPLIC 32 192

FT MUTAGEN 851 851

FT CONFLICT 650 650

FT CONFLICT 1207 1207

SO SEQUENCE 1304 AA; 147253 MW; A08FC2206069BA7 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 1304;

Best Local Similarity 100.0%; Pred. No. 0.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10

Db 918 VNLSLHPYL 927

RESULT 5

Q8RP87 PRELIMINARY; PRT; 747 AA.

AC Q8RP87; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

GN Aconitase protein.

GN Name=acna;

OS Bacteroides fragilis.

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;

OC Bacteroidaceae; Bacteroides.

OX NCBI_Taxid=817;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TW4000;

RC MEDLINE=21927545; PubMed=11880608; DOI=10.1073/pnas.052710199;

RA Baughn A.D., Malamy M.H.;

RT "A mitochondrial-like aconitase in the bacterium Bacteroides fragilis;

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RT implications for the evolution of the mitochondrial Krebs cycle.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:4662-4667 (2002).
DR EMBL: AF434843; AAM10631.1; -.
DR HSSP; P20004; 1AMJ.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0003994; F:aconitate hydratase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR006248; Aconitase_mito.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; Aconitase; 1.
DR Pfam; PF00694; Aconitase; 1.
DR PRINTS; PR000415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR01340; aconitase_mito; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
SQ SEQUENCE 747 AA; 81930 MW; 11B3392621615127 CRC64;

Query Match
Best Local Similarity 79.2%; Score 42; DB 2; Length 747;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
DB 314 INLSLEPYI 323

RESULT 6
Q64PT4 PRELIMINARY; PRT; 747 AA.
AC 064PT4;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Aconitase protein.
GN ORFNames=BF3755;
OS Bacteroides fragilis.
OC Bacteriia; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayaashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2004).
DR EMBL: AP006841; BAD50497.1; -.
DR SEQUENCE 747 AA; 81903 MW; A149C273DC9744A CRC64;

Query Match
Best Local Similarity 79.2%; Score 42; DB 2; Length 747;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
DB 314 INLSLEPYI 323

RESULT 7
Q75FE5 PRELIMINARY; PRT; 757 AA.
AC 075FE5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Aconitase hydratase.
GN Name=acn; OrderedlocusNames=LIC20249;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
```

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OS Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fluoruz L1-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascentino A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovsky-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furian L.R., Gamberini M., Gigliotti E.A.,
RA Geese-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
RA Kurmae E.E., Lemos E.G.M., Lemos M.V.F., Martino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schielefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Secubal J.C., Van Sluys W.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172 (2004).
DR EMBL: AE016824; AAS72270.1; -.
DR HSSP; P16276; 1B0U.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0003994; F:aconitate hydratase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR006248; Aconitase_mito.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; Aconitase; 1.
DR Pfam; PF00694; Aconitase; 1.
DR PRINTS; PR000415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR01340; aconitase_mito; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 757 AA; 81983 MW; E0D29E079F21D1A4 CRC64;

Query Match
Best Local Similarity 79.2%; Score 42; DB 2; Length 757;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
DB 314 INLSLEPYI 323

RESULT 8
Q8EX87 PRELIMINARY; PRT; 757 AA.
AC 08EX87;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Aconitase hydratase (EC 4.2.1.3).
GN Name=acn; OrderedlocusNames=LB327;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar 1a1;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Gloms I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
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RT "Unique physiological and pathogenic features of Leptospira
RT Interrogans revealed by whole-genome sequencing.",
RT Nature 422:888-893(2003).
DR EMBL; AF011619; AAN51886.1; -.
DR HSSP; P20004; 1C96.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0003994; F:aconitase hydratase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR006248; Aconitase_mito.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; Aconitase; 1.
DR Pfam; PF00694; Aconitase_C; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRfam; TIGR01340; aconitase_mito; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Complete proteome.
SQ SEQUENCE 757 AA; 81953 MW; 40D92AE7697CF878 CRC64;

Query Match
Best Local Similarity 79.2%; Score 42; DB 2; Length 757;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNISELHPYL 10
Db 314 VNISELHPYL 323

RESULT 9
Q41865 ID Q41865 PRELIMINARY; PRT; 897 AA.
AC Q41865;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wx-844::En-1;
RA Pereira A., Cuypers H., Gierl A., Schwarz-Sommer Z.S., Saedler H.;
RT "Molecular analysis of the En/Spm transposable element system of Zea
RT mays.";
RL EMBL J. 5:835-841(1986).
DR EMBL; M25427; AAA6266.1; -.
DR PIR; S29329; S29329.
DR InterPro; IPR004242; Transposase_21.
DR Pfam; PF02992; Transposase_21; 1.
KW Hypothetical protein.
SQ SEQUENCE 897 AA; 104551 MW; 7F3BAV43770600DD CRC64;

Query Match
Best Local Similarity 79.2%; Score 42; DB 2; Length 897;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNISELHPYL 9
Db 832 VNISELHPYL 840

RESULT 10
Q68SU0 ID Q68SU0 PRELIMINARY; PRT; 280 AA.
AC Q68SU0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
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DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Reductase AKOR1.
GN Name=AKOR1;
OS Pleurotus djamor.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=34470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RV95/957.30;
RA PubMed=15219565; DOI=10.1016/j.fgb.2004.04.005;
RA James T.Y., Liou S.R., Vilgalys R.;
RT "The genetic structure and diversity of the A and B mating-type genes
RT from the tropical oyster mushroom, Pleurotus djamor.";
RL Fungal Genet. Biol. 41:813-825(2004).
DR EMBL; AY462110; NAS46750.1; -.
DR InterPro; IPR001395; Aldo/ket_red.
DR Pfam; PF00248; Aldo_ket_red; 1.
DR PRINTS; PR00069; ALDKETRDPASE.
DR ProDom; PD000288; Aldo/ket_red; 1.
DR PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
DR SEQUENCE 280 AA; 31444 MW; FD02D7EBABE9D615 CRC64;

Query Match
Best Local Similarity 77.4%; Score 41; DB 2; Length 280;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNISELHPYL 10
Db 162 VNISELHPYL 171

RESULT 11
Q7ZMA4 ID Q7ZMA4 PRELIMINARY; PRT; 289 AA.
AC Q7ZMA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein zgc:56622.
GN ORFNames=zgc:56622;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Brachydanio rerio; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Teleostei; Ostariophysi; Cypriniformes;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=whole body;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Caaveira T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
```

RC TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC049508; AAH49508.1; -.
 DR HSSP; P06632; 1HW6.
 DR ZFIN; ZDB-GENE-030131-4758; zgc:56622.
 DR InterPro; IPR001395; Aldo/ket_red.
 DR Pfam; PF00248; Aldo_ket_red; 1.
 DR PRINTS; PR00069; ALDKETRDASE.
 DR ProDom; PD000288; Aldo/ket_red; 1.
 DR PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
 DR PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 289 AA; 32906 MW; 96142EFD8D1D4AC CRC64;

Query Match 77.4%; Score 41; DB 2; Length 289;
 Best Local Similarity 80.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLSLHPYL 10
 Db 154 VNQVELHPYL 163

RESULT 12

06BVX2 PRELIMINARY; PRT; 314 AA.

DT 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE Similar to tr|Q9HGX9 Zygosaccharomyces rouxi Glycerol

DE dehydrogenase.

GN ORFNames=DEHA0B16181g;

OS Debaryomyces hansenii CBS767.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.

OX NCBI_TaxID=284592;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CBS767;

RG Genolevres;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,

RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,

RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,

RA Boistrane A., Boyer J., Catolico L., Confanioli F., de Darvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,

RA Nicand J.M., Nikolski M., Otae S., Olier-Kalogeropoulos O.,

RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,

RA Sennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,

RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,

RA Bouchier C., Caudon B., Scarpelli C., Galliard C., Weissenbach J.,

RA Wincker P., Souciet J.L.;
 RT "Genome evolution in Yeasts";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CB382134; CAG85661.1; -.
 DR InterPro; IPR001395; Aldo/ket_red.
 DR Pfam; PF00248; Aldo_ket_red; 1.
 DR PRINTS; PR00069; ALDKETRDASE.
 DR ProDom; PD000288; Aldo/ket_red; 1.
 DR PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
 SQ SEQUENCE 314 AA; 35221 MW; FE87A58EB8845AA CRC64;

Query Match 77.4%; Score 41; DB 2; Length 314;

Best Local Similarity 80.0%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLSLHPYL 10
 Db 190 VNQVELHPYL 199

RESULT 13

ID P74308 PRELIMINARY; PRT; 327 AA.

AC P74308; 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Aldehyde reductase.

GN OrderedlocusNames=slr0942;

OS Synecchocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synecchocystis.

OX NCBI_TaxID=1148;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PCC6803;

RX MEDLINE=97061201; PubMed=8905231;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

RA Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT Synecchocystis sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).

DR EMBL; D90914; BA018402.1; -.
 DR PIR; S76143; S76143.

DR HSSP; P14550; 2ALR.

DR InterPro; IPR001395; Aldo/ket_red.

DR Pfam; PF00248; Aldo_ket_red; 1.

DR PRINTS; PR00069; ALDKETRDASE.

DR ProDom; PD000288; Aldo/ket_red; 1.

DR PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.

DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 327 AA; 36014 MW; 4B9415E098A8892D CRC64;

Query Match 77.4%; Score 41; DB 2; Length 327;
 Best Local Similarity 80.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNLSLHPYL 10
 Db 187 VNQVELHPYL 196

RESULT 14

ID O81JF6 PRELIMINARY; PRT; 1541 AA.

AC O81JF6; 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein.

GN ORFNames=PL10_0242;

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Gardner M.J., Hall N., Pung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,

RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.,
 RT "Genome sequence of the human malaria parasite *Plasmodium*
 RT *falciparum*.";
 RL Nature 419:498-511(2002).
 DR EMBL: AE014833; AAN35439.1; -
 KM Hypothetical protein.
 SQ SEQUENCE 1541 AA; 180939 MW; B060D6567D5C9816 CRC64;

Query Match 77.4%; Score 41; DB 2; Length 1541;
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNISELHPYL 10
 :|||:|||||
 DB 1105 INLQDIHPYL 1114

RESULT 15

Q96SJ1 PRELIMINARY; PRT; 220 AA.
 AC Q96SJ1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ14979.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 RA Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Oshima A.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: AK027885; BAB55431.1; -
 DR GO: GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR002350; Prot_inh_Kazal.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4_1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00282; KAZAL; UNKNOWN_1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PSS0089; ZF_RING_2; 1.
 KM DNA-binding; Metal-binding; Zinc; Zinc-finger
 SQ SEQUENCE 220 AA; 24435 MW; E38B4B84C9F77193 CRC64;

Query Match 75.5%; Score 40; DB 2; Length 220;
 Best Local Similarity 70.0%; Pred. No. 28;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNISELHPYL 10
 :|||:|||||
 DB 125 INLSELPYL 134

Search completed: May 3, 2005, 05:59:20
 Job time : 41.5946 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 06:24:23 ; Search time 78 Seconds
(without alignments)
49.585 Million cell updates/sec

Title: US-10-003-983C-6
Perfect score: 53
Sequence: 1 VNISELHPYL 10

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	5	ABG31976 Human CD4
2	53	100.0	764	8	ABO84454 Human can
3	53	100.0	960	8	ADQ39377 Human myo
4	53	100.0	1114	6	ABU05246 Human exp
5	53	100.0	1114	6	ABU05239 Human exp
6	53	100.0	1143	6	ABU05240 Human exp
7	53	100.0	1143	6	ABU05245 Human exp
8	53	100.0	1143	7	AD116232 Human pro
9	53	100.0	1143	8	ADQ18845 Human sol
10	53	100.0	1149	4	AAW41048 Human pol
11	53	100.0	1149	6	ABU05242 Human exp
12	53	100.0	1192	8	ADR39747 Human kin
13	53	100.0	1219	8	ADQ39378 Human myo
14	53	100.0	1256	8	ADM67187 Human adi
15	53	100.0	1256	8	ADP12956 Protein e
16	53	100.0	1258	8	ADQ39376 Human myo
17	53	100.0	1267	8	ADQ39379 Human myo
18	53	100.0	1304	6	ABU05243 Human exp
19	53	100.0	1304	6	ABU05241 Human exp
20	53	100.0	1304	6	ABU05244 Human exp
21	53	100.0	1304	7	AD116230 Human pro
22	53	100.0	1304	7	ADP65158 Human adi
23	53	100.0	1304	8	ADM67209 Human can
24	53	100.0	1304	8	ABO84455 Human can
25	53	100.0	1304	8	ADQ39380 Human myo

26	53	100.0	1306	8	ADQ39375 Human myo
27	49	92.5	9	5	ABG31975 Human CD4
28	43	81.1	273	8	ADN21825 Bacterial
29	43	81.1	273	8	ADN24584 Bacterial
30	43	81.1	322	6	ABU21347 Protein e
31	41	77.4	327	8	ADN20106 Bacterial
32	40	75.5	103	7	ADC31123 Human nov
33	40	75.5	168	4	AAO12222 Human pol
34	40	75.5	168	7	ADC32832 Human nov
35	40	75.5	220	4	AA894801 Human pro
36	40	75.5	220	5	AAU80360 Human cel
37	40	75.5	352	5	AAU80358 Human cel
38	40	75.5	363	4	ABG26905 Novel hum
39	40	75.5	1237	2	AAW44729 Chicken p
40	40	75.5	1237	2	AAW89347 Chicken t
41	39	73.6	747	8	ADS21204 Bacterial
42	39	73.6	813	6	ABU20999 Protein e
43	38	71.7	579	2	ADP90916 Porcine a
44	38	71.7	579	2	AA14306 Ascorbate
45	37	69.8	193	4	AA820086 Mouse CAR

ALIGNMENTS

RESULT 1
ABG31976
ID ABG31976 standard; peptide, 10 AA.
XX
AC ABG31976;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CD45 HLA-binding peptide, huCD45/918.
XX
KW Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
KW antigen-presenting cell; APC; major histocompatibility complex; MHC;
KW antigen; allogenic; T cell receptor; TCR; cancer; tumour;
KW allogenic stem cell transplantation; CFU-GM; leukaemia;
KW colony forming unit-granulocyte macrophage; immunotherapeutic;
KW haematopoietic; malignant.
XX
OS Homo sapiens.
XX
PN MO200244207-A1.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2000; 2000MO-GB004566.
XX
PR 30-NOV-2000; 2000MO-GB004566.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Staus HJ, Amrolia PJ;
XX
DR WPI, 2002-599413/64.
XX
PT Novel peptide comprising leukocyte antigen binding peptide of human CD45
PT polypeptide, useful for producing activated cytotoxic T lymphocytes, for
PT killing cancerous cells e.g. leukemia.
XX
PS Claim 2, Page 38, 56pp; English.
XX
XX The invention discloses a peptide comprising the human leukocyte antigen
XX (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,
XX provided that the peptide is not the intact human CD45 polypeptide. The
XX peptides are useful for producing activated cytotoxic T lymphocyte (CTL)
XX in vitro which involves contacting the CTL with an antigen-presenting
XX cell, where its major histocompatibility complex (MHC) class I molecules
XX are loaded with the peptide, to activate, in an antigen specific manner,
XX where the CTL and the antigen presenting cell are allogenic with respect
XX to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animal models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/918,
CC comprising an HLA-binding peptide of human CD45
CC
CC
SQ Sequence 10 AA;

QY Query Match 100.0%; Score 53; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VNLSLHPYL 10
1 VNLSLHPYL 10

RESULT 2

AB084454
ID AB084454 standard; protein; 764 AA.

AC AB084454;

DT 18-NOV-2004 (first entry)

DE Human cancer-associated protein HP13-011.1.

KW Human; cancer-associated protein; cytosolic; cancer; leukaemia;

KW Lymphoma; CAP.

OS Homo sapiens.

PN WO2004074320-A2.

XX 02-SEP-2004.

PD 17-FEB-2004; 2004WO-US004730.

PF 14-FEB-2003; 2003US-00367094.

PR 14-MAR-2003; 2003US-00388838.

PR 15-APR-2003; 2003US-00417375.

PR 13-JUN-2003; 2003US-00461862.

PR 15-SEP-2003; 2003US-00663431.

PR 15-DEC-2003; 2003US-00737318.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Morris DW, Malandro MS;

XX MPI: 2004-652914/63.

XX N-PSDB; ABD32625.

XX New isolated cancer-associated polynucleotides and polypeptides useful

XX for diagnosing, preventing or treating cancers, especially lymphoma and

XX leukemia, or in screening for agents that modulate cancer.

XX claim 18; seqid 145; 310pp; English.

CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell vector comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
CC
CC
SQ Sequence 764 AA;

QY Query Match 100.0%; Score 53; DB 8; Length 764;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VNLSLHPYL 10
378 VNLSLHPYL 387

RESULT 3

ADQ39377
ID ADQ39377 standard; protein; 960 AA.

AC ADQ39377;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1040.

KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KW Cardiac; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

XX 15-JUL-2004.

PD 22-DEC-2003; 2003WO-US040978.

PF 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

XX (APPL-) APPLERA CORP.

XX Cargill M, Devlin JU, Iakoubova O;

XX MPI: 2004-533949/51.

DR N-PSDB; ADO38549.
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1040; 145bp; English.
PS
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting a SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction.
CC CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 960 AA;
Query Match 100.0%; Score 53; DB 8; Length 960;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNISELHPYL 10
DB 574 VNISELHPYL 583
RESULT 4
ABU05246
ID ABU05246 standard; protein; 1114 AA.
XX
AC ABU05246;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1912.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCO INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
DR
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1912; 134bp; English.
PS
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1114 AA;
Query Match 100.0%; Score 53; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNISELHPYL 10
DB 728 VNISELHPYL 737
RESULT 5
ABU05239
ID ABU05239 standard; protein; 1114 AA.
XX
AC ABU05239;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1905.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.

```
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0338985P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS Example 2; SEQ ID NO 1905; 134pp; English.
XX
XX CC The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1114 AA;
XX
XX Query Match 100.0%; Score 53; DB 6; Length 1114;
XX Best Local Similarity 100.0%; Pred. No. 0.23;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VNLSLHPYL 10
XX |||||
XX Db 728 VNLSLHPYL 737
XX
XX RESULT 6
XX ABU05240
XX ID ABU05240 standard; protein; 1143 AA.
XX AC ABU05240;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1906.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
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PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0338985P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
XX CC The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1143 AA;
XX
XX Query Match 100.0%; Score 53; DB 6; Length 1143;
XX Best Local Similarity 100.0%; Pred. No. 0.24;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VNLSLHPYL 10
XX |||||
XX Db 757 VNLSLHPYL 766
XX
XX RESULT 7
XX ABU05245
XX ID ABU05245 standard; protein; 1143 AA.
XX AC ABU05245;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1911.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
```


PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 1911; 134pp; English.
XX PS The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1143 AA;
XX
XX Query Match 100.0%; Score 53; DB 6; Length 1143;
XX Best Local Similarity 100.0%; Pred. No. 0.24;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
DB 757 VNLSLHPYL 766
XX
XX RESULT 8
XX ADL16232
XX ID ADL16232 standard; protein; 1143 AA.
XX AC ADL16232;
XX DT 06-MAY-2004 (first entry)
XX DE Human protein tyrosine phosphatase #27.
XX KW cytosolic; immunosuppressive; antiallergic;
XX protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
XX inducible signalling pathway; cell proliferation; cancer;
XX guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX cell-cycle abnormality; enzyme.
XX OS Homo sapiens.
XX PN WO2003068984-A2.
XX PD 21-AUG-2003.
XX PF 13-FEB-2003; 2003WO-EP001446.
XX PR 13-FEB-2002; 2002US-0356810P.
XX PR 12-FEB-2003; 2003US-00366547.

XX XX (COLD-) COLD SPRING HARBOR LAB.
XX PA (CEPT-) CEPTYR INC.
XX PA Tonks NK, Tzu-Ching M, Cool DE;
XX PI WPI; 2003-712572/67.
XX DR N-PSDB; ADL16231.
XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX PS Disclosure; SEQ ID NO 81; 238pp; English.
XX CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX SQ Sequence 1143 AA;
XX
XX Query Match 100.0%; Score 53; DB 7; Length 1143;
XX Best Local Similarity 100.0%; Pred. No. 0.24;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
DB 757 VNLSLHPYL 766
XX
XX RESULT 9
XX ADQ18845
XX ID ADQ18845 standard; protein; 1143 AA.
XX AC ADQ18845;
XX DT 26-AUG-2004 (first entry)
XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
XX KW soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human.
XX OS Homo sapiens.
XX PN WO2004048938-A2.
XX PD 10-JUN-2004.
XX PF 26-NOV-2003; 2003WO-US038193.
XX PR 26-NOV-2002; 2002US-0429739P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Aziz N, Ginsburg WM, Zlotnick A;
XX DR WPI; 2004-441208/41.
XX

PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

PS Example 2; SEQ ID NO 1664; 210bp; English.

CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 1143 AA;

Query Match Best Local Similarity 100.0%; Score 53; DB 8; Length 1143;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNLSLHPYL 10

Db 757 VNLSLHPYL 766

RESULT 10

AA041048
ID AA041048 standard; protein; 1149 AA.

XX AA041048;

XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 5979.

XX Human; nocrotic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoclastic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

OS WO20015312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US034263.

PF 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.

DR N-PSDB; AA160204.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

PS Example 2; SEQ ID NO 5979; 10078bp; English.

CC The invention relates to human nucleic acids (AA157298-AA161369) and the
CC encoded polypeptides (AA038642-AA042213) with nocrotic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemoclastic/chemokine activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 1149 AA;

Query Match Best Local Similarity 100.0%; Score 53; DB 4; Length 1149;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNLSLHPYL 10

Db 763 VNLSLHPYL 772

RESULT 11

AB05242
ID AB05242 standard; protein; 1149 AA.

XX AB05242;

XX 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1908.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

OS WO200278524-A2.

PN 10-OCT-2002.

PD 28-MAR-2002; 2002WO-US009671.

PF 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCO INC.

XX Chicz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT

PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

PS Example 2; SEQ ID NO 1908; 134pp; English.

XX
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 1149 AA;

Query Match 100.0%; Score 53; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
| | | | | | | | | |
Db 763 VNLSLHPYL 772

RESULT 12
ADR39747
ID ADR39747 standard; protein; 1192 AA.

XX
AC ADR39747;

XX
DT 18-NOV-2004 (first entry)

XX
DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.

XX
XX human; kinase and phosphatase protein; KPP, enzyme; cytosolic;
KM antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KM cerebroprotective; anti-HIV; anti-allergic; anti-inflammatory;
KM thymic; gene therapy; cell proliferative disorder; cancer;
KM atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
KM stroke; immune disorder; inflammatory disorder; AIDS; allergy;
KM developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KM KPP-20.

XX
OS Homo sapiens.

XX
PN MO2004074453-A2.

XX
PD 02-SEP-2004.

XX
PF 20-FEB-2004; 2004WO-US005092.

XX
PR 20-FEB-2003; 2003US-0449059P.

XX
PR 19-MAR-2003; 2003US-0456932P.

XX
PR 28-MAR-2003; 2003US-0458844P.

XX
PR 09-APR-2003; 2003US-0461678P.

XX
PR 17-APR-2003; 2003US-0463937P.

XX
XX (INCY-) INCYTE CORP.

PA Rankumar J, Marguis JP, Swarnakar A, Chawla NK, Tran UK,
XX Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
PI Jackson AA, Yang J, Gorvad AB;

XX
XX WPI; 2004-635568/51.

DR N-PSDB; ADR39793.

XX
XX
PT New human kinases and phosphatases (KPP) for diagnosing, treating and
PT preventing diseases or conditions associated with aberrant KPP expression
XX e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.

PS Claim 1; SEQ ID NO 20; 299pp; English.

XX
XX
CC The present sequence represents the human kinase and phosphatase protein
CC (KPP), designated KPP-20. The human KPP sequences from the present
CC invention have cytosolic, antiarteriosclerotic, anticonvulsant,
CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, anti-allergic,
CC antiinflammatory and thymic activities, and can be used in gene
CC therapy. The human KPP proteins and polynucleotides can be used in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KPP, such as cell
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They can also be used in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.

XX
SQ Sequence 1192 AA;

Query Match 100.0%; Score 53; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
| | | | | | | | | |
Db 806 VNLSLHPYL 815

RESULT 13
ADQ39378
ID ADQ39378 standard; protein; 1219 AA.

XX
AC ADQ39378;

XX
DT 18-NOV-2004 (first entry)

XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.

XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiant; gene therapy; human.

XX
OS Homo sapiens.

XX
PN MO2004058052-A2.

XX
PD 15-JUL-2004.

XX
PF 22-DEC-2003; 2003WO-US040978.

XX
PR 20-DEC-2002; 2002US-0434778P.

XX
PR 10-MAR-2003; 2003US-0453135P.

XX
PR 30-APR-2003; 2003US-0466412P.

XX
PR 23-SEP-2003; 2003US-0504955P.

XX
PA (APPL-) APPLERA CORP.

XX
XX Cargill M, Devlin UT, Iakoubova O;

PI WPI; 2004-533949/51.

DR N-PSDB; ADQ38550.

XX
PT Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in
 the individual's nucleic acids.

PS Claim 10; SEQ ID NO 1041; 145bp; English.

CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

SO Sequence 1219 AA;

Query Match 100.0%; Score 53; DB 8; Length 1219;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
 Db 833 VNLSLHPYL 842

RESULT 14

ID ADM67187 standard; protein; 1256 AA.

AC ADM67187;

DT 03-JUN-2004 (first entry)

DE Human adipocyte specific PTPase receptor type C protein SegID 541.

KW human; adipocyte specific; adipose tissue; anti-obesity;

KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;

KW adipogenesis; hypertension; cardiovascular disease; anorectic;

KW antidiabetic; hypotensive; PTPase receptor type C.

OS Homo sapiens.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMG-) HMGENE INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

XX WPI; 2004-143846/14.
 DR N-PsDB; ADM66908.

PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.

PS Disclosure; SEQ ID NO 541; 91pp; English.

CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC -obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.

SO Sequence 1256 AA;

Query Match 100.0%; Score 53; DB 8; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
 Db 870 VNLSLHPYL 879

RESULT 15

ID ADP12966 standard; protein; 1256 AA.

AC ADP12966;

DT 12-AUG-2004 (first entry)

DE Protein encoding reference mRNA sequence #51.

KW transplant rejection; immune system; rheumatoid arthritis; lupus;

KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

OS Homo sapiens.

PN WO2004042346-A2.

PD 21-MAY-2004.

PF 24-APR-2003; 2003WO-US012946.

PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

PI Rosenberg S;

DR WPI; 2004-400724/37.

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,

PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2975; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein encoded by an mRNA sequence of the invention which show altered
CC expression in renal transplantation and expression.
XX
SQ Sequence 1256 AA;
Query Match 100.0%; Score 53; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
DB 870 VNLSLHPYL 879
RESULT 16
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.
XX
AC ADQ39376;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
OS cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
XX
PR 30-APR-2003; 2003US-0466412P.
XX
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Iakubova O,
XX
DR N-PSDB; ADQ38548.
XX
DR MPI; 2004-533949/51.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1039; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method

CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1258 AA;
Query Match 100.0%; Score 53; DB 8; Length 1258;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
DB 872 VNLSLHPYL 881
RESULT 17
ADQ39379
ID ADQ39379 standard; protein; 1267 AA.
XX
AC ADQ39379;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
OS cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
XX
PR 30-APR-2003; 2003US-0466412P.
XX
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Iakubova O,
XX
DR N-PSDB; ADQ38551.
XX
DR MPI; 2004-533949/51.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.

XX Claim 10; SEQ ID NO 1042; 145pp; English.
PS
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
SQ
XX
SQ Sequence 1267 AA;
Query Match 100.0%; Score 53; DB 8; Length 1267;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
Db 881 VNLSLHPYL 890
RESULT 18
ABU05243
ID ABU05243 standard; protein; 1304 AA.
XX
AC ABU05243;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1909.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX

PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1909; 134pp; English.
PS
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ
XX
SQ Sequence 1304 AA;
Query Match 100.0%; Score 53; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
Db 918 VNLSLHPYL 927
RESULT 19
ABU05241
ID ABU05241 standard; protein; 1304 AA.
XX
AC ABU05241;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1907.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX

PA (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI, 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;

Query Match 100.0%; Score 53; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
DB 918 VNLSLHPYL 927

RESULT 20
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
XX
DT 29-JAN-2003 (first entry)
XX
XX

DE Human expressed protein tag (EPT) #1910.

XX Translational profiling; expressed protein tag; EPT, kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-027949P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI, 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1910; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;

Query Match 100.0%; Score 53; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNLSLHPYL 10
DB 918 VNLSLHPYL 927

RESULT 21
ADL16230
ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX

DE Human protein tyrosine phosphatase #26.

XX cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
XX

OS Homo sapiens.

PN WO2003068984-A2.

PD 21-AUG-2003.

PF 13-FEB-2003; 2003WO-EP001446.

PR 13-FEB-2002; 2002US-0356810P.

PR 12-FEB-2003; 2003US-00366547.

XX (COLD-) COLD SPRING HARBOR LAB.

PA (CEPT-) CEPTYR INC.

XX Tonke NK, Tzu-Ching M, Cool DE;

XX
DR WPI: 2003-712572/67.
DR N-PSDB; ADL16229.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 79; 238bp; English.
XX
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulphydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. . No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 53; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VNLSLHPYL 10
DB 918 VNLSLHPYL 927
XX
RESULT 22
ADP65158 100.0%; Score 53; DB 7; Length 1304;
ID ADP65158 standard; protein; 1304 AA.
XX
AC ADP65158;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
XX
KW autoimmune disease; arthritis; gene expression analysis; antineumatic;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antineumatic;
KW antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
OS Homo sapiens.
XX
PN WO2003072827-A1.
XX
PD 04-SEP-2003.
XX
PF 31-OCT-2002; 2002WO-US035433.
XX
PR 31-OCT-2001; 2001US-0336220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thornton St;
XX
DR WPI: 2003-712740/67.
DR GENBANK; NP_002829.

XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
PS Disclosure; Page; 56pp; English.
XX
CC The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritis. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritis in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antineumatic, antiarthritis, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritis, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritis. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 53; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VNLSLHPYL 10
DB 918 VNLSLHPYL 927
XX
RESULT 23
ADM67209 100.0%; Score 53; DB 7; Length 1304;
ID ADM67209 standard; protein; 1304 AA.
XX
AC ADM67209;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human adipocyte specific leukocyte common antigen protein SegID 563.
XX
KW human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; leukocyte common antigen.
XX
OS Homo sapiens.
XX
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
XX
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGE-) HMGENCE INC.

XX Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
XX WPI: 2004-143846/14.
DR N-PSDB; ADM66930.
XX
XX Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
XX Disclosure; SEQ ID NO 563; 91pp; English.
XX
XX This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti-
CC obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMG1-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
XX
XX Sequence 1304 AA;
SQ
Query Match 100.0%; Score 53; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
Db 918 VNLSLHPYL 927
RESULT 24
ABO84455
ID ABO84455 standard; protein; 1304 AA.
XX
XX ABO84455;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Human cancer-associated protein HP13-011.2.
DE
XX
XX Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KM lymphoma; CAP.
XX
XX Homo sapiens.
OS
XX
XX WO2004074320-A2.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 17-FEB-2004; 2004WO-US004730.
PF
XX
XX 14-FEB-2003; 2003US-00367094.
PR
XX
XX 14-MAR-2003; 2003US-0038838.
PR
XX
XX 15-APR-2003; 2003US-00417375.
PR
XX
XX 13-JUN-2003; 2003US-00461862.
PR
XX
XX 15-SEP-2003; 2003US-00663431.
PR
XX
XX 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX

PI Morris DW, Morris DW, Malandro MS;
XX
XX WPI: 2004-652914/63.
DR N-PSDB; ABD32626.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
XX claim 18; seqid 147; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1304 AA;
SQ
Query Match 100.0%; Score 53; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNLSLHPYL 10
Db 918 VNLSLHPYL 927
RESULT 25
ADQ39380
ID ADQ39380 standard; protein; 1304 AA.
XX
XX ADQ39380;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
DE
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiant; gene therapy; human.
XX
XX Homo sapiens.
OS
XX
XX WO2004058052-A2.
PN
XX
XX 15-JUL-2004.
PD
XX
XX

```

XX 22-DEC-2003; 2003WO-US040978.
PF 20-DEC-2002; 2002US-0434778P.
XX 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
XX 23-SEP-2003; 2003US-0504955P.
XX (APPL-) APPLERA CORP.
XX Cargill M, Devlin JJ, Iakubova O;
XX WPI; 2004-533949/51.
XX N-PSDB; ADQ38552.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1043; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the nucleotide sequences given in the specification and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1304 AA;

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```

Query Match          100.0%; Score 53; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VNLSLHPYL 10
   |||||
Db 918 VNLSLHPYL 927

```

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RESULT 26
ADQ39375
ID ADQ39375 standard; protein; 1306 AA.
XX
AC ADQ39375;
XX
DT 18-NOV-2004 (First entry)
XX
DB Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX

```

```

OS Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
XX 23-SEP-2003; 2003US-0504955P.
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JJ, Iakubova O;
XX WPI; 2004-533949/51.
XX N-PSDB; ADQ38547.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1038; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1306 AA;

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Query Match          100.0%; Score 53; DB 8; Length 1306;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VNLSLHPYL 10
   |||||
Db 920 VNLSLHPYL 929

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Search completed: May 3, 2005, 07:28:18
Job time : 138 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds
(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-7

Perfect score: 44

Sequence: 1 LLAFCFAFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	1304	1 A46546	leukocyte common a
2	39	88.6	213	2 S73011	hypothetical prote
3	39	88.6	336	2 G87202	probable membrane
4	38	86.4	24	2 I57644	transmembrane glyc
5	38	86.4	183	2 A28335	leukocyte common a
6	38	86.4	1291	1 A28334	protein-tyrosine-p
7	37	84.1	1237	2 A54080	protein-tyrosine-p
8	36	81.8	481	2 T23729	hypothetical prote
9	36	79.5	721	2 AH3417	lipa protein (lipo
10	35	79.5	351	2 C64646	dihydroorotate deh
11	35	79.5	351	2 E71935	dihydroorotate deh
12	35	79.5	1132	2 T03844	telomerase catalyt
13	35	77.3	188	2 A71801	hypothetical prote
14	34	77.3	220	2 D64717	hypothetical prote
15	34	77.3	256	2 F89955	conserved hypochet
16	34	77.3	259	2 H69445	conserved hypochet
17	34	77.3	321	2 AC0658	peptide transport
18	34	77.3	321	2 P90862	peptide transport
19	34	77.3	321	2 C85756	peptide transport
20	34	77.3	321	2 H64877	peptide transport
21	34	77.3	321	2 S39586	peptide transport
22	34	77.3	355	2 P96020	probable iron ABC
23	34	77.3	430	2 B95892	probable ABC trans
24	34	77.3	482	2 T43855	cytochrome-c oxida
25	34	77.3	512	2 T09801	cytochrome-c oxida
26	34	77.3	513	2 T11999	cytochrome-c oxida
27	34	77.3	592	2 E70488	cytochrome-c oxida
28	34	77.3	672	2 B84782	probable receptor-
29	34	77.3	708	2 T29669	hypothetical prote

30	33	75.0	98	2 T14136	NADH2 dehydrogenas
31	33	75.0	331	2 AE3372	toluene tolerance
32	33	75.0	347	2 G90444	hypothetical prote
33	33	75.0	397	2 C84078	hypothetical prote
34	33	75.0	404	2 H83249	sodium/glutamate s
35	33	75.0	406	2 T31778	hypothetical prote
36	33	75.0	431	2 C95023	competence-induced
37	33	75.0	450	2 T21515	hypothetical prote
38	33	75.0	514	2 T11103	cytochrome-c oxida
39	33	75.0	518	2 F97894	hypothetical prote
40	33	75.0	558	2 S08270	cytochrome-c oxida
41	33	75.0	585	2 H83941	ABC transporter (A
42	33	75.0	718	2 AB1258	hypothetical prote
43	33	75.0	718	2 AF1620	hypothetical prote
44	32	72.7	56	2 D82138	hypothetical prote
45	32	72.7	81	2 S71165	RNA-directed DNA p

ALIGNMENTS

RESULT 1

A46546
leukocyte common antigen long splice form precursor - human
N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext. change 09-Jul-2004
C:Accession: A46546; B46546; C46546; A29449; B29449; I57658
R:Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
J. Title: Differential usage of three exons generates at least five different mRNAs enco
A:Reference number: A46546; MUID:88061067; PMID:2824653
A:Accession: A46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1304 <STR>
A:Cross-references: UNIPROT:P08575; GB:Y00638
A:Experimental source: clone LCA.6/2
A:Accession: B46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-32,99-264 <STR>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.111 and clone LCA.260
A:Accession: C46546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-31,193-264 <STR>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.1
R:Rajp, S.U.; Thomas, W.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
J. Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A:Reference number: A91066; MUID:87275816; PMID:2956090
A:Accession: A29449
A:Molecule type: mRNA
A:Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAU>
A:Cross-references: GB:Y00622; MUID:934275; PIND:CAA68269.1; PID:934276
A:Experimental source: clones pHLC-1 and lambdaHLCL1
A:Accession: B29449
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 32-192 <RA2>
A:Experimental source: clone HLC-2
R:Tsal, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
J. Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative ;
A:Reference number: I57658; MUID:90066468; PMID:2531281
A:Accession: I57658
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 146-192 <RES>

A:Molecule type: DNA
A:Residues: 1-481 <WIL>
A:Cross-references: UNIPROT:Q21517; EMBL:Z71265; PDB:CAA5636.1; GSPDB:GN00019; CESP:MC
A:Experimental source: clone M05B5
C:Gene: CESP:M05B5.6
A:Map position: 1
A:Introns: 50/2; 99/1; 133/3; 185/3; 229/3; 402/3; 457/3

Query Match 81.8%; Score 36; DB 2; Length 481;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
|:|||||:
238 LIAFGFAFL 246

RESULT 9
AH3417
lpsA protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AH3417
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
.: Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-721 <KUR>
A:Cross-references: UNIPROT:Q8Y636; GB:AE008917; PDB:1AL52507.1; PID:G17983318; GSPDB:G
A:Experimental source: strain 16M
C:Gene: BME11326
A:Map position: 1

Query Match 81.8%; Score 36; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LIAFGFAFL 8
|:|||||:
697 LIAFGFAFL 703

Db 697 LIAFGFAFL 703

RESULT 10
C64646
dihydroorotate dehydrogenase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: C64646
R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khakh, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.
Nature 386, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; PMID:97394467; PMID:9252185
A:Accession: C64646
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-351 <TOM>
A:Cross-references: UNIPROT:Q25655; GB:AE000609; GB:AE000511; NID:G2314150; PDB:1AAD0805
C:Superfamily: dihydroorotate oxidase

Query Match 79.5%; Score 35; DB 2; Length 351;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9

Db 79 LIAFGFAFL 87
|:|||||:
79 LIAFGFAFL 87

RESULT 11
E71935
dihydroorotate dehydrogenase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71935
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ivee, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; PMID:99120557; PMID:9923682
A:Accession: E71935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <ARN>
A:Cross-references: UNIPROT:Q9ZM11; GB:AE001475; GB:AE001439; NID:G4154939; PDB:1AAD0599
A:Experimental source: strain J99
C:Gene: pyd
C:Superfamily: dihydroorotate oxidase

Query Match 79.5%; Score 35; DB 2; Length 351;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
|:|||||:
79 LIAFGFAFL 87

Db 79 LIAFGFAFL 87

RESULT 12
T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: Z15111; PMID:97400623; PMID:9252327
A:Accession: T03844
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NMK>
A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:G2330016; PDB:1AAC51672.1; PID:G2
A:Experimental source: Kidney
C:Gene: TRT
A:Map position: 5p

Query Match 79.5%; Score 35; DB 2; Length 1132;
Best Local Similarity 77.8%; Pred. No. 95;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
|:|||||:
96 LIAFGFAFL 104

Db 96 LIAFGFAFL 104

RESULT 13
A71801
hypothetical protein jhp1487 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: A71801
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; PMID:99120557; PMID:9923682
A;Accession: A71801
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <ARN>
A;Cross-references: UNIPROT:Q92J31; GB:AE001570; GB:AE001439; NID:94156108; PIDN:AMD0706
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp1487

Query Match 77.3%; Score 34; DB 2; Length 198;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAFGPFL 9
|:|:|:|:
Db 156 LIAWGFAYL 164

RESULT 14
D64717
hypothetical protein HP1580 - Helicobacter pylori (strain 26695) .
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: D64717
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Gilek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; PMID:97394467; PMID:9252185
A;Accession: D64717
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-220 <TCM>
A;Cross-references: UNIPROT:Q26100; GB:AE000655; GB:AE000511; NID:92314757; PIDN:AMD0862

Query Match 77.3%; Score 34; DB 2; Length 220;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAFGPFL 9
|:|:|:|:
Db 178 LIAWGFAYL 186

RESULT 15
F89955
conserved hypothetical protein SAI536 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89955
R;Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: F89955
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <KUR>
A;Cross-references: UNIPROT:Q99TB9; GB:BA000018; PID:913701509; PIDN:BA842803.1; GSPDB:G
C;Genetics:
A;Experimental source: strain N315
A;Gene: SAI536

Query Match 77.3%; Score 34; DB 2; Length 256;
Best Local Similarity 77.8%; Pred. No. 35;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LLAFGPFL 9
|:|:|:|:
Db 166 LIAWGFAYL 174

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Job time : 27.6892 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:35:45 ; Search time 47.8421 Seconds

(without alignments)
96.332 Million cell updates/sec

Title: US-10-003-983c-7

Perfect score: 44

Sequence: 1 ILAFGFAPL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	100.0	34	2	Q9H3X6	Q9h3x6 homo sapien
2	44	100.0	126	2	Q8M1N3	Q8m1n3 equus caball
3	44	100.0	240	2	Q6Q1P2	Q6q1p2 homo sapien
4	44	100.0	453	2	Q9GMB6	Q9gmb6 bos indicus
5	44	100.0	454	2	Q6S280	Q6s280 sus scrofa
6	44	100.0	461	2	Q9GMB4	Q9gmb4 bos taurus
7	44	100.0	463	2	Q9GMB5	Q9gmb5 bos indicus
8	44	100.0	465	2	Q9GMB1	Q9gmb1 syncerus ca
9	44	100.0	466	2	Q6S281	Q6s281 sus scrofa
10	44	100.0	501	2	Q6S282	Q6s282 sus scrofa
11	44	100.0	517	2	Q6S283	Q6s283 sus scrofa
12	44	100.0	567	2	Q6S284	Q6s284 sus scrofa
13	44	100.0	583	2	Q6S285	Q6s285 sus scrofa
14	44	100.0	756	2	Q6P1K7	Q6p1k7 homo sapien
15	44	100.0	1290	2	Q6ED60	Q6ed60 aotus vociferans
16	44	100.0	1303	2	Q6ED61	Q6ed61 aotus nancy
17	44	100.0	1303	2	Q6ED62	Q6ed62 aotus nancy
18	44	100.0	1304	1	CD45_HUMAN	P08175 homo sapien
19	40	90.9	568	2	Q62M14	Q62m14 burkholderia
20	40	90.9	568	2	Q63X68	Q63x68 burkholderia
21	39	88.6	213	2	Q49930	Q49930 mycobacterium
22	39	88.6	336	2	Q69510	Q69510 mycobacterium
23	39	88.6	459	2	Q83123	Q83123 enterococcus
24	38	86.4	22	2	Q78BF1	Q78bf1 mus musculus
25	38	86.4	24	2	Q61815	Q61815 mus musculus
26	38	86.4	183	2	Q61814	Q61814 mus musculus
27	38	86.4	272	2	Q8DXT2	Q8dxt2 streptococcus
28	38	86.4	878	2	Q8C6Q7	Q8c6q7 mus musculus
29	38	86.4	1152	1	CD45_MOUSE	P06800 mus musculus
30	38	86.4	1291	2	Q61812	Q61812 mus musculus
31	38	86.4	1343	2	Q64730	Q64730 mus musculus

32	37	84.1	198	2	Q9FMX8	Q9fmx8 arabidopsis
33	37	84.1	230	2	Q6F753	Q6f753 acinetobact
34	37	84.1	1237	2	Q91976	Q91976 gallus gall
35	36	81.8	138	2	Q8XK73	Q8xk73 clostridium
36	36	81.8	153	2	Q635B8	Q635b8 burkholderi
37	36	81.8	254	2	Q621Q7	0621q7 burkholderi
38	36	81.8	260	2	Q8CHM8	Q8chm8 rattus norv
39	36	81.8	371	2	Q973W8	Q973w8 sulfobolus
40	36	81.8	475	2	Q97A92	Q97a92 thermoplas
41	36	81.8	475	2	Q6ANSL	Q6ansl deaurefalte
42	36	81.8	481	2	Q21517	Q21517 caenorhabdi
43	36	81.8	703	2	Q8VP06	Q8vp06 bruceella ab
44	36	81.8	703	2	Q8G1T9	Q8g1t9 bruceella su
45	36	81.8	721	2	Q8VG36	Q8vg36 bruceella me

ALIGNMENTS

RESULT 1

Q9H3X6 PRELIMINARY; PRT; 34 AA.
AC Q9H3X6;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE T200 Leukocyte common antigen (Fragment).
GN Name=PTPRC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=8909812; PubMed=2971720;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
antigen (CD45) gene.";
RL J. Immunol. 141:2781-2787 (1988).
DR EMBL; M23463; AAC26082.1;
DR EMBL; M23461; AAC26082.1; JOINED.
DR EMBL; M23462; AAC26082.1; JOINED.
FT CHAIN
FT NON_TER 32 >34 T200 leukocyte common antigen.
SQ SEQUENCE 34 AA; 3749 MW; OC261F8943734758 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 34;
Best local similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILAFGFAPL 9
|||||
Db 7 ILAFGFAPL 15

RESULT 2

Q8M1N3 PRELIMINARY; PRT; 126 AA.
AC Q8M1N3;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Leukocyte common antigen (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY114350; AAM76678.1; --

FT NON TER 126 126
SQ SEQUENCE 126 AA; 12927 MW; B3D35062F709F14C CRC64;

Query Match 100.0%; Score 44; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAFGFAFL 9
| | | | |
| | | | |
Db 7 LIAFGFAFL 15

RESULT 3

O6Q1P2 PRELIMINARY; PRT; 240 AA.

AC O6Q1P2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 transcript variant (Fragment).
GN Name=PTPRC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li D., Backenridge S., Sreaton G.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY567999; AAS75254.1; -.
FT NON TER 240
SQ SEQUENCE 240 AA; 25329 MW; 65067EDA0312DE87 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAFGFAFL 9
| | | | |
| | | | |
Db 7 LIAFGFAFL 15

RESULT 4

O9GMB6 PRELIMINARY; PRT; 453 AA.

AC O9GMB6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Membrane tyrosine phosphatase (Fragment).
GN Name=cd45;
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Born; TISSUE=Periphereal blood;
RC MEDLINE=21115144; PubMed=1120630; DOI=10.1007/s002510000276;
RX Ballingall K.T., Walbooch L., Holmes E.C., Woelk C.H., Machugh N.D.,
RA Lufte V., McKeever D.J.;
RT "The CD45 locus in cattle: allelic polymorphism and evidence for
RT exceptional positive natural selection."
RL Immunogenetics 52:276-283(2001).
DR EMBL; AJ400865; CAC05415.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS50853; FN3; 2.
FT NON TER 453
SQ SEQUENCE 453 AA; 51211 MW; 2E01CBE6F6C5268 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAFGFAFL 9
| | | | |
| | | | |
Db 7 LIAFGFAFL 15

RESULT 5

O6SZ80 PRELIMINARY; PRT; 454 AA.

AC O6SZ80;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 antigen isoform 6 (EC 3.1.3.48) (Fragment).
GN Name=CD45;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY444871; AAR16435.1; -.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Hydrolase.
FT NON TER 454
SQ SEQUENCE 454 AA; 50996 MW; 9FD5CCAE96DF48B CRC64;

Query Match 100.0%; Score 44; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAFGFAFL 9
| | | | |
| | | | |
Db 7 LIAFGFAFL 15

RESULT 6

O9GMB4 PRELIMINARY; PRT; 461 AA.

AC O9GMB4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Membrane tyrosine phosphatase (Fragment).
GN Name=cd45;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Periphereal blood;
RC MEDLINE=21115144; PubMed=1120630; DOI=10.1007/s002510000276;
RX Ballingall K.T., Walbooch L., Holmes E.C., Woelk C.H., Machugh N.D.,
RA Lufte V., McKeever D.J.;
RT "The CD45 locus in cattle: allelic polymorphism and evidence for
RT exceptional positive natural selection."
RL Immunogenetics 52:276-283(2001).
DR EMBL; AJ400864; CAC05417.1; -.
DR InterPro; IPR003961; FN_III.

DR InterPro: IPR008957; FN_III-like.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PSS0853; FN3; 2.
 FT NON_TER 461 461
 SQ SEQUENCE 461 AA; 51941 MW; 8736F59346454240 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 461;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
 |||||
 DB 7 LIAFGFAFL 15

RESULT 7
 Q9GMB5 PRELIMINARY; PRT; 463 AA.

AC Q9GMB5; 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Membrane tyrosine phosphatase (Fragment).
 GN Name=cd45;

OS Bos indicus (Zebu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 ON NCBI_TaxID=9915;

RP SEQUENCE FROM N.A.
 RC STRAIN=Boian; TISSUE=peripheral blood;
 RX MEDLINE=21115144; PubMed=11220630; DOI=10.1007/s002510000276;
 RA Ballingali K.T., Waibochi L., Holmes E.C., Woelk C.H., MacHugh N.D.,
 RA Lurie V., McKeever D.J.;
 RT "The CD45 locus in cattle: allelic polymorphism and evidence for
 RT exceptional positive natural selection.";
 RL Immunogenetics 52:276-283(2001).
 DR EMBL; AJ400866; CAC05416.1; -.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PSS0853; FN3; 2.
 FT NON_TER 463 463

SQ SEQUENCE 463 AA; 52236 MW; FAEF7F83F87596F CRC64;

Query Match 100.0%; Score 44; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
 |||||
 DB 7 LIAFGFAFL 15

RESULT 8
 Q9GMB1 PRELIMINARY; PRT; 465 AA.

AC Q9GMB1; 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Membrane tyrosine phosphatase (Fragment).
 GN Name=cd45;

OS Syncerus caffer (Cape buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Syncerus.
 ON NCBI_TaxID=9970;
 RN (1)
 RP SEQUENCE FROM N.A.

RC TISSUE=peripheral blood;
 RX MEDLINE=21115144; PubMed=11220630; DOI=10.1007/s002510000276;
 RA Ballingali K.T., Waibochi L., Holmes E.C., Woelk C.H., MacHugh N.D.,
 RA Lurie V., McKeever D.J.;
 RT "The CD45 locus in cattle: allelic polymorphism and evidence for
 RT exceptional positive natural selection.";
 RL Immunogenetics 52:276-283(2001).
 DR EMBL; AJ400867; CAC05420.1; -.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PSS0853; FN3; 2.
 FT NON_TER 465 465

SQ SEQUENCE 465 AA; 52289 MW; 9415673F219A368A CRC64;

Query Match 100.0%; Score 44; DB 2; Length 465;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
 |||||
 DB 7 LIAFGFAFL 15

RESULT 9
 Q6S281 PRELIMINARY; PRT; 466 AA.

AC Q6S281; 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE CD45 antigen isoform 5 (BC 3.1.3.48) (Fragment).
 GN Name=CD45;

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 ON NCBI_TaxID=9823;

RP SEQUENCE FROM N.A.
 RA Schultzein W.M., Zuckermann F.A.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY444870; AAR16434.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PSS0853; FN3; 2.
 KW Hydrolase.
 FT NON_TER 466 466

SQ SEQUENCE 466 AA; 52183 MW; 377CF34BAE18A28 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGFAFL 9
 |||||
 DB 7 LIAFGFAFL 15

RESULT 10
 Q6S282 PRELIMINARY; PRT; 501 AA.

AC Q6S282; 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE CD45 antigen isoform 4 (EC 3.1.3.48) (Fragment).
 GN Name=CD45;
 OS Sus scrofa (Pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY444869; ARI16433.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 501 AA; 55600 MW; B9E514C9183E3689 CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 501;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGPAPL 9
DB 7 LIAFGPAPL 15

RESULT 11
Q6SZ83 PRELIMINARY; PRT; 517 AA.
ID Q6SZ83;
AC Q6SZ83;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 antigen isoform 3 (EC 3.1.3.48) (Fragment).
GN Name=CD45;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY444869; ARI16432.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 517 AA; 57184 MW; D4BD2C74EB186339 CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 517;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGPAPL 9
DB 7 LIAFGPAPL 15

RESULT 12
Q6SZ84 PRELIMINARY; PRT; 567 AA.
ID Q6SZ84;
AC Q6SZ84;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

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DE CD45 antigen isoform 2 (EC 3.1.3.48) (Fragment).
GN Name=CD45;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY444867; ARI16431.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 567 AA; 62298 MW; 5CDBB886254187FD CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 567;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGPAPL 9
DB 7 LIAFGPAPL 15

RESULT 13
Q6SZ85 PRELIMINARY; PRT; 583 AA.
ID Q6SZ85;
AC Q6SZ85;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 antigen isoform 1 (EC 3.1.3.48) (Fragment).
GN Name=CD45;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY444866; ARI16430.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 583 AA; 63951 MW; 52PAA170EF02B83E CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 583;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIAFGPAPL 9
DB 7 LIAFGPAPL 15

RESULT 14
Q6PUK7 PRELIMINARY; PRT; 756 AA.
ID Q6PUK7;
AC Q6PUK7;

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DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)
 DE 05-JUL-2004 (TReMBLrel. 27, last annotation update)
 DE PTPRC protein (Fragment).
 GN Name=PTPRC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Mulvaney S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014239; AAH14239.1; -.
 DR HSSP: P18031; 1AAX.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPC; 2.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS50053; FN3; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 DR FT NON_TER 756
 FT 756
 SQ SEQUENCE 756 AA; 85430 MW; 8A9A863827BD69B6 CRC64;
 Query Match 100.0%; Score 44; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 8.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LIAFGFAFL 9
 Db 7 LIAFGFAFL 15
 RESULT 15
 Q6ED60 PRELIMINARY; PRT; 1290 AA.
 AC Q6ED60;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
 DE CD45.
 OS Actus vociferans (Spix's owl monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.
 NCBI_TaxID=57176;
 [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human";
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL: AY445818; AAS06903.1; -.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003961; FN_III-like.
 DR InterPro: IPR008957; PTPC_motif.
 DR InterPro: IPR003585; PTPC_motif.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 2.
 DR SMART: SM00404; PTPC_motif; 2.
 DR PROSITE: PS50053; FN3; 2.
 DR PROSITE: PS50083; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR KW HydroLase.
 SQ SEQUENCE 1290 AA; 145616 MW; 99EB10C75D932824 CRC64;
 Query Match 100.0%; Score 44; DB 2; Length 1290;
 Best Local Similarity 100.0%; Pred. No. 14; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LIAFGFAFL 9
 Db 9 LIAFGFAFL 17
 RESULT 16
 Q6ED61
 ID Q6ED61 PRELIMINARY; PRT; 1303 AA.
 AC Q6ED61;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, last annotation update)
 DE CD45.
 OS Actus nancyanae (Ma's night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.
 NCBI_TaxID=37293;
 [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human";
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL: AY445817; AAS06902.1; -.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003585; PTPC_motif.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPC; 2.
 DR SMART: SM00404; PTPC_motif; 2.

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DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolyase.
SQ SEQUENCE 1303 AA; 146929 MW; DOEB0C640D1D17E8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 1303;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLAFGPAFL 9
   |||||
Db 9 LLAFGPAFL 17

RESULT 17
ID 06ED62 PRELIMINARY; PRT; 1303 AA.
AC 06ED62;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DE CD45.
OS Aotus nigricape (Black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_Taxid=57175;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
RT vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL; AA445816; AAS06901.1; -.
DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPc_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPc; 2.
DR SMART; SM00404; PTPc_motif; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolyase.
SQ SEQUENCE 1303 AA; 146586 MW; 9BB023EBF4BC165 CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 1303;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLAFGPAFL 9
   |||||
Db 9 LLAFGPAFL 17

RESULT 18
CD45 HUMAN STANDARD; PRT; 1304 AA.
AC P08575; Q16614; Q9H0Y6;
DT 01-NOV-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)

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DE (T200).
GN Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RX MEDLINE=88061067; PubMed=2824653;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different
RT mRNAs encoding human leukocyte common antigens.";
RL J. Exp. Med. 166:1548-1566(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RX MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge T.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common
RT antigen).";
RL EMBO J. 6:1251-1257(1987).
RN [3]
RP SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89009812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
RT antigen (CD45) gene.";
RL J. Immunol. 141:2781-2787(1988).
RN [4]
RP FUNCTION.
RX MEDLINE=89017162; PubMed=2845400;
RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
RT protein tyrosine phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
RN [5]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Struelli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
RT domains of the receptor-linked protein tyrosine phosphatases LCA and
RT LAR.";
RL EMBO J. 9:2399-2407(1990).
RN [6]
RP FUNCTION: Required for T-cell activation through the antigen
RP receptor. The first PTPase domain has enzymatic activity, while
RP the second one seems to affect the substrate specificity of the
RP first one.
CC -! CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -! SUBUNIT: Binds CANAR and PRKSH (By similarity).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=At least 8 isoforms are produced;
CC Name=1;
CC IsoId=P08575-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P08575-2; Sequence=VSP_007780;
CC -! PTM: Heavily N- and O-glycosylated.
CC -! SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 1/6 subfamily.
CC -! SIMILARITY: Contains 2 fibronectin type III domains.
CC -! SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -! DATABASE: NAME=PROV; NOTE=CD guide CD45 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd45.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/

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CC or send an email to licensee@sb-sib.ch).
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DR EMBL; Y00638; CA68669.1; -.
DR EMBL; Y00662; CA68268.1; -.
DR EMBL; M23492; AAD15273.2; -.
DR EMBL; M23496; AAD15273.2; JOINED.
DR EMBL; M23466; AAD15273.2; JOINED.
DR EMBL; M23467; AAD15273.2; JOINED.
DR EMBL; M23468; AAD15273.2; JOINED.
DR EMBL; M23469; AAD15273.2; JOINED.
DR EMBL; M23470; AAD15273.2; JOINED.
DR EMBL; M23471; AAD15273.2; JOINED.
DR EMBL; M23472; AAD15273.2; JOINED.
DR EMBL; M23473; AAD15273.2; JOINED.
DR EMBL; M23474; AAD15273.2; JOINED.
DR EMBL; M23475; AAD15273.2; JOINED.
DR EMBL; M23476; AAD15273.2; JOINED.
DR EMBL; M23477; AAD15273.2; JOINED.
DR EMBL; M23478; AAD15273.2; JOINED.
DR EMBL; M23479; AAD15273.2; JOINED.
DR EMBL; M23480; AAD15273.2; JOINED.
DR EMBL; M23481; AAD15273.2; JOINED.
DR EMBL; M23482; AAD15273.2; JOINED.
DR EMBL; M23483; AAD15273.2; JOINED.
DR EMBL; M23484; AAD15273.2; JOINED.
DR EMBL; M23485; AAD15273.2; JOINED.
DR EMBL; M23486; AAD15273.2; JOINED.
DR EMBL; M23487; AAD15273.2; JOINED.
DR EMBL; M23488; AAD15273.2; JOINED.
DR EMBL; M23489; AAD15273.2; JOINED.
DR EMBL; M23490; AAD15273.2; JOINED.
DR EMBL; M23491; AAD15273.2; JOINED.
DR PIR; A46546; A46546.
DR HSSP; P18031; 1C88.
DR Intact; P08575; -.
DR GlycoSuiteDB; P08575; -.
DR Genew; HGNC:9666; PTPRC.
DR MIM; 151460; -.
DR GO; GO:0005687; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; TYR_Pp.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRVYPHPTASE.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50853; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50853; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1304
FT DOMAIN 24 575
FT TRANSMEM 576 597
FT DOMAIN 598 1304
FT DOMAIN 390 478
FT DOMAIN 482 570
FT DOMAIN 670 919
FT DOMAIN 961 1235
FT ACT_SITE 851 851
FT ACT_SITE 1167 1167
FT CARBOHYD 78 78
FT CARBOHYD 90 90
FT CARBOHYD 95 95
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 197 197

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FT CARBOHYD 232 232 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 260 260 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 270 270 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 276 276 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 335 335 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 378 378 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 419 419 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 468 468 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 488 488 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 529 529 N-linked (GlcNAc. .) (Potential).
FT VARSPPLIC 32 192 Missing (in isoform 2).
FT MUTAGEN 851 851 C->S: loss of activity.
FT CONFLICT 650 650 L -> P (in Ref. 1).
FT CONFLICT 1207 1207 P -> L (in Ref. 1).
SQ SEQUENCE 1304 AA, 147253 MW, A08FC2D069BAF7 CRC64;

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Query Match 100.0%; Score 44; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LIAFGPAFL 9
Db 7 LIAFGPAFL 15

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Search completed: May 3, 2005, 07:40:45
Job time : 95.8421 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds

(without alignments)
129,455 Million cell updates/sec

Title: US-10-003-983C-8

Perfect score: 48

Sequence: 1 VLYNKETKL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	1304	1 A46546	leukocyte common a
2	38	79.2	793	2 T41703	dipeptidyl aminope
3	38	79.2	1520	2 T23620	hypothetical prote
4	37	77.1	705	2 B82885	hypothetical prote
5	37	77.1	856	1 A45394	env polypeptide pr
6	37	77.1	1817	2 H71611	probable secreted
7	35	72.9	185	2 A81327	probable lipoprote
8	35	72.9	200	2 G81316	hypothetical prote
9	35	72.9	255	2 B71868	hypothetical prote
10	35	72.9	263	2 T17771	hypothetical prote
11	35	72.9	328	2 H83641	hypothetical prote
12	35	72.9	659	2 JC4910	heparin-sulfate ly
13	35	72.9	725	2 T52158	hypothetical prote
14	35	72.9	873	2 E90581	hypothetical prote
15	35	72.9	1398	2 H71606	hypothetical prote
16	34	70.8	63	1 TIMTC3	chymotrypsin inhib
17	34	70.8	123	2 C81441	probable protein-e
18	34	70.8	146	2 AB3612	transcription regu
19	34	70.8	267	1 KCHUM	matrilysin (EC 3.4
20	34	70.8	291	2 T14950	hypothetical prote
21	34	70.8	433	2 T27731	hypothetical prote
22	34	70.8	444	2 A72209	hypothetical prote
23	34	70.8	465	2 S69038	hypothetical prote
24	34	70.8	468	2 T40223	HMG-box containing
25	34	70.8	468	2 A41518	transcription fact
26	34	70.8	528	2 PC4025	intercellular adhe
27	34	70.8	532	1 A29849	intercellular adhe
28	34	70.8	577	2 C84936	DNA primase (limpor
29	34	70.8	598	2 S63617	cymH protein - Kle

30	34	70.8	647	2 S67651	hypothetical prote
31	34	70.8	756	2 AB1088	chitinase B homolo
32	34	70.8	756	2 AB1452	chitinase B homolo
33	34	70.8	816	2 C88196	protein ZK1127.7 l
34	34	70.8	855	1 JQ2003	env polypeptide -
35	34	70.8	855	2 F45557	external glycoprot
36	34	70.8	879	2 A56277	DNA-directed DNA p
37	34	70.8	979	2 E72236	clostridin-relate
38	34	70.8	1104	2 S36773	GTPase-activating
39	34	70.8	1810	2 T31092	probable voltage-g
40	34	70.8	2052	2 T18290	FYVE finger-contai
41	34	70.8	5138	2 B96695	hypothetical prote
42	33.5	69.8	204	2 T46363	hypothetical prote
43	33	68.8	67	2 S64713	formin binding pro
44	33	68.8	120	2 T26779	hypothetical prote
45	33	68.8	150	1 WZVZB1	vaccinia virus 18k

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N/Contents: leukocyte common antigen, intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text change 09-Jul-2004
R/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A/Reference number: A46546; PMID:88061067; PMID:2824653
A/Accession: A46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.111 and clone LCA.260
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-31,193-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.1
R/Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A/Reference number: A91066; PMID:87275816; PMID:295690
A/Accession: A29449
A/Molecule type: mRNA
A/Residues: 1-31,193-649, 'L', 651-869, 'G', 871-972, 'A', 874-1206, 'P', 1208-1304 <RAL>
A/Cross-references: GB:Y00662; NID:934275; PIND:CA68269.1; PID:934276
A/Experimental source: clones pHLC-1 and lambdaHLCL1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Rtsal, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative
A/Reference number: I57658; PMID:9006468; PMID:2531281
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:g187020; PIDN:AAA59497.1; PID:g553521
 C:Genetics:
 A:Gene: GDB:PTPRC; CD45
 A:Cross-references: GDB:119768; OMIM:151460
 A:Map position: 1q31-1q32
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 48; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETK 9
 DB 237 YLYNKETKL 245

RESULT 2
 T41703
 dipeptidyl aminopeptidase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T41703
 R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 Submitted to the EMBL Data Library, August 1998
 A:Reference number: Z22011
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-793 <MR>
 A:Cross-references: UNIPROT:O14073; EMBL:AL031180; PIDN:CAA0138.1; GSPDB:GN00066
 A:Experimental source: strain 972h-; cosmid c2E11 -climetic
 C:Genetics:
 A:Gene: SPAC2E11.08
 A:Map position: 1
 C:Superfamily: dipeptidyl-peptidase IV

Query Match 79.2%; Score 38; DB 2; Length 793;
 Best Local Similarity 87.5%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLYNKETK 8
 DB 150 YLYNKETK 157

RESULT 3
 T23620
 hypothetical protein K12D12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T23620; T28109
 R:Coles, L.
 Submitted to the EMBL Data Library, April 1995
 A:Reference number: Z19772
 A:Accession: T23620
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1520 <MT>
 A:Cross-references: UNIPROT:Q23670; EMBL:Z49069; PIDN:CAA88867.1; GSPDB:GN00020; CESP:K1
 A:Experimental source: clone K12D12
 R:Swindburne, J.
 Submitted to the EMBL Data Library, March 1996
 A:Reference number: Z20470
 A:Accession: T28109
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1520 <MT>
 A:Cross-references: EMBL:Z70213; PIDN:CAA94177.1; GSPDB:GN00020; CESP:K12D12.1

A:Experimental source: clone ZK930
 C:Genetics:
 A:Gene: CESP:K12D12.1
 A:Map position: 2
 A:Intron: 34/1; 146/2; 390/3; 471/3; 611/2; 1351/3; 1486/2
 C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd

Query Match 79.2%; Score 38; DB 2; Length 1520;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETK 8
 DB 719 YLYNKDTR 726

RESULT 4
 B82885
 hypothetical protein U0485 [imported] - Ureaplasma urealyticum
 C:Species: Ureaplasma urealyticum
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: B82885
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casseil, G.H.
 Submitted to GenBank, February 2000
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A:Reference number: A82870
 A:Accession: B82885
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-705 <GLA>
 A:Cross-references: GB:AE002146; GB:AF222894; NID:g6899479; PIDN:AAF30897.1; GSPDB:GN001
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: U0485
 A:Genetic code: SGC3

Query Match 77.1%; Score 37; DB 2; Length 705;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YNKETKL 9
 DB 605 YNKETKL 611

RESULT 5
 A45394
 env polypeptide precursor - feline immunodeficiency virus (strain UT-113)
 N:Alternate names: coat polypeptide
 N:Contains: surface glycoprotein; transmembrane glycoprotein
 C:Species: feline immunodeficiency virus
 A>Note: host Felis silvestris catus (domestic cat)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A45394; S16030
 R:Verchoor, E.J.; Hulskotte, E.G.J.; Ederveen, J.; Koolen, M.J.M.; Horzinek, M.C.; Rott
 Virology 193, 433-438, 1993
 A:Title: Post-translational processing of the feline immunodeficiency virus envelope pre
 A:Reference number: A45394; MUID:93174954; PMID:8382405
 A:Accession: A45394
 A:Molecule type: mRNA
 A:Residues: 1-856 <VER>
 A:Cross-references: UNIPROT:O03804; EMBL:X60725; NID:g1092; PIDN:CAA43131.1; PID:g1093
 C:Comment: This protein lacks an N-terminal signal sequence, and one of the three intern
 C:Genetics:
 A:Gene: env
 C:Superfamily: feline immunodeficiency virus env polypeptide
 C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
 F:1-611/Product: surface glycoprotein #status predicted <SGP>
 F:95-111/Region: hydrophobic
 F:151-169/Region: hydrophobic
 F:612-856/Product: transmembrane glycoprotein #status predicted <TGP>
 F:616-640/Region: hydrophobic
 F:786-812/Domain: transmembrane #status predicted <TMN>

F:220,258,269,274,298,330,336,342,418,422,448,469,481,499,518,531,548,551,556,717,721,724

Query Match 77.1%; Score 37; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYNNKTK 8
|||||
DB 309 LYNNKTK 315

RESULT 6
H71611
Probable secreted protein PFB0565w - malaria parasite (Plasmodium falciparum)
C/Species: Plasmodium falciparum
C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C/Accession: H71611
R/Gardner, M.J.; Tetzelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pereira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A/Reference number: A71600; MUID:99021743; PMID:9804551
A/Accession: H71611
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1817 <GAR>
A/Cross-references: UNIPROT:Q96205; GB:AE001403; GB:AE001362; NID:G3845216; PIDN:AACT7190
C/Experimental source: clone 3D7
C/Genetics:
A/Gene: PFB0565w

Query Match 77.1%; Score 37; DB 2; Length 1817;
Best Local Similarity 100.0%; Pred. No. 16+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYNNKTK 8
|||||
DB 805 LYNNKTK 811

RESULT 7
A81327
Probable 110proteins thiredoxin Cj1207c [imported] - Campylobacter jejuni (strain NCTC 11168)
C/Species: Campylobacter jejuni
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: A81327
R/Faircliff, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
A/Reference number: A81250; MUID:20150912; PMID:10688204
A/Accession: A81327
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-185 <PAR>
A/Cross-references: UNIPROT:Q9PN88; GB:AL139077; GB:AL111168; NID:G6968444; PIDN:CAW7346
C/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Gene: Cj1207c

Query Match 72.9%; Score 35; DB 2; Length 185;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LYNNKTK 9
|||||
DB 155 LYNNKTK 163

RESULT 8
G81316
probable galactosyltransferase Cj1124c [imported] - Campylobacter jejuni (strain NCTC 11168)
C/Species: Campylobacter jejuni

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: G81316
R/Faircliff, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
A/Reference number: A81250; MUID:20150912; PMID:10688204
A/Accession: G81316
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-200 <PAR>
A/Cross-references: UNIPROT:Q9PN80; GB:AL139077; GB:AL111168; NID:G6968444; PIDN:CAW733
C/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
A/Gene: wjaH; Cj1124c
C/Superfamily: pss2 protein

Query Match 72.9%; Score 35; DB 2; Length 200;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYNNKTK 9
|||||
DB 120 LYNNKTK 127

RESULT 9
B71868
hypothetical protein jhp0944 - Helicobacter pylori (strain J99)
C/Species: Helicobacter pylori
A/Variety: strain J99
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: B71868
R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat
A/Reference number: A71800; MUID:99120557; PMID:9923682
A/Accession: B71868
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-255 <ARN>
A/Cross-references: UNIPROT:Q9ZKJ1; GB:AE001524; GB:AE001439; NID:G4155523; PIDN:AA0065;
C/Experimental source: strain J99
C/Genetics:
A/Gene: jhp0944

Query Match 72.9%; Score 35; DB 2; Length 255;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYNNKTK 8
|||||
DB 240 LYNNKTK 247

RESULT 10
T17771
hypothetical protein A274R - Chlorella virus PBCV-1
C/Species: Chlorella virus PBCV-1
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T17771
R/Graves, M.V.; Van Etten, J.L.
Submitted to the EMBL Data Library, May 1999
A/Reference number: Z18806
A/Accession: T17771
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-263 <GRA>
A/Cross-references: UNIPROT:Q84591; EMBL:U42580; NID:G4028896; PIDN:AA096442.1
A/Experimental source: specific host Chlorella strain NC64A
C/Genetics:
A/Note: A274R

Query Match 72.9%; Score 35; DB 2; Length 263;
 Best Local Similarity 72.8%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 DB 170 YLYNKEHTL 178

RESULT 11

H83641
 hypothetical protein PA0026 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: H83641
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,
 .; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: H83641

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-328 <STO>

A/Cross-references: UNIPROT:Q917A4; GB:AE004442; GB:AE004091; NID:9945843; PIDN:AA0341

A/Experimental source: strain PA01

C/Genetics: PA0026

Query Match 72.9%; Score 35; DB 2; Length 328;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLYNKETK 8
 |||||
 DB 150 YLYNRELK 157

RESULT 12

JC4910
 heparin-sulfate lyase (EC 4.2.2.8) - Flavobacterium heparinum

N/Alternate names: heparin-sulfate eliminase; heparinase III

C/Species: Flavobacterium heparinum

C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C/Accession: JC4910

R/Godavarti, R.; Davis, M.; Venkataraman, G.; Cooney, C.; Langer, R.; Sasisekharan, R.

Biochem. Biophys. Res. Commun. 225, 751-758, 1996

A/Title: Heparinase III from Flavobacterium heparinum: Cloning and recombinant expressio

A/Reference number: JC4910; MUID:96374394; PMID:8780685

A/Accession: JC4910

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-659 <GOD>

A/Cross-references: UNIPROT:Q59289

A/Note: the authors translated the codon ACC for residue 313 as Asn

C/Suprafamily: Flavobacterium heparinum heparitin-sulfate lyase

C/Keywords: carbon-oxygen lyase

Query Match 72.9%; Score 35; DB 2; Length 659;
 Best Local Similarity 75.0%; Pred. No. 89;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLYNKETK 8
 |||||
 DB 588 YLYNRELK 595

RESULT 13

T52158
 hypothetical protein Ca49C10.14 [imported] - yeast (Candida albicans)

C/Species: Candida albicans

C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C/Accession: T52158

R/Taylor, K.; Harris, D.

submitted to the EMBL Data Library, November 1998

A/Reference number: Z25985

A/Accession: T52158

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-725 <TAY>

A/Cross-references: UNIPROT:Q94028; EMBL:AL033497; PIDN:CAA21978.1

A/Experimental source: strain 1161; cosmid Ca49C10

C/Genetics: A/Map position: 1

A/Note: Ca49C10.14

Query Match 72.9%; Score 35; DB 2; Length 725;
 Best Local Similarity 66.7%; Pred. No. 98;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 DB 333 YLYNKRSLK 341

RESULT 14

B90581
 hypothetical protein MYPV_5570 [imported] - Mycoplasma pulmonis (strain UAB CT1P)

C/Species: Mycoplasma pulmonis

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: B90581

R/Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A/Reference number: A95512; MUID:21267165; PMID:11353084

A/Accession: B90581

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-873 <KUR>

A/Cross-references: UNIPROT:Q98012; GB:AL445566; PID:gl4089972; PIDN:CAC13730.1; GSPDB:G

A/Experimental source: strain UAB CT1P

C/Genetics: A/Genetic code: SGC3

C/Suprafamily: alanyl-tRNA ligase

Query Match 72.9%; Score 35; DB 2; Length 873;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 DB 468 YLYNSELK 476

RESULT 15

H71606
 hypothetical protein PFB0755w - malaria parasite (Plasmodium falciparum)

C/Species: Plasmodium falciparum

C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C/Accession: H71606

R/Gardner, M.J.; Tetteilin, H.; Caracci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

Science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A/Reference number: A71600; MUID:99021743; PMID:9804551

A/Accession: H71606

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1398 <GAR>

A/Cross-references: UNIPROT:Q96244; GB:AE001416; GB:AE001362; NID:g845268; PIDN:AACT194

A/Experimental source: clone 3D7

C/Genetics:

A:Gene: PFB0755w

Query Match 72.9%; Score 35; DB 2; Length 1398;

Best Local Similarity 77.8%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;

QY 1 YLYNKEITKL 9
| | | | |
Db 1268 YCINKETKL 1276

Search completed: May 3, 2005, 06:16:16
Job time : 37.6892 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-8

Perfect score: 48

Sequence: 1 YLYNKETKL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	72	2	O6QIN1	O6QIN1. homo sapien
2	48	100.0	72	2	O6QIM8	O6QIM8. pongo pygma
3	48	100.0	72	2	O6QIM9	O6QIM9. gorilla gor
4	48	100.0	72	2	O6QIN0	O6QIN0. pan troglod
5	48	100.0	756	2	O6PJK7	O6PJK7. homo sapien
6	48	100.0	1304	1	CD45_HUMAN	P08575. homo sapien
7	41	85.4	383	2	O6C2W7	O6C2W7. yarrowia li
8	40	83.3	816	1	LEP1A_DROME	P11995. drosophila
9	39	81.2	77	2	O6QIM5	O6QIM5. cercopithee
10	39	81.2	77	2	O6QIM6	O6QIM6. macaca neme
11	39	81.2	77	2	O6QIM7	O6QIM7. hylobates m
12	39	81.2	455	2	O9RM84	O9RM84. clostridium
13	39	81.2	715	2	O59208	O59208. bacillus li
14	39	81.2	2228	2	O7RC88	O7RC88. plasmodium
15	38	79.2	226	2	O9NMB3	O9NMB3. mytilus edu
16	38	79.2	316	2	O7ZTV7	O7ZTV7. brachydanio
17	38	79.2	350	2	O9PZ20	O9PZ20. xestia c-ni
18	38	79.2	466	2	O7XSM2	O7XSM2. lactobacilli
19	38	79.2	532	2	O8MPL1	O8MPL1. plasmodium
20	38	79.2	713	2	O81ZG1	O81ZG1. plasmodium
21	38	79.2	793	1	YEAB_SCHPO	O14073. schizosacch
22	38	79.2	1520	1	TOP2_CAEEL	O23630. caenorhabdi
23	38	79.2	1547	1	TOP2_BOMMO	O16140. bombyx mori
24	37	77.1	543	2	O73D64	O73D64. bacillus ce
25	37	77.1	553	2	O8A269	O8A269. bacteroides
26	37	77.1	567	2	O7NAT2	O7NAT2. bacteroides
27	37	77.1	705	2	O9PQ05	O9PQ05. ureaplasma
28	37	77.1	789	1	LP1B_DROME	P11996. drosophila
29	37	77.1	840	2	O6S515	O6S515. cryptospori
30	37	77.1	853	2	O8O5O4	O8O5O4. feline immu
31	37	77.1	854	1	ENV_FITWO	O05312. feline immu

32	37	77.1	854	2	O90QK4	O90QK4. feline immu
33	37	77.1	854	2	O6J4Y9	O6J4Y9. feline immu
34	37	77.1	856	1	ENV_FITVU1	O03804. feline immu
35	37	77.1	856	2	O03800	O03800. feline immu
36	37	77.1	856	2	O03801	O03801. feline immu
37	37	77.1	856	2	O9PZ25	O9PZ25. feline immu
38	37	77.1	859	2	O90QK5	O90QK5. feline immu
39	37	77.1	3990	2	O96205	O96205. plasmodium
40	36	75.0	108	2	O9X9M3	O9X9M3. streptococc
41	36	75.0	171	2	O6BXD9	O6BXD9. debaryomyce
42	36	75.0	235	2	O8BSB7	O8BSB7. mus musculu
43	36	75.0	235	2	O8C180	O8C180. mus musculu
44	36	75.0	241	2	O7P2X6	O7P2X6. fusobacteri
45	36	75.0	257	2	O8RHK2	O8RHK2. fusobacteri

ALIGNMENTS

RESULT 1
ID O6QIN1 PRELIMINARY; PRT; 72 AA.
AC O6QIN1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPXC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/meh11;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL; AY393691; M546946.1; -.
FT NON_TER
FT TER
SQ SEQUENCE 72 AA; 8003 MW; 2EAC733A3290D4E4 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YLYNKETKL 9
DB 10 YLYNKETKL 18
RESULT 2
ID O6QIM8 PRELIMINARY; PRT; 72 AA.
AC O6QIM8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPXC;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/meh11;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).

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DR EMBL; AY539694; AAS46949.1; -.
FT NON_TER 1 1
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8303 MM; BAAAAFB3D47CSA42 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
Db 10 YLYNKETKL 18

RESULT 3
O6QIM9 PRELIMINARY; PRT; 72 AA.
AC O6QIM9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL; AY539693; AAS46948.1; -.
FT NON_TER 1 1
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8063 MM; 42ACT73A3297AD52 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
Db 10 YLYNKETKL 18

RESULT 4
O6QINO PRELIMINARY; PRT; 72 AA.
AC O6QINO;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Pan troglodytes (chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL; AY539692; AAS46947.1; -.
FT NON_TER 1 1
FT NON_TER 72 72
SQ SEQUENCE 72 AA; 8063 MM; 42ACT73A3297AD52 CRC64;
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Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
Db 10 YLYNKETKL 18

RESULT 5
O6PUK7 PRELIMINARY; PRT; 756 AA.
AC O6PUK7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE PTPRC protein (Fragment).
GN Name=PTPRC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Bueltow K.H., Scheeter C.F., Bhat N.K.,
RA Hopkins R.F., Jordan D.M., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshlyuk S., Carrincci P., Prange C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalski J., Smalton D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
RL Strausberg R.;
DR EMBL; BC014239; AAH14239.1; -.
DR HSSP; P18031; IAHX.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
FT NON_TER 756 756
SQ SEQUENCE 756 AA; 85430 MM; 8A9A863827BD69E6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 756;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
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Db 189 YLYNKERTL.197

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RESULT 6
CD45_HUMAN
ID CD45_HUMAN STANDARD; PRT; 1304 AA.
AC P08575; Q16614; Q9H0Y6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)
DE (T200).
GN Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different mRNAs encoding human leukocyte common antigens.";
RL J. Exp. Med. 166:1548-1566(1987).
[2]
SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RA MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common antigen).";
RL EMBO J. 6:1251-1257(1987).
[3]
SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE=89009812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intern organization of the human leukocyte common antigen (CD45) gene.";
RL J. Immunol. 141:2781-2787(1988).
[4]
FUNCTION.
RA MEDLINE=89017162; PubMed=2845400;
RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
[5]
MUTAGENESIS.
RA MEDLINE=90316093; PubMed=1695145;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";
RL EMBO J. 9:2399-2407(1990).
-1- FUNCTION: Required for T-cell activation through the antigen receptor. The first PTPase domain has enzymatic activity, while the second one seems to affect the substrate specificity of the first one.
-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
-1- SUBUNIT: Binds GANAB and PKCSH (By similarity).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=At least 8 isoforms are produced;
Name=1;
IsoId=P08575-1; Sequence=Displayed;
CC Name=2;
IsoId=P08575-2; Sequence=VSP_007780;
-1- PTM: Heavily N- and O-glycosylated.
-1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.

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CC CC Receptor class 1/6 subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -1- DATABASE: NAME=PTPRC; NOTE=CD guide CD45 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/row/cd/cd45.htm".
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC EMBL; Y00638; CAA68669.1; -
CC EMBL; Y00662; CAA68269.1; -
CC EMBL; M23492; AAD15273.2; -
CC EMBL; M23496; AAD15273.2; JOINED.
CC EMBL; M23466; AAD15273.2; JOINED.
CC EMBL; M23467; AAD15273.2; JOINED.
CC EMBL; M23468; AAD15273.2; JOINED.
CC EMBL; M23469; AAD15273.2; JOINED.
CC EMBL; M23470; AAD15273.2; JOINED.
CC EMBL; M23471; AAD15273.2; JOINED.
CC EMBL; M23472; AAD15273.2; JOINED.
CC EMBL; M23473; AAD15273.2; JOINED.
CC EMBL; M23474; AAD15273.2; JOINED.
CC EMBL; M23475; AAD15273.2; JOINED.
CC EMBL; M23476; AAD15273.2; JOINED.
CC EMBL; M23477; AAD15273.2; JOINED.
CC EMBL; M23478; AAD15273.2; JOINED.
CC EMBL; M23479; AAD15273.2; JOINED.
CC EMBL; M23480; AAD15273.2; JOINED.
CC EMBL; M23481; AAD15273.2; JOINED.
CC EMBL; M23482; AAD15273.2; JOINED.
CC EMBL; M23483; AAD15273.2; JOINED.
CC EMBL; M23484; AAD15273.2; JOINED.
CC EMBL; M23485; AAD15273.2; JOINED.
CC EMBL; M23486; AAD15273.2; JOINED.
CC EMBL; M23487; AAD15273.2; JOINED.
CC EMBL; M23488; AAD15273.2; JOINED.
CC EMBL; M23489; AAD15273.2; JOINED.
CC EMBL; M23490; AAD15273.2; JOINED.
CC EMBL; M23491; AAD15273.2; JOINED.
CC PIR; A46546; A46546.
CC HSSP; P18031; 1C88.
CC Inlact; P08575; -.
CC GlycoSuiteDB; P08575; -.
CC GeneW; HGNC:9666; PTPRC.
CC MIM; 151460; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR000387; TYR phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00041; fn3; 2.
CC PRINTS; PR00700; PRTYPHPTASE.
CC PROSITE; PS00553; FN3; 2.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
CC PROSITE; PS00556; TYR_PHOSPHATASE_2; 2.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
CC Alternative splicing; Antigen; Glycoprotein; Hydrolase;
CC Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
CC Transmembrane.
CC SIGNAL 1 23
CC CHAIN 24 1304 Leukocyte common antigen.
CC DOMAIN 24 575 Extracellular (Potential).
CC TRANSMEM 576 597 Potential.
CC DOMAIN 598 1304 Cytoplasmic (Potential).
CC DOMAIN 390 478 Fibronectin type-III 1.

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FT DOMAIN 482 570 Fibronection type-III 2.
FT DOMAIN 670 919 Protein-tyrosine phosphatase 1.
FT ACT_SITE 961 1235 Protein-tyrosine phosphatase 2.
FT ACT_SITE 851 851 Phosphotyrosine intermediate.
FT ACT_SITE 1167 1167 Phosphotyrosine intermediate (By
similarity).
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 164 184 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 190 184 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 197 197 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 260 260 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 335 335 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 378 378 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 419 419 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 468 468 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 529 529 N-linked (GlcNAc...) (Potential)
FT VARSPPLIC 32 192 Missing (in isoform 2).
FT MUTAGEN 851 851 /FTid=VSP_007780.
FT CONFLICT 650 650 C->S: Loss of activity.
FT CONFLICT 1207 1207 L->P (in Ref. 1).
SQ SEQUENCE 1304 AA; 147253 MW; A08FC22D606B9BA7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 1; Length 1304;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETK 9
DB 237 YLYNKETKL 245

RESULT 7
OC62W7 PRELIMINARY; PRT; 383 AA.
ID OC62W7
AC 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Similar to tr|Q8TRF8 Trichoderma virens Class V chitinase.
GN ORFNames=YAL10P045328;
OS Yarrowia lipolytica CL1899.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_Taxid=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1899;
RG Genolevures;
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchon S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissiere A., Boyer J., Catolico L., Contandoli F., de Darivar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Duizat H., Groppi A.,
RA Hantreva F., Hennequin C., Jauniaux N., Juyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennen S., Tekala F., Wesolowski-Jouvet M., Westhof E., Witth B.,
RA Zenzou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudon B., Scarpelli C., Galliardin C., Weissenbach J.,
RA Winkler P., Souciet J.L.;
RA "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RP SEQUENCE FROM N.A.

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RC STRAIN=CL1899;
RA Genoscope;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR382132; CAG77802.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase II.
DR InterPro; IPR01223; Glyco_hydro_18.
DR InterPro; IPR01579; Glyco_hydro_18A5.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Chitinase II; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KV Glycosidase; Hydrolase.
SQ SEQUENCE 383 AA; 43844 MW; 228CAFDA1D50361 CRC64;

Query Match
Best Local Similarity 85.4%; Score 41; DB 2; Length 383;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETK 8
DB 306 YLYNKDTX 313

RESULT 8
ID LPLA_DROME STANDARD; PRT; 816 AA.
AC P11955; Q9VYM4;
DT 01-OCT-1989 (Rel. 12, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Larval serum protein 1 alpha chain precursor (Hexamerin 1 alpha).
GN Name=Lsp1-alpha; Synonyms=LSP1-a; ORFNames=CG2559;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.D., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelber W.M., Glaser K.,
RA Glisdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Heiman J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibbegan C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclbo J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

```

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochkin S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN
RP SEQUENCE OF 1-84 FROM N.A.
RX MEDLINE=87060914; PubMed=3097321;
RA Delaney S.J., Smith D.F., McClelland A., Sunkel C., Glover D.M.;
RT "Sequence conservation around the 5' ends of the larval serum protein
RT 1 genes of *Drosophila melanogaster*.";
RN J. Mol. Biol. 189:1-11(1986).
RN
RP SEQUENCE OF 1-52 FROM N.A.
RA Jowett T.;
RT "The regulatory domain of a larval serum protein gene in *Drosophila
RT melanogaster*.";
RL EMBO J. 4:3789-3795(1985).
CC
CC -1- FUNCTION: Larval storage protein (LSP) which may serve as a store
CC of amino acids for synthesis of adult proteins (By similarity).
CC
CC -1- SUBUNIT: Heterohexamer, composed of three subunits, alpha, beta
CC and gamma.
CC
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC
CC -1- TISSUE SPECIFICITY: Larval hemolymph.
CC
CC -1- SIMILARITY: Belongs to the hemocyanin family.
CC
CC -----
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CC -----
DR EMBL, AE003489; AAF48168.2; -;
DR EMBL, X03872; CAA27506.1; -;
DR EMBL, X03368; CAA27066.1; -;
DR PIR: A27144; A27144.
DR HSSP: P04253; ILIA.
DR FlyBase, FBgn0002562; Lsp1-alpha.
DR GO: GO:0005616; C:larval serum protein complex; IDA.
DR InterPro, IPR000896; Hemocyanin.
DR InterPro, IPR005203; hemocyanin_C.
DR InterPro, IPR005204; hemocyanin_N.
DR Pfam, PF03723; Hemocyanin_C_1.
DR Pfam, PF03722; Hemocyanin_M_1.
DR Pfam, PF03722; Hemocyanin_N_1.
DR PRINTS, PR00187; HAEMOCYANIN.
DR PROSITE, PS00209; HEMOCYANIN_1; FALSE_NEG.
DR PROSITE, PS00210; HEMOCYANIN_2; 1.
DR GlycoProtein; Hemolymph; Multifigene family; Signal; Storage protein.
FT SIGNAL 1 16
FT CHAIN 17 816 Larval serum protein 1 alpha chain.
SQ SEQUENCE 816 AA; 98867 MW; 2D1C44176EB76194 CRC64;
Query Match 83.3%; Score 40; DB 1; Length 816;

Best Local Similarity 77.8%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLYNKETKL 9
DB 306 YLYNBSKTL 314
RESULT 9
QOQIM5 PRELIMINARY; PRT; 77 AA.
AC QOQIM5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OC Cercopithecus neglectus (Debrazza's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/meh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL, AY539697; AAS46952.1; -;
FT NON_TER 1 1
FT NON_TER 77 77
SQ SEQUENCE 77 AA; 8815 MW; 6DDDE13DEDE1184 CRC64;
Query Match 81.2%; Score 39; DB 2; Length 77;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YLYNKETKL 9
DB 10 YLYNHQTKL 18
RESULT 10
QOQIM6 PRELIMINARY; PRT; 77 AA.
AC QOQIM6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OC Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/meh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL, AY539696; AAS46951.1; -;
FT NON_TER 1 1
FT NON_TER 77 77
SQ SEQUENCE 77 AA; 8918 MW; D82A0CB0CEB66758 CRC64;
Query Match 81.2%; Score 39; DB 2; Length 77;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YLYNKETK 9
| | | | |
Db 10 YLYNKETK 18

RESULT 11

OQOIM7 PRELIMINARY; PRT; 77 AA.
AC OQOIM7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE CD45 (Fragment).
OS Name=PTPRC;
OS Hylobates muelleri (Mueller's gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OK NCBI_TaxID=9588;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates."
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL; AY539695; AAS46950.1; -.
FT NON_TER
SQ SEQUENCE 77 AA; 8782 MW; 65B19539595ED7CA CRC64;

Query Match 81.2%; Score 39; DB 2; Length 77;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETK 8
| | | | |
Db 10 YLYNKETK 17

RESULT 12

OQRM84 PRELIMINARY; PRT; 455 AA.
ID OQRM84;
AC OQRM84;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative transposase.
OS Clostridium beijerinckii (Clostridium MP).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OK NCBI_TaxID=1520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8052;
RA MEDLINE=20391274; PubMed=10937495;
RA Liyanage H., Holcroft P., Evans V.J., Keis S., Wilkinson S.R.,
RA Kashek E.R., Young M.;
RT "A new insertion sequence, ISCb1, from Clostridium beijerinckii NCIMB
RT 8052."
RL J. Mol. Microbiol. Biotechnol. 2:107-113(2000).
DR EMBL; AJ250468; CAB60193.1; -.
SQ SEQUENCE 455 AA; 52691 MW; 5C1902030A9F5E94 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 455;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETK 8
| | | | |
Db 367 YLYNKETK 374

RESULT 13

O59208 PRELIMINARY; PRT; 715 AA.
ID O59208;
AC O59208;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Esterase (EC 3.1.1.1).
GN Name=est;
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OK NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LCB40;
RA Alvarez-Macario E., Augter-Magro V., Guzzo J., Baratt J.;
RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U35855; AAA79183.1; -.
DR GO; GO:0004091; F:carboxylesterase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004607; F:phosphatidylcholine-sterol O-acyltransferase . .; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR003386; LACT.
DR InterPro; IPR007280; Pept_Bact_C.
DR Pfam; PF02450; LACT; 1.
DR Pfam; PF04151; PC; 2.
KW Hydrolase.

SQ SEQUENCE 715 AA; 81570 MW; B6E829B5A755D975 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 715;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YLYNKETK 9
| | | | |
Db 170 YLYNKETK 178

RESULT 14

O7RG88 PRELIMINARY; PRT; 2228 AA.
ID O7RG88;
AC O7RG88;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Guanylyl cyclase-related.
GN Name=PY04459;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OK NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow N.J., van Aken S.E., Riedmuller S.B., Felblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R., III, Raine J.D., Sinden K.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABU01001358; BAA16324.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001757; ATPase_E1-E2.

DR InterPro; IPR005834; Dehal_like_hydro.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PROSITE; PS00154; ATPase_E1_E2; UNKNOWN 1.
 SQ SEQUENCE 2228 AA; 262353 MW; 452E8463DBF9AF77 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 2228;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YLYNKETK 9
 :|||||
 Db 1606 YLYNKETK 1613

RESULT 15

O9NHB3 PRELIMINARY; PRT; 226 AA.
 ID O9NHB3
 AC O9NHB3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Topoisomerase II (Fragment).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_Taxid=6550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Luedeking A., Winzer K., Koehler A.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF227976; AAF5892.1; -.
 DR HSP; P06786; 1BJT.
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
 DR GO; GO:0016853; F:Isomerase activity; IEA.
 DR GO; GO:0006265; P:DNA topological change; IEA.
 DR InterPro; IPR011558; DNA_gyrase_B.
 DR InterPro; IPR001241; DNA_topoisomII.
 DR InterPro; IPR002205; DNA_topoisomIV.
 DR Pfam; PF00521; DNA_topoisomIV; 1.
 DR PRINTS; PR00418; TP12FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR ProDom; PD000742; DNA_topoisomIV; 1.
 KW Isomerase.
 FT NON_TER 1
 FT NON_TER 226
 SQ SEQUENCE 226 AA; 26529 MW; 7CCF8F06D819C544 CRC64;

Query Match 79.2%; Score 38; DB 2; Length 226;
 Best Local Similarity 87.5%; Pred. NO. 33;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLYNKETK 8
 :|||||
 Db 139 YLYNKETK 146

Search completed: May 3, 2005, 05:59:51
 Job time : 54.1351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:28:27 ; Search time 38.6757 Seconds
(without alignments)
90.001 Million cell updates/sec

Title: US-10-003-983C-8

Perfect score: 48

Sequence: 1 YLYNKETKL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseq1980s:***
2: geneseq1990s:***
3: geneseq2000s:***
4: geneseq2001s:***
5: geneseq2002s:***
6: geneseq2003as:***
7: geneseq2003bs:***
8: geneseq2004s:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	ABG31978	Abg31978 Human CD4
2	48	100.0	553	AAW35856	Aaw35856 Human CD4
3	48	100.0	553	ABU07335	Abu07335 Human exp
4	48	100.0	641	AAW23689	Aaw23689 Human EST
5	48	100.0	641	ABU07333	Abu07333 Human exp
6	48	100.0	664	AAW39262	Aaw39262 Human pol
7	48	100.0	664	ABU07334	Abu07334 Human exp
8	48	100.0	1114	ABU05246	Abu05246 Human exp
9	48	100.0	1114	ABU05239	Abu05239 Human exp
10	48	100.0	1143	ABU05240	Abu05240 Human exp
11	48	100.0	1143	ABU05245	Abu05245 Human exp
12	48	100.0	1143	ADL16232	Adl16232 Human pro
13	48	100.0	1143	ADL18845	Adl18845 Human sof
14	48	100.0	1149	AAW10448	Aaw10448 Human pol
15	48	100.0	1149	ABU05242	Abu05242 Human exp
16	48	100.0	1192	ADR39747	Adr39747 Human kin
17	48	100.0	1219	ADQ39378	Adq39378 Human myo
18	48	100.0	1256	ADM67187	Adm67187 Human adi
19	48	100.0	1256	ADP12966	Adp12966 Protein e
20	48	100.0	1258	ADQ39376	Adq39376 Human myo
21	48	100.0	1267	ADQ39379	Adq39379 Human myo
22	48	100.0	1304	ABU05243	Abu05243 Human exp
23	48	100.0	1304	ABU05241	Abu05241 Human exp
24	48	100.0	1304	ABU05244	Abu05244 Human exp
25	48	100.0	1304	ADL16230	Adl16230 Human pro

26	48	100.0	1304	ADP65158	Adp65158 Human pro
27	48	100.0	1304	ADM67209	Adm67209 Human adi
28	48	100.0	1304	ABO84455	Ab084455 Human can
29	48	100.0	1304	ADQ39380	Adq39380 Human myo
30	48	100.0	1306	ADQ39375	Adq39375 Human myo
31	40	83.3	789	ABB59220	Abb59220 Protein d
32	39	81.2	793	ADA95085	Ada95085 Protein d
33	38	79.2	793	ADN19590	Adn19590 Bacterial
34	38	79.2	1520	ADN22943	Adn22943 Bacterial
35	38	79.2	1520	ADN22944	Adn22944 Bacterial
36	37	77.1	34	ADA95111	Ada95111 Protein d
37	37	77.1	568	ABM67293	Abm67293 Phototrab
38	37	77.1	705	ABU48943	Abu48943 Protein e
39	37	77.1	789	ABB60269	Abb60269 Drosophill
40	37	77.1	854	AAR44957	Aar44957 Feline im
41	37	77.1	856	AAR51253	Aar51253 FIV DUTCH
42	37	77.1	856	AAR51247	Aar51247 FIV envel
43	37	77.1	856	AAR51254	Aar51254 FIV DUTCH
44	37	77.1	1817	AAB18255	Aab18255 Plasmodiu
45	36	75.0	312	AAC00952	Aac00952 Human pol

ALIGNMENTS

RESULT 1
ID ABG31978 standard, peptide, 9 AA.
XX
AC ABG31978;
XX

DT 05-NOV-2002 (first entry)
XX

DE Human CD45 HLA-binding peptide, huCD45/237.
XX

KW Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
XX antigen-presenting cell; APC; major histocompatibility complex; MHC;

KW antigen; allogenic; T cell receptor; TCR; cancer; tumour;
XX

KW allogenic stem cell transplantation; CFU-GM; leukaemia;
XX colony forming unit-granulocyte macrophage; immunotherapeutic;

KW haematopoietic; malignant.
XX

OS Homo sapiens.
XX

PN WO200244207-A1.
XX

PD 06-JUN-2002.
XX

PF 30-NOV-2000; 2000WO-GB004566.
XX

PR 30-NOV-2000; 2000WO-GB004566.
XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX

Stausas HJ, Amrolia PJ;
XX

WPI; 2002-599413/64.
XX

Novel peptide comprising leukocyte antigen binding peptide of human CD45 polypeptide, useful for producing activated cytotoxic T lymphocytes, for killing cancerous cells e.g. leukemia.
XX

Claim 2; Page 38; 56pp; English.
XX

The invention discloses a peptide comprising the human leukocyte antigen (HLA)-binding peptide of human CD45 polypeptide, its portion or variant, provided that the peptide is not the intact human CD45 polypeptide. The peptides are useful for producing activated cytotoxic T lymphocyte (CTL) in vitro which involves contacting the CTL with an antigen-presenting cell, where its major histocompatibility complex (MHC) class I molecules are loaded with the peptide, to activate, in an antigen specific manner, where the CTL and the antigen presenting cell are allogenic with respect to the class I MHC molecule that is presenting peptides of CD45. The

antigen-presenting cell contains an expression vector including the polynucleotide encoding the CD45 peptide. The activated CTLs are useful for killing, and in the manufacture of a medicament for, target cells expressing the CD45 peptide in a patient. A T cell receptor (TCR), recognising cells expressing the CD45 peptides, is useful for killing target cells (cancer cells) in a patient which involves obtaining CTLs from the patient, introducing into the CTLs the polynucleotide encoding the TCR and then introducing the cells thus produced into the patient who has undergone an allogeneic stem cell transplantation. Tumour reactive CTLs have been shown to mediate tumour regression in animal models by the inhibition of colony forming unit-granulocyte macrophage (CFU-GM) colony formation. The cancer is leukaemia which expresses the CD45 polypeptide. The method is useful as an immunotherapeutic for treating a patient with haematopoietic malignancy or to target and kill cells which express the CD45 polypeptide. This advantage this method provides is that the CTLs destroy the malignant haematopoietic cells but not the transplanted cells. The sequence presented is the peptide, huCD45/237, comprising an HLA-binding peptide of human CD45

Sequence 9 AA;

Query Match 100.0%; Score 48; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
|||||||
Db 1 YLYNKETKL 9

RESULT 2
AAW35856
ID AAW35856 standard; protein; 553 AA.

AC AAW35856;

DT 27-APR-1998 (first entry)

DE Human CD45 for use in T lymphocyte veto molecule.

Human; CD45; T lymphocyte veto molecule; chimeric molecule;
targeting polypeptide; suppression; immune response; treatment;
autoimmune disease; allergy; immunological disorder;
transplant rejection.

OS Homo sapiens.

PN WO9737687-A1.

PD 16-OCT-1997.

PF 10-APR-1997; 97WO-US005943.

PR 10-APR-1996; 96US-00630172.

PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

PI Staerz UD;

DR WPI; 1997-512419/47.

T lymphocyte veto molecule comprising response cell activating protein -
linked to molecule that targets stimulator cell marker, used for
selective suppression of immune response, e.g. prevention of graft
rejection or treatment of auto-immune disease.

Claim 37; Page 70-72; 309pp; English.

A novel T lymphocyte veto molecule is a chimeric molecule comprising a
protein, e.g. the present sequence, linked to a targeting polypeptide
that binds a molecule, which differentiates a host cell from a tissue
graft cell, or selectively targets a stimulator cell involved in the
autoimmune response. A veto molecule, in which the protein binds a

molecule that targets stimulator cells, can be used to suppress an immune
response and therefore treat autoimmune diseases, e.g. systemic lupus
erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
thyroiditis, Addison's or Grave's diseases and rheumatoid arthritis,
allergies and other immunological disorders. Where the protein binds a
molecule that differentiates graft and host cells, the veto molecule can
be used to reduce transplant rejection. The veto molecule provides
specific regulation of particular stimulator cells that can kill graft
cells or respond to autoantigens, but leave other stimulator cells
unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
affecting the other. The veto molecule can be administered locally to
minimise generalised immunosuppression

Sequence 553 AA;

Query Match 100.0%; Score 48; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
|||||||
Db 214 YLYNKETKL 222

RESULT 3
ABU07335
ID ABU07335 standard; protein; 553 AA.

AC ABU07335;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #2036.

Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
kinase; protease; protease inhibitor; transporter; cytoskeletal protein;
receptor; transcription factor; cancer; MHC;
major histocompatibility complex; myeloma; colon cancer; gastric cancer;
adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCO INC.

PI Chicx RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
cytoskeletal proteins, receptors or transcription factors), useful for
treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
leukemia.

Example 2; SEQ ID NO 2036; 134pp; English.

The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 48; DB 6; Length 553;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
DB 214 YLYNKETKL 222

RESULT 4
ID AAM23689 standard; protein; 641 AA.
XX
AC AAM23689;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1214.
XX
KM Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KM diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KM gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang U, Wehrman T;
XX
DR WPI; 2001-476164/51.
XX
PT N-PSDB; AAH98348.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 875-876; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensic, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 48; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
DB 78 YLYNKETKL 86

RESULT 5
ID ABU07333 standard; protein; 641 AA.
XX
AC ABU07333;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2034.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2034; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 641 AA;
Query Match 100.0%; Score 48; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YLYNKETKL 9
DB 78 YLYNKETKL 86
RESULT 6
AAM39262
ID AAM39262 standard; protein; 664 AA.
AC AAM39262;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2407.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
XX
PR 21-JAN-2000; 2000US-00488725.
XX
PR 25-APR-2000; 2000US-00552317.
XX
PR 20-JUN-2000; 2000US-00598042.
XX
PR 19-JUL-2000; 2000US-00620312.
XX
PR 03-AUG-2000; 2000US-00653450.
XX
PR 14-SEP-2000; 2000US-00662191.
XX
PR 19-OCT-2000; 2000US-00693036.
XX
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
XX
DR N-PSDB; AAI58418.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2407; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 664 AA;
Query Match 100.0%; Score 48; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YLYNKETKL 9
DB 78 YLYNKETKL 86
RESULT 7
ABU07334
ID ABU07334 standard; protein; 664 AA.
XX
AC ABU07334;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2035.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2035; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
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CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 664 AA;

Query Match 100.0%; Score 48; DB 6; Length 664;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 Db 78 YLYNKETKL 86

RESULT 8
 ABU05246
 ID ABU05246 standard; protein; 1114 AA.

XX AC ABU05246;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1912.

XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOs INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX PS Example 2; SEQ ID NO 1912; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 1114 AA;

Query Match 100.0%; Score 48; DB 6; Length 1114;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 Db 47 YLYNKETKL 55

RESULT 9
 ABU05239
 ID ABU05239 standard; protein; 1114 AA.

XX AC ABU05239;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1905.

XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOs INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX PS Example 2; SEQ ID NO 1905; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 1114 AA;

Query Match 100.0%; Score 48; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 9.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

OY 1 YLYNKETKL 9
|||
DB 47 YLYNKETKL 55

RESULT 10

ABU05240
ID ABU05240 standard; protein; 1143 AA.

XX
AC ABU05240;

XX
DT 29-JAN-2003 (first entry)

XX
DE Human expressed protein tag (EPT) #1906.

XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX
OS Homo sapiens.

XX
PN WO200278524-A2.

XX
PD 10-OCT-2002.

XX
PF 28-MAR-2002; 2002MO-US009671.

XX
PR 28-MAR-2001; 2001US-0279495P.

XX
PR 21-MAY-2001; 2001US-0292544P.

XX
PR 08-AUG-2001; 2001US-0310801P.

XX
PR 01-OCT-2001; 2001US-0326370P.

XX
PR 04-DEC-2001; 2001US-0336780P.

XX
PR 20-FEB-2002; 2002US-0358985P.

XX
PA (ZYCO-) ZYCOS INC.

XX
PI Chicx RM, Tomlinson AJ, Urban RG;

XX
PI WPI; 2003-040607/03.

XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX
PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 1143 AA;

Query Match 100.0%; Score 48; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 9.9; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

OY 1 YLYNKETKL 9
|||
DB 76 YLYNKETKL 84

RESULT 11

ABU05245
ID ABU05245 standard; protein; 1143 AA.

XX
AC ABU05245;

XX
DT 29-JAN-2003 (first entry)

XX
DE Human expressed protein tag (EPT) #1911.

XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX
OS Homo sapiens.

XX
PN WO200278524-A2.

XX
PD 10-OCT-2002.

XX
PF 28-MAR-2002; 2002MO-US009671.

XX
PR 28-MAR-2001; 2001US-0279495P.

XX
PR 21-MAY-2001; 2001US-0292544P.

XX
PR 08-AUG-2001; 2001US-0310801P.

XX
PR 01-OCT-2001; 2001US-0326370P.

XX
PR 04-DEC-2001; 2001US-0336780P.

XX
PR 20-FEB-2002; 2002US-0358985P.

XX
PA (ZYCO-) ZYCOS INC.

XX
PI Chicx RM, Tomlinson AJ, Urban RG;

XX
PI WPI; 2003-040607/03.

XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX
PS Example 2; SEQ ID NO 1911; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 1143 AA;

Query Match 100.0%; Score 48; DB 6; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 76 YLYNKETKL 84

RESULT 12

ADL16232
 ID ADL16232 standard; protein; 1143 AA.

XX
 AC ADL16232;

XX
 DT 06-MAY-2004 (first entry)

XX
 DE Human protein tyrosine phosphatase #27.

XX
 KM cytostatic; immunosuppressive; antiallergic;
 KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KM inducible signalling pathway; cell proliferation; cancer;
 KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KM cell-cycle abnormality; enzyme.

XX
 OS Homo sapiens.

XX
 EN WO2003068984-A2.

XX
 PD 21-AUG-2003.

XX
 PF 13-FEB-2003; 2003WO-EP001446.

XX
 PR 13-FEB-2002; 2002US-0356810P.

XX
 PR 12-FEB-2003; 2003US-00366547.

XX
 PA (COLD-) COLD SPRING HARBOR LAB.

XX
 PA (CEPT-) CEPTYR INC.

XX
 PI Tonks NK, Tzu-Ching M, Cool DE;

XX
 DR WPI; 2003-712572/67.

XX
 DR N-PSDB; ADL16231.

PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.

XX
 PS Disclosure; SEQ ID NO 81; 238pp; English.

XX
 CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulphydryl-reactive agent (II) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle

CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.

XX
 SQ Sequence 1143 AA;

Query Match 100.0%; Score 48; DB 7; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 76 YLYNKETKL 84

RESULT 13

ADQ18845
 ID ADQ18845 standard; protein; 1143 AA.

XX
 AC ADQ18845;

XX
 DT 26-AUG-2004 (first entry)

XX
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.

XX
 KM soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX
 OS Homo sapiens.

XX
 PN WO2004048938-A2.

XX
 PD 10-JUN-2004.

XX
 PF 26-NOV-2003; 2003WO-US038193.

XX
 PR 26-NOV-2002; 2002US-0429739P.

XX
 PA (PROT-) PROTEIN DESIGN LABS INC.

XX
 PI Aziz N, Ginsburg WM, Zlotnick A;

XX
 DR WPI; 2004-441208/41.

PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.

XX
 PS Example 2; SEQ ID NO 1664; 210pp; English.

XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.

XX
 SQ Sequence 1143 AA;

Query Match 100.0%; Score 48; DB 8; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 76 YLYNKETKL 84

RESULT 14
AAM41048
ID AAM41048 standard; protein; 1149 AA.
XX
XX AAM41048;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5979.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200153312-A1.
XX
XX PD 26-JUL-2001.
XX
XX PF 26-DEC-2000; 2000WO-US034263.
XX
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX PA
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX DR N-PSDB; AAI60204.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX PS Example 2; SEQ ID NO 5979; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX SQ Sequence 1149 AA;

Query Match 100.0%; Score 48; DB 4; Length 1149;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9

Db 81 YLYNKETKL 89
|||||||
RESULT 15
ABU05242
ID ABU05242 standard; protein; 1149 AA.
XX
XX ABU05242;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1908.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0278495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX PI Chicz RM, Tomlinson AJ, Urban RG;
XX
XX DR WPI; 2003-040607/03.
XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX PS Example 2; SEQ ID NO 1908; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1149 AA;

Query Match 100.0%; Score 48; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9

Db 81 YLYNKETKL 89

RESULT 16

ADR39747

ID ADR39747 standard; protein, 1192 AA.

AC ADR39747;

DT 18-NOV-2004 (first entry)

DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.

XX human: kinase and phosphatase protein; KPP; enzyme; cytosolic;
XX antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
XX thymoprotective; anti-HIV; antiallergic; antiinflammatory;
XX thymomimetic; gene therapy; cell proliferative disorder; cancer;
XX atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
XX stroke; immune disorder; inflammatory disorder; AIDS; allergy;
XX developmental disorder; Hypochyroidism; Cushing's syndrome; infection;
XX KPP-20.

OS Homo sapiens.

PN WO2004074453-A2.

PD 02-SEP-2004.

PF 20-FEB-2004; 2004WO-US005092.

PR 20-FEB-2003; 2003US-0449059P.

PR 19-MAR-2003; 2003US-0456932P.

PR 28-MAR-2003; 2003US-0458644P.

PR 09-APR-2003; 2003US-0461678P.

PR 17-APR-2003; 2003US-0463937P.

XX (INCY-) INCYTE CORP.

PA Rankumar J, Marguis JP, Swarnakar A, Chawla NK, Tran UK;

PI Becha SD, Lee SY, Hafalia AJA, Richardson TW, Knare R, Jiang X;

PI Jackson AA, Yang J, Gorvad AE;

DR WPI; 2004-635568/61.

DR N-PSDB; ADR39793.

PT New human kinases and phosphatases (KPP) for diagnosing, treating and

PT preventing diseases or conditions associated with aberrant KPP expression

PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.

XX Claim 1; SEQ ID NO 20; 299pp; English.

XX The present sequence represents the human kinase and phosphatase protein
XX (KPP), designated KPP-20. The human KPP sequences from the present
XX invention have cytosolic, antiarteriosclerotic, anticonvulsant,
XX neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
XX antiinflammatory and thymomimetic activities, and can be used in gene
XX therapy. The human KPP proteins and polynucleotides can be used in
XX diagnosing, treating and preventing diseases or conditions associated
XX with the decreased expression or overexpression of KPP, such as cell
XX proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
XX epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
XX allergies) and developmental (e.g. Hypochyroidism, Cushing's syndrome)
XX disorders, or infections. They can also be used in assessing the effects
XX of exogenous compounds on the expression of nucleic acid and amino acid
XX sequences of KPP. The KPP or its fragments are useful in screening
XX compounds for effectiveness as agonist or antagonist of the polypeptides,
XX or in altering the expression of the target polynucleotide and compounds
XX that specifically bind to or modulate the activity of the polypeptide.

XX Sequence 1192 AA;

Query Match

100.0%; Score 48; DB 8; Length 1192;

Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9

Db 125 YLYNKETKL 133

RESULT 17

ADQ39378

ID ADQ39378 standard; protein, 1219 AA.

AC ADQ39378;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;

XX cardiac; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

XX (APPL-) APPLERA CORP.

PA Cargill M, Devlin JJ, Iakubova O;

PI WPI; 2004-533949/51.

DR N-PSDB; ADQ38550.

PT Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

XX Claim 10; SEQ ID NO 1041; 145pp; English.

XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide
XX comprising an amino acid sequence given in the specification; an antibody
XX that specifically binds to the polypeptide or its antigen-binding
XX fragment; an amplified polynucleotide containing an SNP given in the
XX specification and which is between about 16 and 1000 nucleotides in
XX length; a kit for detecting an SNP in a nucleic acid, comprising the
XX polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX method for identifying an agent useful in treating or preventing
XX myocardial infarction. The novel detection method has cardiac activity.
XX The nucleic acids of the invention may be used in gene therapy. The
XX method is useful in identifying an individual who has an increased or
XX decreased risk for developing myocardial infarction and for preparing a
XX composition for treating or preventing myocardial infarction. This
XX sequence represents the protein of a human myocardial infarction-
XX associated gene containing one or more SNPs of the invention. Note: This
XX sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1219 AA;
Query Match 100.0%; Score 48; DB 8; Length 1219;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLYNKETKL 9
| | | | | | | | | |
DB 152 YLYNKETKL 160
RESULT 18
ADM67187
ID ADM67187 standard; protein; 1256 AA.
AC ADM67187;
DT 03-JUN-2004 (first entry)
DE Human adipocyte specific PTPase receptor type C protein SegID 541.
XX
XX human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; PTPase receptor type C.
XX
OS Homo sapiens.
XX
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
PR 12-JUN-2003; 2003US-0478206P.
XX
XX (HMGE-) HMGNE INC.
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
PI WPI; 2004-143846/14.
DR N-PSDB; ADM66908.
DR
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 541; 91pp; English.
XX
XX This invention relates to a novel method for identifying genes that are
XX over-expressed in adipose tissue and as such it provides targets for anti-
XX -obesity pharmaceutical compositions. Specifically, it refers to a high
XX mobility group I-C protein (HMGI-C) that is associated with obesity and
XX is epistatic to leptin, furthermore, it refers to the ob gene where an
XX autosomal recessive trait is linked to obesity and diabetes. The present
XX invention describes performing differential gene expression analysis
XX between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
XX of any two different mice selected from a group consisting of wild-type,
XX HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
XX this method novel nucleotides and the encoded proteins thereof were
XX identified that are adipocyte specific, and as such can be used for
XX preventing adipogenesis, diagnosing and treating diabetes, obesity,
XX hypertension and cardiovascular disease, as well as screening for
XX compounds that can modulate or prevent adipogenesis and treat diabetes or
XX obesity. These compositions exhibit anorectic, antidiabetic and
XX hypotensive activities. This polypeptide sequence is a human homologue of
XX a murine adipocyte specific protein sequence of the invention.
XX
SQ Sequence 1256 AA;

Query Match 100.0%; Score 48; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLYNKETKL 9
| | | | | | | | | |
DB 189 YLYNKETKL 197
RESULT 19
ADP12966
ID ADP12966 standard; protein; 1256 AA.
AC ADP12966;
DT 12-AUG-2004 (first entry)
DE Protein encoding reference mRNA sequence #51.
XX
XX
DE Protein encoding reference mRNA sequence #51.
XX
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
PI WPI; 2004-400724/37.
DR
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2975; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprises detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX protein encoded by an mRNA sequence of the invention which show altered
XX expression in renal transplantation and expression.
XX
SQ Sequence 1256 AA;
Query Match 100.0%; Score 48; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLYNKETKL 9
| | | | | | | | | |
DB 189 YLYNKETKL 197

RESULT 20
ADQ39376
ID ADQ39376 standard; protein: 1258 AA.
XX
AC ADQ39376;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLEA CORP.
XX
PI Cargill M, Devlin JJ, Iakubova O;
DR WPI; 2004-533949/51.
DR N-PDB; ADQ38548.
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1039; 145bp; English.
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SO Sequence 1258 AA;
Query Match 100.0%; Score 48; DB 8; Length 1258;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLYNKEFKL 9
Db 191 YLYNKEFKL 199
RESULT 21
ADQ39379
ID ADQ39379 standard; protein: 1267 AA.
XX
AC ADQ39379;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLEA CORP.
XX
PI Cargill M, Devlin JJ, Iakubova O;
DR WPI; 2004-533949/51.
DR N-PDB; ADQ38551.
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1042; 145bp; English.
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX

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SQ Sequence 1267 AA;
Query Match          100.0%; Score 48; DB 8; Length 1267;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
   |||||
DB 200 YLYNKETKL 208

RESULT 22
ABU05243
ID ABU05243 standard; protein; 1304 AA.
XX
AC ABU05243;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1909.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1909; 134pp; English.
XX
XX
The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a
mammal an immunogenic response directed against any of the purified
polypeptide. The purified polypeptide, or the antibody that binds to this
polypeptide, is useful for treating cancer. The polypeptide is also
useful for identifying compounds that binds to a naturally processed
class I or class II MHC-binding polypeptide. The polypeptides and
polynucleotides are particularly useful for treating or preventing
myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
lymphoma or leukaemia. These are also useful for screening agents for
treating the above mentioned diseases. This sequence represents an
expressed protein tag (EPT) isolated from human tissue for translational
profiling. Note: This sequence does not appear in the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
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```
SQ Sequence 1304 AA;
Query Match          100.0%; Score 48; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YLYNKETKL 9
   |||||
DB 237 YLYNKETKL 245

RESULT 23
ABU05241
ID ABU05241 standard; protein; 1304 AA.
XX
AC ABU05241;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1907.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
XX
The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a
mammal an immunogenic response directed against any of the purified
polypeptide. The purified polypeptide, or the antibody that binds to this
polypeptide, is useful for treating cancer. The polypeptide is also
useful for identifying compounds that binds to a naturally processed
class I or class II MHC-binding polypeptide. The polypeptides and
polynucleotides are particularly useful for treating or preventing
myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
lymphoma or leukaemia. These are also useful for screening agents for
treating the above mentioned diseases. This sequence represents an
expressed protein tag (EPT) isolated from human tissue for translational
profiling. Note: This sequence does not appear in the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
```

SQL Sequence 1304 AA;

Query Match 100.0%; Score 48; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
| | | | | | | | | |
Db 237 YLYNKETKL 245

RESULT 24
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1910.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1910; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polypeptides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQL Sequence 1304 AA;

Query Match 100.0%; Score 48; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
| | | | | | | | | |
Db 237 YLYNKETKL 245

RESULT 25
ADL16230
ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #26.
XX
KM cytostatic; immunosuppressive; antiallergic;
KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KM inducible signalling pathway; cell proliferation; cancer;
KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KM cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-BP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-00366547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
XX
PI Tonke NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-P8DB; ADL16229.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 79; 238pp; English.
XX
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. . No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
SQ Sequence 1304 AA;

Query Match 100.0%; Score 48; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 DB 237 YLYNKETKL 245

RESULT 26

ADP65158
 ID ADP65158 standard; protein; 1304 AA.

AC ADP65158;
 XX

DT 12-AUG-2004 (first entry)

DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.

XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antirheumatic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.

OS Homo sapiens.

PN WO2003072827-A1.

PD 04-SEP-2003.

PF 31-OCT-2002; 2002WO-US035433.

PR 31-OCT-2001; 2001US-0336220P.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

PI Hirsch R, Thornton SL;

DR WPI; 2003-712740/67.

DR GENBANK; NP_002829.

PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

PS Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analyzing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analyzing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment

CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 48; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 DB 237 YLYNKETKL 245

RESULT 27

ADM67209
 ID ADM67209 standard; protein; 1304 AA.

AC ADM67209;
 XX

DT 03-JUN-2004 (first entry)

DE Human adipocyte specific leukocyte common antigen protein SegID 563.

XX human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; leukocyte common antigen.

OS Homo sapiens.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMGE-) HMGNE INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66930.

PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.

PS Disclosure; SEQ ID NO 563; 91pp; English.

XX This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C^{-/-}, ob/ob, or HMGI-C^{-/-} ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.

XX Sequence 1304 AA;
SQ Query Match 100.0%; Score 48; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YLYNKETKL 9
|||||
Db 237 YLYNKETKL 245

RESULT 28
ABO84455
ID ABO84455 standard; protein; 1304 AA.
XX ABO84455;
XX
XX
XX
DT 18-NOV-2004 (first entry)
XX
XX Human cancer-associated protein HPI3-011.2.
DE Human cancer-associated protein HPI3-011.2.
XX
XX Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW lymphoma; CAP.
XX
XX Homo sapiens.
OS
XX WO2004074320-A2.
XX
XX 02-SEP-2004.
XX
XX 17-FEB-2004; 2004WO-US004730.
XX
XX 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
PI
XX WPI; 2004-652914/63.
XX
XX N-PSDB; ABD32626.
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
XX claim 18; seqid 147; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
XX in the specification, or its complement. The nucleic acids encode cancer-
XX associated proteins. Also included are an expression vector comprising
XX the isolated nucleic acid cited above, a host cell comprising the above
XX recombinant nucleic acid or expression vector, a microarray for detecting
XX a cancer-associated (CA) nucleic acid comprising at least one probe
XX comprising at least 10 contiguous nucleotides of any of the above-
XX mentioned nucleotide sequences, an isolated polypeptide (encoded within
XX an open reading frame of a CA sequence selected from any of the 95
XX polynucleotide sequences as mentioned in the specification, or its
XX complement), an isolated antibody, (or its antigen binding fragment) that
XX binds to the above polypeptide, a hybridoma that produces the above
XX monoclonal antibody, a pharmaceutical composition comprising the above
XX antibody and a pharmaceutical excipient, a kit for detecting cancer
XX cells (comprising the antibody cited above, methods for diagnosing cancer
XX or for detecting the presence or absence of cancer cells in an
XX individual, a method for inhibiting growth of cancer cells in an
XX individual, a method for delivering a therapeutic agent to cancer cells
XX in an individual, an electronic library comprising the above

CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1304 AA;
Query Match 100.0%; Score 48; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YLYNKETKL 9
|||||
Db 237 YLYNKETKL 245

RESULT 29
ADQ39380
ID ADQ39380 standard; protein; 1304 AA.
XX ADQ39380;
XX
XX
XX
DT 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiac; gene therapy; human.
XX
XX Homo sapiens.
OS
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JJ, Yakubova O;
PI
XX WPI; 2004-533949/51.
XX
XX N-PSDB; ADQ38552.
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1043; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide

comprising an amino acid sequence given in the specification; an antibody
 that specifically binds to the polypeptide or its antigen-binding
 fragment; an amplified polynucleotide containing an SNP given in the
 specification and which is between about 16 and 1000 nucleotides in
 length; a kit for detecting an SNP in a nucleic acid, comprising the
 polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 nucleic acid molecule; a method of detecting a variant polypeptide; and a
 method for identifying an agent useful in treating or preventing
 myocardial infarction. The novel detection method has cardiant activity.
 The nucleic acids of the invention may be used in gene therapy. The
 method is useful in identifying an individual who has an increased or
 decreased risk for developing myocardial infarction and for preparing a
 composition for treating or preventing myocardial infarction. This
 sequence represents the protein of a human myocardial infarction-
 associated gene containing one or more SNP's of the invention. Note: This
 sequence was not shown in the specification. The sequence has come from
 an electronic sequence listing downloaded from the WIPO website.

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 48; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 Db 239 YLYNKETKL 245

RESULT 30
 ADQ39375
 ID ADQ39375 standard; protein; 1306 AA.

AC ADQ39375;
 DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.

KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human.

OS Homo sapiens.

PN MO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin JT, Iakubova O;

DR WPI; 2004-533949/51.

DR N-PSDB; ADQ38547.

PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.

PS Claim 10; SEQ ID NO 1038; 145pp; English.

CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleic acid sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an

altered risk for myocardial infarction in the individual. The invention
 further comprises: an isolated nucleic acid molecule comprising at least
 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 the specification or its complement and encoding any one of the amino
 acid sequences given in the specification; an isolated polypeptide
 comprising an amino acid sequence given in the specification; an antibody
 that specifically binds to the polypeptide or its antigen-binding
 fragment; an amplified polynucleotide containing an SNP given in the
 specification and which is between about 16 and 1000 nucleotides in
 length; a kit for detecting an SNP in a nucleic acid, comprising the
 polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 nucleic acid molecule; a method of detecting a variant polypeptide; and a
 method for identifying an agent useful in treating or preventing
 myocardial infarction. The novel detection method has cardiant activity.
 The nucleic acids of the invention may be used in gene therapy. The
 method is useful in identifying an individual who has an increased or
 decreased risk for developing myocardial infarction and for preparing a
 composition for treating or preventing myocardial infarction. This
 sequence represents the protein of a human myocardial infarction-
 associated gene containing one or more SNP's of the invention. Note: This
 sequence was not shown in the specification. The sequence has come from
 an electronic sequence listing downloaded from the WIPO website.

XX SQ Sequence 1306 AA;

Query Match 100.0%; Score 48; DB 8; Length 1306;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLYNKETKL 9
 |||||
 Db 239 YLYNKETKL 247

Search completed: May 3, 2005, 07:35:35
 Job time : 52.6757 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds
(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-9

Perfect score: 46

Sequence: 1 L1IDVPPGV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	1304	1 A46546	leukocyte common a
2	42	91.3	137	2 S32461	lectin, 205K, larg
3	39	84.8	350	2 H83679	ATP-binding Mtp pr
4	39	84.8	354	2 A90012	hypothetical prote
5	38	82.6	242	2 A75178	mtp protein homolo
6	38	82.6	257	2 C83005	conserved hypotet
7	38	82.6	331	2 T51894	related to nucleot
8	38	82.6	369	2 AG0776	conserved hypotet
9	38	82.6	379	2 H64978	probable ATPase m
10	38	82.6	379	2 G90993	probable ATPase [l
11	38	82.6	379	2 B85839	probable ATPase m
12	38	82.6	388	2 AG2663	mtp protein [impor
13	38	82.6	390	2 F97445	mtp protein homolo
14	37	80.4	217	2 F82788	thymidylate kinase
15	37	80.4	242	2 D71036	probable ATP-bindi
16	37	80.4	277	2 H97266	mind family ATPase
17	37	80.4	282	2 C84654	hypothetical prote
18	37	80.4	296	2 A90191	MRF protein homolo
19	37	80.4	318	2 G71721	hypothetical prote
20	37	80.4	319	2 C97720	mtp protein [impor
21	37	80.4	330	2 H70508	probable mtp prote
22	36	78.3	202	2 E72688	hypothetical prote
23	36	78.3	350	2 F75448	mtp protein - Dein
24	36	78.3	352	2 A69743	ATP-binding Mtp-l
25	36	78.3	353	2 S74379	probable ATPase -
26	36	78.3	356	2 AC1888	hypothetical prote
27	36	78.3	364	2 G70364	conserved hypotet
28	36	78.3	370	2 AG0185	conserved hypotet
29	36	78.3	382	2 E82249	mtp protein VCI037

30	36	78.3	383	2 B87044	MRF-family ATP-bin
31	36	78.3	386	2 A64114	probable ATPase m
32	36	78.3	435	2 T45199	probable mtp prote
33	36	78.3	602	2 G75278	N-acetylmutamoyl-L
34	36	78.3	608	2 T39094	WD domain, G-beta
35	35	76.1	194	2 H83060	peptidyl-L-cRNA hyd
36	35	76.1	194	2 S16753	aminoacyl-L-cRNA hyd
37	35	76.1	194	2 B85700	peptidyl-L-cRNA hyd
38	35	76.1	194	2 E90842	peptidyl-L-cRNA hyd
39	35	76.1	196	2 C82107	peptidyl-L-cRNA hyd
40	35	76.1	202	2 A10720	aminoacyl-L-cRNA hyd
41	35	76.1	209	2 D72029	endonuclease III C
42	35	76.1	209	2 C86595	endonuclease III C
43	35	76.1	254	2 F69547	nucleotide-binding
44	35	76.1	254	2 E69533	nucleotide-binding
45	35	76.1	263	2 T04056	hypothetical prote

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N/Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 09-Jul-2004
C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Salto, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A/Reference number: A46546; MUID:88061067; PMID:2824653
A/Accession: A46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.6/2
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-31,193-264 <ST3>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.1
R/Ralph, S.U.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A/Reference number: A91066; MUID:87275816; PMID:2956090
A/Accession: A29449
A/Molecule type: mRNA
A/Residues: 1-31,193-649,'L',651-869,'G',871-872,'A',874-1206,'P',1208-1304 <RAL>
A/Cross-references: GB:Y00062; MUID:934275; PIND:CAA68269.1; PID:934276
A/Experimental source: clones pHL-C1 and lambdaHLG1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Tsai, A.Y.; Streuli, M.; Salto, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative;
A/Reference number: I57658; MUID:9006468; PMID:2531281
A/Accession: I57658
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:G187020; PIDN:AAA59497.1; PID:G553521
C:Genetics:
A:Gene: GDB:PTPRC: CD45
A:Cross-references: GDB:119768; OMIM:151460
A:Map position: 1q31-1q32
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolog
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
F:851/Active site: Cys (phosphotyrosine intermediate) #status predicted
F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 46; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 9
DB 293 LILDVPPGV 301

RESULT 2
S32461
lectin, 205K, large granular lymphocyte - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S32461
R:Bezouska, K.; Krahanzl, A.; Pospisil, M.; Kubrycht, J.; Stajner, K.; Felberg, J.; Kc
Eur. J. Biochem. 213, 1303-1313, 1999
A:Title: Characterization of the high-affinity oligosaccharide-binding site of the 205-K
A:Reference number: S32461; MUID:93279332; PMID:8504822
A:Accession: S32461
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-137 <BEZ>
A:Cross-references: UNIPROT:Q7M2R0
C:Superfamily: pig lectin, 205K, large granular lymphocyte

Query Match 91.3%; Score 42; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 8
DB 48 LILDVPPGV 55

RESULT 3
H83679
ATP-binding Mrp protein (Mrp/Mrp35 family) BH0240 [imported] - Bacillus halodurans (stra
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: H83679
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeki, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H83679
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <STO>
A:Cross-references: UNIPROT:Q9KG72; GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BAB039
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0240
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 84.8%; Score 39; DB 2; Length 350;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 8
DB 111 LILDVPPGV 8

DB 217 LILDVPPGV 224

RESULT 4
A90012
hypothetical protein SA1969 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A90012
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A90012
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <KDR>
A:Cross-references: UNIPROT:Q99SA0; GB:BA000018; PID:G13701966; PIDN:BAB43258.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1969
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 84.8%; Score 39; DB 2; Length 354;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 8
DB 220 LILDVPPGV 227

RESULT 5
A75178
mrp protein homolog PAB0400 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A75178
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: A75178
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <KAN>
A:Cross-references: UNIPROT:Q9V147; GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CAB4950
C:Genetics:
A:Experimental source: strain Orsay
A:Gene: mrp-like; PAB0400
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 82.6%; Score 38; DB 2; Length 242;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 9
DB 127 LILDVPPGV 135

RESULT 6
CB3005
conserved hypothetical protein PA5135 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: CB3005
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lam,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: G83005
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-257 <STO>
A/Cross-references: UNIPROT:Q9HU49; GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AMG0852
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA5135

Query Match 82.6%; Score 38; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LILDVPPG 9
Db 50 VLDPGCV 57

RESULT 7
T51894
related to nucleotide-binding protein [imported] - *Neurospora crassa*
N/Alternate names: protein B23111.60
C/Species: *Neurospora crassa*
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C/Accession: T51894
R/Schulte, U.; Align, V.; Hehse, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, August 2000
A/Reference number: Z25858
A/Accession: T51894
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-331 <SCH>
A/Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.60
C/Genetics:
A/Gene: NCSP:B23111.60
A/Map position: 6
A/Intons: 34/3; 60/3; 87/1
C/Superfamily: conserved probable membrane protein YIL003W

Query Match 82.6%; Score 38; DB 2; Length 331;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPG 8
Db 185 LVLDLPPG 192

RESULT 8
AG0776
conserved hypothetical protein STY2363 [imported] - *Salmonella enterica* subsp. *enterica*
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A/Note: this species has also been called *Salmonella typhi*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AG0776
R/Farkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connelton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AG0776
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-369 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD02533.1; PID:gl6503394; GSPDB:GN00176
C/Genetics:
A/Gene: STY2363
C/Superfamily: conserved probable membrane protein YIL003W

Query Match 82.6%; Score 38; DB 2; Length 369;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPG 8
Db 219 LVLDMPG 226

RESULT 9
H64978
probable ATPase mrp - *Escherichia coli* (strain K-12)
C/Species: *Escherichia coli*
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: H64978; S11948
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: H64978
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-379 <BLAT>
A/Cross-references: UNIPROT:Q8X7E8; GB:AE000300; GB:U00096; NID:gl788425; PIDN:AACT5174
A/Experimental source: strain K-12, substrain MG1655
R/Bardel, F.; Panvert, M.; Fayat, G.
Mol. Gen. Genet. 223, 121-133, 1990
A/Title: Transcription and regulation of expression of the *Escherichia coli* methionyl-t.
A/Reference number: S11948; MUID:91080852; PMID:2259334
A/Accession: S11948
A/Molecule type: DNA
A/Residues: 11-379 <DAR>
A/Cross-references: EMBL:X55791; NID:g42015; PIDN:CAA39316.1; PID:g42017
C/Genetics:
A/Gene: mrp
C/Superfamily: conserved probable membrane protein YIL003W
C/Keywords: nucleotide binding; P-loop
F,125-132/Region: nucleotide-binding motif A (P-loop)

Query Match 82.6%; Score 38; DB 2; Length 379;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPG 8
Db 229 LVLDMPG 236

RESULT 10
G90993
probable ATPase [imported] - *Escherichia coli* (strain O157:H7, substrain RIMD 0509952)
C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: G90993
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: G90993
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-379 <HAY>
A/Cross-references: UNIPROT:Q8X7E8; GB:BA000007; PIDN:BA836342.1; PID:gl3362388; GSPDB:G
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: EC92919
C/Superfamily: conserved probable membrane protein YIL003W

Query Match 82.6%; Score 38; DB 2; Length 379;
Best Local Similarity 75.0%; Pred. No. 26;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 L1LDVPPG 8
|:|:|:|:|
Db 229 LVLDMPG 236

RESULT 11
B85839
probable ATPase mmp [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B85839

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.U.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimlant, E.; Potamoculis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85839
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <STO>
A:Cross-references: UNIPROT:Q8X7B8; GB:AE005174; NID:g12516326; PIDN:AA657174.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: mmp
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 82.6%; Score 38; DB 2; Length 379;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 L1LDVPPG 8
|:|:|:|:|
Db 229 LVLDMPG 236

RESULT 12
AG2663
mmp protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG2663

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2663
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-388 <KUR>
A:Cross-references: UNIPROT:Q8UHH3; GB:AE008689; PIDN:AA141725.1; PID:g17739074; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0709
A:Map position: circular chromosome
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 82.6%; Score 38; DB 2; Length 388;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 L1LDVPPG 8
|:|:|:|:|
Db 240 LVLDMPG 247

RESULT 13
F97445

mmp protein homolog [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97445
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Woliam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: F97445
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-390 <KUR>
A:Cross-references: UNIPROT:Q8UHH3; GB:AE007869; PIDN:AA66519.1; PID:g15155675; GSPDB:C
C:Genetics:
A:Gene: AGR_C1282
A:Map position: circular chromosome
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 82.6%; Score 38; DB 2; Length 390;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 L1LDVPPG 8
|:|:|:|:|
Db 242 LVLDMPG 249

RESULT 14
F82788
thymidylate kinase Xf0580 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: F82788
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82788
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <SIM>
A:Cross-references: GB:AE003904; GB:AE003849; NID:g9105433; PIDN:AAF83390.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Britones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincan, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teuhako, M.H.; Vailade, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0580
C:Superfamily: dtmp kinase

Query Match 80.4%; Score 37; DB 2; Length 217;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 L1LDVPPG 9
|:|:|:|:|
Db 132 LVLDMPG 140

RESULT 15

D71036
probable ATP-binding protein - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: D71036
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Onitoku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679134
A:Accession: D71036
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-242 <KAW>
A:Cross-references: UNIPROT:O59268; GB:AP000006; NID:G3236133; PIDN:BAA30692.1; PID:G323
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1580

Query Match 80.4%; Score 37; DB 2; Length 242;
Best local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLDVPPGV 9
|:::|::|:
Db 127 LVIDMPGTL 135

Search completed: May 3, 2005, 06:16:23
Job time : 13.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-9

Perfect score: 46

Sequence: 1 RLIDVPPGV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	756	2 Q6PK7	Q6PK7 homo sapien
2	46	100.0	1304	1 CDA5 HUMAN	P08575 homo sapien
3	42	91.3	137	2 Q7M2R0	Q7M2R0 sus scrofa
4	40	87.0	880	2 Q931Y1	Q931Y1 streptomyce
5	40	87.0	980	2 Q821G2	Q821G2 streptomyce
6	39	84.8	231	2 Q6AVH8	Q6AVH8 oryza sativ
7	39	84.8	306	2 Q83B30	Q83B30 coxiella bu
8	39	84.8	350	2 Q9KG72	Q9KG72 bacillus ha
9	39	84.8	354	2 Q99SA0	Q99SA0 staphylococ
10	39	84.8	354	2 Q7A0A1	Q7A0A1 staphylococ
11	39	84.8	354	2 Q7A4A8	Q7A4A8 staphylococ
12	39	84.8	354	2 Q6G7E8	Q6G7E8 staphylococ
13	39	84.8	354	2 Q6GER2	Q6GER2 staphylococ
14	39	84.8	1303	2 Q6ED62	Q6ED62 actus nigri
15	38	82.6	57	1 RPOK_PYRFU	Q8U0E8 pyrococcus
16	38	82.6	245	2 Q9V147	Q9V147 pyrococcus
17	38	82.6	252	2 Q6QEH0	Q6QEH0 burkholderi
18	38	82.6	255	2 Q63J94	Q63J94 burkholderi
19	38	82.6	257	2 Q9HU49	Q9HU49 pseudomonas
20	38	82.6	309	2 Q7S6P7	Q7S6P7 neurospora
21	38	82.6	354	2 Q81VP5	Q81VP5 bacillus an
22	38	82.6	354	2 Q6HPM2	Q6HPM2 bacillus th
23	38	82.6	355	2 Q63H54	Q63H54 bacillus ce
24	38	82.6	355	2 Q73F59	Q73F59 bacillus ce
25	38	82.6	355	2 Q81J10	Q81J10 bacillus ce
26	38	82.6	358	2 Q8RDC2	Q8RDC2 thermomater
27	38	82.6	359	1 MRP_ECOLI	P21550 escherichia
28	38	82.6	359	2 Q8Z5C4	Q8Z5C4 salmonella
29	38	82.6	359	2 Q8ZNN5	Q8ZNN5 salmonella
30	38	82.6	359	2 Q7UCA4	Q7UCA4 shigella fl
31	38	82.6	359	2 Q6D7B5	Q6D7B5 erwania car

32	38	82.6	379	2 Q7ACU7	Q7ACU7 escherichia
33	38	82.6	379	2 Q8X7E8	Q8X7E8 escherichia
34	38	82.6	379	2 Q83QY1	Q83QY1 shigella fl
35	38	82.6	388	2 Q8DHM3	Q8DHM3 agrobacteri
36	38	82.6	390	2 Q7D0V6	Q7D0V6 agrobacteri
37	38	82.6	533	2 Q9C9Z9	Q9C9Z9 arabidopsis
38	38	82.6	1290	2 Q6ED60	Q6ED60 actus vocif
39	37	80.4	162	2 Q7SD13	Q7SD13 neurospora
40	37	80.4	208	1 KTHY_XYLF	Q9P5E7 xyloella fas
41	37	80.4	229	2 Q7QNT8	Q7QNT8 anopheles g
42	37	80.4	231	2 Q7PV10	Q7PV10 anopheles g
43	37	80.4	242	2 Q59268	Q59268 pyrococcus
44	37	80.4	275	2 Q33969	Q33969 streptomyce
45	37	80.4	277	2 Q97EX4	Q97EX4 clostridium

ALIGNMENTS

RESULT 1
ID Q6PK7 PRELIMINARY, PRT, 756 AA.
AC Q6PK7;
DT 05-JUL-2004 (TREMBLrel, 27, Created)
DT 05-JUL-2004 (TREMBLrel, 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel, 27, Last annotation update)
DE PRPC protein (Fragment).
GN Name=PRPC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RT Jones S.J., Maier M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.,
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC014239, ANH14239.1; -.
DR HSSP, P18031, IAAK.
DR GO, GO:0004725, F:protein tyrosine phosphatase activity, IEA.
DR GO, GO:000470, P:protein amino acid dephosphorylation, IEA.
DR InterPro, IPR003961, FN III.
DR InterPro, IPR008957, FN III-like.
DR InterPro, IPR002452, Ty_PP.
DR Pfam, PF00041, fn3; 2.
DR Pfam, PF00102, Y_phosphatase, 1.
DR PRINTS, PR00700, PTPYHPHPTASE.
DR SMART, SM00060, FN3; 2.
DR SMART, SM00194, PRPC, 1.

DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50055; TYR PHOSPHATASE_PTP; 1.
FT NON TER 756 756
SQ SEQUENCE 756 AA; 85430 MW; 8A9A863827BD69E6 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LILDPVPGV 9
Db 245 LILDPVPGV 253

RESULT 2
CD45_HUMAN STANDARD; PRT; 1304 AA.
AC P08575; Q16614; Q9H0Y6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen) (T200).
DE Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RX MEDLINE=88061067; PubMed=2824653;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "differential usage of three exons generates at least five different mRNAs encoding human leukocyte common antigens.";
RT J. Exp. Med. 166:1548-1566 (1987).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RX MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common antigen).";
RT J. Biol. Chem. 262:1251-1257 (1987).
RL [3]
RP SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89009812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common antigen (CD45) gene.";
RT J. Immunol. 141:2781-2787 (1988).
RL [4]
RP FUNCTION.
RX MEDLINE=89017162; PubMed=2845400;
RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase.";
RT Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186 (1988).
RL [5]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA andLAR.";
RT EMBO J. 9:2399-2407 (1990).
RL [6]
RP FUNCTION. Required for T-cell activation through the antigen receptor. The first PTPase domain has enzymatic activity, while the second one seems to affect the substrate specificity of the first one.
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
CC -I- SUBUNIT: Binds GANAB and PKC8 (By similarity).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=At least 8 isoforms are produced;
CC Name=1;
CC IsoId=P08575-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P08575-2; Sequence=VSP_007780;
CC -I- PTM: Heavily N- and O-glycosylated.
CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -I- SIMILARITY: Contains 2 fibronectin type III domains.
CC -I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD45 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00638; CAA68669.1; -;
CC EMBL; Y00062; CAA68269.1; -;
CC EMBL; M23492; AAD15273.2; -;
CC EMBL; M23496; AAD15273.2; JOINED.
CC EMBL; M23466; AAD15273.2; JOINED.
CC EMBL; M23467; AAD15273.2; JOINED.
CC EMBL; M23468; AAD15273.2; JOINED.
CC EMBL; M23469; AAD15273.2; JOINED.
CC EMBL; M23470; AAD15273.2; JOINED.
CC EMBL; M23471; AAD15273.2; JOINED.
CC EMBL; M23472; AAD15273.2; JOINED.
CC EMBL; M23473; AAD15273.2; JOINED.
CC EMBL; M23474; AAD15273.2; JOINED.
CC EMBL; M23475; AAD15273.2; JOINED.
CC EMBL; M23476; AAD15273.2; JOINED.
CC EMBL; M23477; AAD15273.2; JOINED.
CC EMBL; M23478; AAD15273.2; JOINED.
CC EMBL; M23479; AAD15273.2; JOINED.
CC EMBL; M23480; AAD15273.2; JOINED.
CC EMBL; M23481; AAD15273.2; JOINED.
CC EMBL; M23482; AAD15273.2; JOINED.
CC EMBL; M23483; AAD15273.2; JOINED.
CC EMBL; M23484; AAD15273.2; JOINED.
CC EMBL; M23485; AAD15273.2; JOINED.
CC EMBL; M23486; AAD15273.2; JOINED.
CC EMBL; M23487; AAD15273.2; JOINED.
CC EMBL; M23488; AAD15273.2; JOINED.
CC EMBL; M23489; AAD15273.2; JOINED.
CC EMBL; M23490; AAD15273.2; JOINED.
CC EMBL; M23491; AAD15273.2; JOINED.
CC PIR; A46546; A46546.
CC HSSP; P18031; 1C88.
CC InFact; P08575; -;
CC GlycoSuiteDB; P08575; -;
CC GeneW; HGNC:9666; PTPRC.
CC MIM; 151460; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
CC InterPro; IPR003861; FN_III.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR000387; TYR_phosphatase.
CC Pfam; PF000441; fn3_2.
CC Pfam; PF00102; Y_PTPHPTASE.
CC PRINTS; PRO0700; PTPHPTASE.
CC PROSITE; PS50853; FN3; 2.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.

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DR PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.  
KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;  
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;  
KW Transmembrane.  
FT SIGNAL 1 23  
FT CHAIN 24 1304  
FT DOMAIN 24 575  
FT TRANSMEM 576 597  
FT DOMAIN 598 1304  
FT DOMAIN 390 478  
FT DOMAIN 482 570  
FT DOMAIN 670 919  
FT ACT_SITE 961 1235  
FT ACT_SITE 851 851  
FT ACT_SITE 1167 1167  
FT CARBOHYD 78 78  
FT CARBOHYD 90 90  
FT CARBOHYD 95 95  
FT CARBOHYD 184 184  
FT CARBOHYD 190 190  
FT CARBOHYD 197 197  
FT CARBOHYD 232 232  
FT CARBOHYD 260 260  
FT CARBOHYD 270 270  
FT CARBOHYD 276 276  
FT CARBOHYD 335 335  
FT CARBOHYD 378 378  
FT CARBOHYD 419 419  
FT CARBOHYD 468 468  
FT CARBOHYD 488 488  
FT CARBOHYD 529 529  
FT VARBPLIC 32 192  
FT MUTAGEN 851 851  
FT CONFLICT 650 650  
FT CONFLICT 1207 1207  
SQ SEQUENCE 1304 AA; 147253 MW; A08FC22D6069BAF7 CRC64;  
Query Match 100.0%; Score 46; DB 1; Length 1304;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LILDVPGV 9  
DB 293 LILDVPGV 301  
RESULT 3  
Q7M2R0 PRELIMINARY; PRT; 137 AA.  
AC Q7M2R0;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE lectin, 205k, large granular lymphocyte.  
OS Sus scrofa domestica (domestic pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI_TaxId=9825;  
RN [1]  
RP SEQUENCE  
RA MEDLINE=93279332; PubMed=8504822;  
RA Bezouska K., Krajhanzl A., Pospisil M., Kubrycht J., Strajner K.,  
RA Felberg J., Kocourek J.;  
RT "Characterization of the high-affinity oligosaccharide-binding site of  
RT the 205-kDa porcine large granular lymphocyte lectin, a member of the  
RT leukocyte common antigen family."  
RL Eur. J. Biochem. 213:1303-1313(1993).  
DR FIR; S32461;  
SQ SEQUENCE 137 AA; 14936 MW; 84DBA4FBA700194 CRC64;  
Query Match 91.3%; Score 42; DB 2; Length 137;
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Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LILDVPGV 8  
DB 48 LILDVPGV 55  
RESULT 4  
Q931Y1 PRELIMINARY; PRT; 880 AA.  
AC Q931Y1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein SC05104.  
GN ORFNames=SCBAC2861.10;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.  
OX NCBI_TaxId=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieseer H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieseer T., Larke L., Murthy L.D., Oliver K., O'Neill S.,  
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL939123; CAC44217.1; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0004871; F:signal transducer activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003594; ATPbind_ATPase.  
DR InterPro; IPR003018; ATP.  
DR InterPro; IPR002345; Lipocalin.  
DR InterPro; IPR000014; PAS.  
DR InterPro; IPR010822; PP2C-like.  
DR Pfam; PF01590; GAF; 1.  
DR Pfam; PF02518; HATPase_C; 1.  
DR Pfam; PF00989; PAS; 2.  
DR Pfam; PF07228; SpoIIE; 1.  
DR SMART; SM00065; GAF; 1.  
DR SMART; SM00387; HATPase_C; 1.  
DR SMART; SM00091; PAS; 2.  
DR SMART; SM00331; PP2C_SIG; 1.  
DR TIGRFAMs; TIGR00229; sensory_box; 1.  
DR PROSITE; PS00113; LIPOCALIN; UNKNOWN_1.  
DR PROSITE; PS50112; PAS; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 880 AA; 94778 MW; 4EB9867390CB8436E CRC64;  
Query Match 87.0%; Score 40; DB 2; Length 880;  
Best Local Similarity 77.8%; Pred. No. 1.6e+02;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LILDVPGV 9  
DB 646 LILDVPGV 654  
RESULT 5  
Q821G2
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ID Q82IG2 PRELIMINARY; PRT; 980 AA.
AC Q82IG2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SAV3185;
OS Streptomyces avermiltis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211431198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermiltis: deducing the ability of producing secondary
RT metabolites.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S., Shinose M., Kikuchi H., Shiba T.,
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermiltis.";
RT Nat. Biotechnol. 21:526-531(2003).
RL EMBL; AP005034; BAC70896.1; -
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0008824; P:catalytic activity; IEA.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR010822; SpoIIE.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF07228; SpoIIE; 1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00091; PAS; 2.
DR TIGRPFAM; TIGR00229; sensory_box; 2.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PS00112; PAS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 980 AA; 104505 MW; 255878478345C3 CRC64;

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Query Match 87.0%; Score 40; DB 2; Length 980;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LILDVPGV 9
DB 746 LMLDVPFGM 754

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RESULT 6
ID Q6AVH8 PRELIMINARY; PRT; 231 AA.
AC Q6AVH8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSJNBa0079G12.6 (Hypothetical protein

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DE OSJNBa0079J18.25).
GN Name=OSJNBa0079G12.6; Synonym=OSJNBa0027J18.25;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=33947;
RN [1]
RP SEQUENCE FROM N.A.
RC Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBa0079G12 genomic sequence.";
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Buell R.;
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBa0027J18 genomic sequence.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC103550; AAT77885.1; -
DR EMBL; AC096689; AAT77895.1; -
DR InterPro; IPR006460; DUF_A_thal_3588.
DR Pfam; PF04759; DUF617; 1.
KW Hypothetical protein.
SQ SEQUENCE 231 AA; 24730 MW; CCFCEB7218499516 CRC64;

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Query Match 84.8%; Score 39; DB 2; Length 231;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LILDVPGV 9
DB 103 LVLDLPGVL 111

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RESULT 7
ID Q83B30 PRELIMINARY; PRT; 306 AA.
AC Q83B30;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mip protein, putative.
GN OrderedLocustNames=CBU1689;
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OC NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidson T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carly H.A., Scanlan D., Heinen R.A.,
RA Thompson H.A., Samuel J.B., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
RT burnetii.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
RL EMBL; AE016965; AA091184.1; -

```


DR HSSP; 029562; 1HYQ.
 DR TIGR; CBUI689; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR000808; MRP.
 DR PROSITE; PS01215; MRP; 1.
 DR Complete proteome.
 SQ SEQUENCE 306 AA; 32537 MW; 28EBB2ECD9D99385 CRC64;

Query Match 84.8%; Score 39; DB 2; Length 306;
 Best Local Similarity 87.5%; Pred. No. 82;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LILDVPPG 8
 Db 152 LILDLPPG 159

RESULT 8
 ID 09KG72 PRELIMINARY; PRT; 350 AA.
 AC 09KG72;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE ATP-binding MRP protein (Mrp/Nbp35 family).
 GN OrderedLocuNames=BH0240;
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Maeno N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AF001507; BAB03959.1; -.
 DR PIR; H83679; H83679.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR002744; DUF59.
 DR InterPro; IPR000808; MRP.
 DR Pfam; PF01883; DUF59; 1.
 DR ProDom; PD005595; DUF59; 1.
 DR PROSITE; PS01215; MRP; 1.
 DR ATP-binding; Complete proteome.
 SQ SEQUENCE 350 AA; 37949 MW; 8CBB15467D5BCBF CRC64;

Query Match 84.8%; Score 39; DB 2; Length 350;
 Best Local Similarity 87.5%; Pred. No. 94;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LILDVPPG 8
 Db 217 LILDLPPG 224

RESULT 9
 Q99SAO PRELIMINARY; PRT; 354 AA.
 ID 099SAO;
 AC 099SAO;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE ATP-binding protein MRP-like protein.
 GN OrderedLocuNames=SAV2165;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003364; BAB58327.1; -.
 DR PIR; A90012; A90012.
 DR GO; GO:0005786; C:signal recognition particle (sensu Eukaryota); IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0006114; P:SRP-dependent cotranslational protein-membr. .; IEA.
 DR InterPro; IPR000897; SRP54.
 DR ProDom; PD000819; SRP54; 1.
 DR ATP-binding; Complete proteome.
 SQ SEQUENCE 354 AA; 38358 MW; 730E4D806920A691 CRC64;

Query Match 84.8%; Score 39; DB 2; Length 354;
 Best Local Similarity 87.5%; Pred. No. 95;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LILDVPPG 8
 Db 220 LILDLPPG 227

RESULT 10
 ID 07A0A1 PRELIMINARY; PRT; 354 AA.
 AC 07A0A1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE MW2092 protein.
 GN OrderedLocuNames=MW2092;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Maeno K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AP004829; BAB95957.1; -.
 DR GO; GO:0005786; C:signal recognition particle (sensu Eukaryota); IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0006114; P:SRP-dependent cotranslational protein-membr. .; IEA.
 DR InterPro; IPR000897; SRP54.
 DR ProDom; PD000819; SRP54; 1.
 DR Complete proteome.
 SQ SEQUENCE 354 AA; 38358 MW; 730E4D806920A691 CRC64;

Query Match 84.8%; Score 39; DB 2; Length 354;
 Best Local Similarity 87.5%; Pred. No. 95;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LILDVPPG 8
 Db 220 LILDLPPG 227

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RESULT 11
O7A4A8      PRELIMINARY;      PRT;      354 AA.
AC  O7A4A8;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE  SAI969 protein.
GN  OrderedLocNames=SAI969;
OS  Staphylococcus aureus (strain N315).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=158879;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA  Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA  Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
RA  Kanamori M., Matsumaru H., Maruyama A., Murakami H.,
RA  Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA  Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA  Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA  Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT  "Whole genome sequencing of methicillin-resistant Staphylococcus
RT  aureus."
RL  Lancet 357:1225-1240(2001).
DR  EMBL; AP003136; BAB43258.1; -.
DR  GO; GO:0005786; C:signal recognition particle (sensu Bkaryota); IEA.
DR  GO; GO:0005525; F:GTP binding; IEA.
DR  GO; GO:0003723; F:RNA binding; IEA.
DR  GO; GO:0006614; P:SRP-dependent cotranslational protein-membr. .; IEA.
DR  InterPro; IPR000897; SRP54.
DR  ProDom; PD000819; SRP54; 1.
KW  Complete proteome.
SQ  SEQUENCE 354 AA; 38358 MW; 730E4D806920A691 CRC64;

Query Match
Best Local Similarity 84.8%; Score 39; DB 2; Length 354;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 LILDVPPG 8
DB  220 LILDVPPG 227

RESULT 12
O6G7E8      PRELIMINARY;      PRT;      354 AA.
AC  O6G7E8;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE  SAI969 protein.
GN  OrderedLocNames=SAI969;
OS  Staphylococcus aureus (strain MSSA476).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=282459;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA  Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA  Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA  James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA  Spratt B.G., Parkhill J.;
RT  "Complete genomes of two clinical Staphylococcus aureus strains:
RT  evidence for the rapid evolution of virulence and drug resistance.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR  EMBL; BX571857; CAG43875.1; -.
DR  GO; GO:0005786; C:signal recognition particle (sensu Bkaryota); IEA.

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DR  GO; GO:0005525; F:GTP binding; IEA.
DR  GO; GO:0003723; F:RNA binding; IEA.
DR  GO; GO:0006614; P:SRP-dependent cotranslational protein-membr. .; IEA.
DR  InterPro; IPR000897; SRP54.
DR  ProDom; PD000819; SRP54; 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 354 AA; 38358 MW; 730E4D806920A691 CRC64;

Query Match
Best Local Similarity 84.8%; Score 39; DB 2; Length 354;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 LILDVPPG 8
DB  220 LILDVPPG 227

RESULT 13
O6GER2      PRELIMINARY;      PRT;      354 AA.
AC  O6GER2;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE  SAI969 protein.
GN  OrderedLocNames=SAI969;
OS  Staphylococcus aureus (strain MRSA252).
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=282458;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA  Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA  Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA  Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA  James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA  Spratt B.G., Parkhill J.;
RT  "Complete genomes of two clinical Staphylococcus aureus strains:
RT  evidence for the rapid evolution of virulence and drug resistance.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR  EMBL; BX571856; CAG41235.1; -.
DR  GO; GO:0005786; C:signal recognition particle (sensu Bkaryota); IEA.
DR  GO; GO:0005525; F:GTP binding; IEA.
DR  GO; GO:0003723; F:RNA binding; IEA.
DR  GO; GO:0006614; P:SRP-dependent cotranslational protein-membr. .; IEA.
DR  InterPro; IPR000897; SRP54.
DR  ProDom; PD000819; SRP54; 1.
KW  Complete proteome.
SQ  SEQUENCE 354 AA; 38400 MW; 1A2C5018A62A0082 CRC64;

Query Match
Best Local Similarity 87.5%; Score 39; DB 2; Length 354;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 LILDVPPG 8
DB  220 LILDVPPG 227

RESULT 14
O6ED62      PRELIMINARY;      PRT;      1303 AA.
AC  O6ED62;
DT  25-OCT-2004 (TrEMBLrel. 28, Created)
DT  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE  SAI969 protein.
GN  OrderedLocNames=SAI969;
OS  Aotus nigricans (Black-headed owl monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 RT vs. human."
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL: AY445816; AA06901.1; -.
 DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003595; PTPC motif.
 DR InterPro; IPR000387; TYR_Phosphatase.
 DR InterPro; IPR00242; TYR_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC_motif; 2.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolyase.
 KW SEQUENCE 1303 AA; 146586 MW; 98B023BFF4BC1165 CRC64;

Query Match 84.8%; Score 39; DB 2; Length 1303;
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LILDVPPGV 9
 | |||||
 Db 293 LKLDVPPGV 301

RESULT 15
 RPOK_PYRFU STANDARD; PRT; 57 AA.
 AC 08U0E8;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE DNA-directed RNA polymerase subunit K (EC 2.7.7.6).
 GN Name=rpok; OrderedLocustNames=PF1642;
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome."
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC -1- {RNA} (N).
 CC -1- SIMILARITY: Belongs to the archaeal rpok / eukaryotic RPB6 RNA
 CC polymerase subunit family.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC EMBL: AE010263; AAL81766.1; -.
 DR HSSP; P20435; 1150.
 DR HAMAP; MF_00192; -. 1.
 DR InterPro; IPR006111; RNA_polK_14kDa.
 DR InterPro; IPR006110; RNA_polY_Rpb6.
 DR InterPro; IPR009026; RNAPol_RPB5_like.
 DR Pfam; PF01192; RNA_pol_Rpb6; 1.
 DR PROSITE; PS01111; RNA_POL_K_14KD; 1.
 KW Complete proteome; DNA-directed RNA polymerase; Transcription;
 KW Transferase.
 KW SEQUENCE 57 AA; 6236 MW; E5F00E89304F9709 CRC64;

Query Match 82.6%; Score 38; DB 1; Length 57;
 Best Local Similarity 55.6%; Pred. No. 21;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LILDVPPGV 9
 | |||||
 Db 26 VLIDVPPGI 34

Search completed: May 3, 2005, 06:00:18
 Job time : 58.1351 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 7.43243 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-10

Sequence: 1 TLILDVPPGV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	1304	1	A46546	leukocyte common a
2	47	92.2	137	2	S32461	lectin, 205K, larg
3	39	76.5	350	2	H83679	ATP-binding Mrp pr
4	39	76.5	354	2	A90012	hypothetical prote
5	38	74.5	242	2	A75178	mrp protein homolo
6	38	74.5	250	2	AE2896	transcription regu
7	38	74.5	250	2	G97671	probable transcrip
8	38	74.5	257	2	C83005	conserved hypochet
9	38	74.5	264	2	A83590	probable stomatin-
10	38	74.5	331	2	TS1894	related to nucleot
11	38	74.5	359	2	AG0776	conserved hypochet
12	38	74.5	379	2	H64978	probable ATPase mr
13	38	74.5	379	2	G90993	probable ATPase [1
14	38	74.5	379	2	B85839	probable ATPase mr
15	38	74.5	388	2	AG2663	mrp protein (impor
16	38	74.5	390	2	F97445	mrp protein homolo
17	38	74.5	528	2	T41362	hypothetical prote
18	38	74.5	533	2	T39025	hypothetical prote
19	37	72.5	212	2	AH0195	thymidylate kinase
20	37	72.5	217	2	F82788	thymidylate kinase
21	37	72.5	242	2	D71036	probable ATP-bind
22	37	72.5	277	2	H97266	mind family ATPase
23	37	72.5	282	2	C84654	hypothetical prote
24	37	72.5	296	2	A90191	MRP protein homolo
25	37	72.5	318	2	G71721	hypothetical prote
26	37	72.5	319	2	C97720	mrp protein (impor
27	37	72.5	390	2	H70508	probable mrp prote
28	37	72.5	765	2	T35719	chitinase - strept
29	36.5	71.6	390	2	AH2346	hypothetical prote

30	36	70.6	111	2	S51860	probable membrane
31	36	70.6	202	2	E72688	hypothetical prote
32	36	70.6	350	2	F75448	mrp protein - Dein
33	36	70.6	352	2	A69743	ATP-binding Mrp-11
34	36	70.6	353	2	S74379	probable ATPase -
35	36	70.6	356	2	AC1888	hypothetical prote
36	36	70.6	364	2	G70364	conserved hypochet
37	36	70.6	370	2	AG0185	conserved hypochet
38	36	70.6	382	2	B82249	mrp protein YC1037
39	36	70.6	383	2	B87044	MRP-family ATP-bin
40	36	70.6	386	2	A64114	probable ATPase mr
41	36	70.6	435	2	T45199	probable mrp prote
42	36	70.6	602	2	G75278	N-acetylmuramoyl-L
43	36	70.6	608	2	T39094	MD domain, G-beta
44	36	70.6	1119	2	AC0045	probable membrane
45	35	68.6	194	2	H83060	peptidyl-trRNA hydr

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N/Alternate names: CD45; Protein-tyrosine-phosphatase; receptor type c; T200 glycoprote
N/Contents: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #ext, change 09-Jul-2004
C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Salto, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A/Reference number: A46546; MID:88061067; PMID:2824653
A/Accession: A46546
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.6/2
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-32,99-264 <STR>
A/Cross-references: GB:Y00638
A/Residues: 1-31,193-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.1
R/Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A/Reference number: A91066; MID:87275816; PMID:2956090
A/Accession: A29449
A/Molecule type: mRNA
A/Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
A/Cross-references: GB:Y00062; MID:934275; PIDN:CAA68269.1; PID:934276
A/Experimental source: clones pHLC-1 and lambdaHLG1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Tsai, A.Y.; Streuli, M.; Salto, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative ;
A/Reference number: I57658; MID:90066468; PMID:2531281
A/Accession: I57658
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:g187020; PIDN:AA59497.1; PID:g553521
 C:Genetics:
 A:Gene: GDB:PTPRC; CD45
 A:Cross-references: GDB:119768; OMIM:151460
 A:Map position: 1q31-1q32
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolog
 C:Species: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:594-123/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:575-899/Domain: protein-tyrosine-phosphatase homology <PT>
 F:551/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:557/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 51; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPPGV 10
 |||||
 DB 292 TLILDVPPGV 301

RESULT 2
 S32461
 lectin, 205K, large granular lymphocyte - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S32461
 R:Bezonska, K.; Krähanzl, A.; Possi, M.; Kubrycht, J.; Stajner, K.; Felsberg, J.; Kd
 Eur. J. Biochem. 213, 1303-1313, 1993
 A:Title: Characterization of the high-affinity oligosaccharide-binding site of the 205-K
 A:Reference number: S32461; PMID:93279332; PMID:8504822
 A:Accession: S32461
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-137 <BEZ>
 A:Cross-references: UNIPROT:Q7M2R0
 C:Superfamily: pig lectin, 205K, large granular lymphocyte

Query Match 92.2%; Score 47; DB 2; Length 137;
 Best Local Similarity 100.0%; Pred. No. 0.28; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPPG 9
 |||||
 DB 47 TLILDVPPG 55

RESULT 3
 H83679
 ATP-binding Mrp protein (Mrp/Nbp35 family) BH0240 (imported) - Bacillus halodurans (stra
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: H83679
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; PMID:20512582; PMID:11058132
 A:Accession: H83679
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <STO>
 A:Cross-references: UNIPROT:Q9KG72; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB039
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0240
 C:Superfamily: conserved probable membrane protein YIL003w

Query Match 76.5%; Score 39; DB 2; Length 350;
 Best Local Similarity 87.5%; Pred. No. 21; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLILDVPPG 9
 |||||

DB 217 TLILDPPG 224

RESULT 4
 A90012
 hypothetical protein SA1969 (imported) - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: A90012
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; PMID:2111952; PMID:11418146
 A:Accession: A90012
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <KUR>
 A:Cross-references: UNIPROT:Q99SA0; GB:BA000018; PID:g13701966; PIDN:BAB43258.1; GSPDB:G
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA1969
 C:Superfamily: conserved probable membrane protein YIL003w

Query Match 76.5%; Score 39; DB 2; Length 354;
 Best Local Similarity 87.5%; Pred. No. 21; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLILDVPPG 9
 |||||
 DB 220 TLILDPPG 227

RESULT 5
 A75178
 mrp protein homolog PAB0400 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: A75178
 R:anonymous, GenomeScope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: A75178
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-242 <KAW>
 A:Cross-references: UNIPROT:Q9V147; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4950
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: mrp-like; PAB0400
 C:Superfamily: conserved probable membrane protein YIL003w

Query Match 74.5%; Score 38; DB 2; Length 242;
 Best Local Similarity 66.7%; Pred. No. 21; Indels 0; Gaps 0;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLILDVPPGV 10
 |||||
 DB 127 TLILDPPGV 135

RESULT 6
 AE2896
 transcription regulator, GntR family Atu2606 (imported) - Agrobacterium tumefaciens (str
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AE2896
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, L
 erage, G.; Gilliet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, B.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB25777; MUID:21608550; PMID:11743193
A:Accession: AE2896
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <RUR>
A:Cross-references: UNIPROT:Q8UC92; GB:AE008688; PIDD:PAL43567.1; PID:917741104; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2606
A:Map position: circular chromosome

Query Match 74.5%; Score 38; DB 2; Length 250;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLIDVPPG 9
Db 201 TLIDVPPG 209

RESULT 7
G97671
Probable transcription regulator (PA3757) [imported] - *Agrobacterium tumefaciens* (strain C)
C:Species: *Agrobacterium tumefaciens*
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97671
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitzoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
A:; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <RUR>
A:Cross-references: UNIPROT:Q8UC92; GB:AE007869; PIDD:MAK88328.1; PID:915157806; GSPDB:C
C:Genetics:
A:Gene: AGR_C_4722
A:Map position: circular chromosome

Query Match 74.5%; Score 38; DB 2; Length 250;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TLIDVPPG 9
Db 201 TLIDVPPG 209

RESULT 8
C83005
conserved hypothetical protein PA5135 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: C83005
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitzoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
A:; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lhm,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: C83005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <STO>
A:Cross-references: UNIPROT:Q9HU49; GB:AE004926; GB:AE004091; NID:99951424; PIDD:MA0852
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5135

Query Match 74.5%; Score 38; DB 2; Length 257;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILIDVPPG 10
Db 50 VLIDVPPG 57

RESULT 9
AB3590
Probable stomatin-like protein PA0452 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: AB3590
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitzoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
A:; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lhm,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: AB3590
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPROT:Q9I666; GB:AE004482; GB:AE004091; NID:99946303; PIDD:MA038
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0452
C:Superfamily: erythrocyte band 7 integral membrane protein

Query Match 74.5%; Score 38; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TLIDVPP 8
Db 65 TLIDVPP 72

RESULT 10
T51894
related to nucleotide-binding protein [imported] - *Neurospora crassa*
N:Alternate names: protein B23111.60
C:Species: *Neurospora crassa*
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C:Accession: T51894
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25858
A:Accession: T51894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <SCH>
A:Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.60
A:Experimental source: BAC clone B23111; strain OR74A
C:Genetics:
A:Gene: NCSP:B23111.60
A:Map position: 6
A:Intons: 34/3; 60/3; 87/1
C:Superfamily: conserved probable membrane protein YTL003w

Query Match 74.5%; Score 38; DB 2; Length 331;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLIDVPPG 9
Db 185 VLIDVPPG 192

RESULT 11
AG0776

conserved hypothetical protein SRY2383 [imported] - *Salmonella enterica* subsp. *enterica*
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A:Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0776
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moul, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG0776
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-369 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02533.1; PID:g16503394; GSPDB:GN00176
C:Gene: SRY2383
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 74.5%; Score 38; DB 2; Length 369;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 L1LDVPPG 9
Db 219 LVLDMPG 226

RESULT 12
H64978
probable ATPase mrp - *Escherichia coli* (strain K-12)
C:Species: *Escherichia coli*
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: H64978; S11948
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:9742617; PMID:9278503
A:Accession: H64978
A:Residues: 1-379 <BLAT>
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown; translation not shown
A:Cross-references: UNIPROT:Q8X7E8; GB:AE000300; GB:U00096; NID:g1788425; PIDN:AACT5174.
A:Experimental source: strain K-12, substrain MG1655
R:Dardel, F.; Panvert, M.; Payat, G.
Mol. Gen. Genet. 223, 121-133, 1990
A:Title: Transcription and regulation of expression of the *Escherichia coli* methionyl-tRNA
A:Reference number: S11948; MUID:91080852; PMID:2259334
A:Accession: S11948
A:Molecule type: DNA
A:Residues: 1-379 <DAR>
A:Cross-references: EMBL:X55791; NID:g42015; PIDN:CAA39316.1; PID:g42017
C:Gene: mrp
C:Superfamily: conserved probable membrane protein Y1L003w
C:Keywords: nucleotide binding; P-loop
F:125-132/Region: nucleotide-binding motif A (P-loop)

Query Match 74.5%; Score 38; DB 2; Length 379;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 L1LDVPPG 9
Db 229 LVLDMPG 236

RESULT 13
G90993
probable ATPase [imported] - *Escherichia coli* (strain O157:H7, substrain R1MD 0509952)

C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: G90993
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gatawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G90993
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <HAY>
A:Cross-references: UNIPROT:Q8X7E8; GB:BA000007; PIDN:BA836342.1; PID:g13362388; GSPDB:G
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Gene: BGS2919
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 74.5%; Score 38; DB 2; Length 379;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 L1LDVPPG 9
Db 229 LVLDMPG 236

RESULT 14
B85839
probable ATPase mrp [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B85839
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11266551
A:Accession: B85839
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <STO>
A:Cross-references: UNIPROT:Q8X7E8; GB:AE005174; NID:g12516326; PIDN:AA057174.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Gene: mrp
C:Superfamily: conserved probable membrane protein Y1L003w

Query Match 74.5%; Score 38; DB 2; Length 379;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 L1LDVPPG 9
Db 229 LVLDMPG 236

RESULT 15
AG2663
mrp protein [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C:Species: *Agrobacterium tumefaciens*
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG2663
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Teo, Y.; Biddle, P.; Jung, M.; Kreppan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2663
A:Status: preliminary

A;Molecule type: DNA
A;Residues: 1-388 <KUR>
A;Cross-references: UNIPROT:Q8UHH3; GB:AE008686; PID:AAI41725.1; PID:G17739074; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0709
A;Map position: circular chromosome
C;Superfamily: conserved probable membrane protein YII003w

Query Match 74.5%; Score 38; DB 2; Length 388;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LILDVPRG 9
|:|:|:|
Db 240 LVLDMPG 247

Search completed: May 3, 2005, 06:16:26
Job time : 10.4324 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 34.5946 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-10

Perfect score: 51

Sequence: 1 TLRIDVDPGV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	756	2 O6PUK7	O6PUK7 homo sapien
2	51	100.0	1304	1 CD45 HUMAN	P08575 homo sapien
3	47	92.2	137	2 Q7M2EO	Q7M2EO sus scrofa
4	44	86.3	1303	2 O6ED62	O6ED62 aotus nigri
5	43	84.3	1290	2 O6ED60	O6ED60 aotus vocif
6	41	80.4	72	2 O6QIN1	O6QIN1 homo sapien
7	40	78.4	880	2 O93IY1	O93IY1 streptomyc
8	40	78.4	980	2 O82IG2	O82IG2 streptomyc
9	39	76.5	72	2 O6QIM9	O6QIM9 gorilla gor
10	39	76.5	72	2 O6QIM9	O6QIM9 pan troglod
11	39	76.5	231	2 O6AVH8	O6AVH8 oryza sativ
12	39	76.5	306	2 O83B30	O83B30 coxiella bu
13	39	76.5	350	2 O9KG72	O9KG72 bacillus ha
14	39	76.5	354	2 O99SA0	O99SA0 staphylococ
15	39	76.5	354	2 Q7A0A1	Q7A0A1 staphylococ
16	39	76.5	354	2 Q7A4A8	Q7A4A8 staphylococ
17	39	76.5	354	2 O6G7E8	O6G7E8 staphylococ
18	39	76.5	354	2 O6GER2	O6GER2 staphylococ
19	39	76.5	380	2 O9GSD3	O9GSD3 melanoplus
20	39	76.5	933	2 O8CIT7	O8CIT7 streptomyc
21	39	76.5	1040	2 O86LJ2	O86LJ2 dictyostell
22	39	76.5	1199	2 Q7XTL8	Q7XTL8 oryza sativ
23	39	76.5	2066	2 Q7QX44	Q7QX44 glaria lam
24	39	76.5	3331	2 Q7XPS4	Q7XPS4 oryza sativ
25	38	74.5	87	1 RPOK PYRFU	RPOK PYRFU
26	38	74.5	87	1 O8IDJ1	O8IDJ1 bacillus ce
27	38	74.5	90	2 O82VT0	O82VT0 nitrosomona
28	38	74.5	194	2 O6ETU0	O6ETU0 monellima a
29	38	74.5	242	2 O9V147	O9V147 pyrococcus
30	38	74.5	250	2 O8UC92	O8UC92 agrobacteri
31	38	74.5	255	2 O6OEHO	O6OEHO burkholderi

ALIGNMENTS

RESULT 1	ID	Q6PUK7	PRELIMINARY	PRT	756 AA.
AC	O6PUK7				
DT	05-JUL-2004 (T-EMBLrel. 27, Created)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)				
DE	PTPRC protein (Fragment).				
GN	Name=PTPRC;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RX	MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsien F.,				
RA	Diatchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,				
RA	Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaracne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,				
RA	Krzywnicki M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,				
RT	Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RA	Strausberg R.;				
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, BC014239; AA014239.1; -.				
DR	HSSP, P18031; IMAK.				
DR	GO, GO:0004725; P:protein tyrosine phosphatase activity; IEA.				
DR	GO, GO:0006470; P:protein amino acid dephosphorylation; IEA.				
DR	InterPro, IPR003961; FN III.				
DR	InterPro, IPR008957; FN III-like.				
DR	InterPro, IPR000242; Tyr_PP.				
DR	Pfam, PF00061; fn3; 2.				
DR	Pfam, PF00102; Y_phosphatase; 1.				
DR	PRINTS, PR00700; PRTYPHPTASE.				
DR	SMART, SM00060; FN3; 2.				
DR	SMART, SM00194; PTPC; 1.				

32	38	74.5	255	2	O63J94	O63J94 burkholderi
33	38	74.5	257	2	O9HU49	O9HU49 pseudomonas
34	38	74.5	264	2	O91666	O91666 pseudomonas
35	38	74.5	309	2	O7S6P7	O7S6P7 neurospora
36	38	74.5	309	2	O9TA64	O9TA64 calathus ci
37	38	74.5	354	2	O81VP5	O81VP5 bacillus th
38	38	74.5	354	2	O6HVM2	O6HVM2 bacillus th
39	38	74.5	355	2	O63H54	O63H54 bacillus ce
40	38	74.5	355	2	O73F59	O73F59 bacillus ce
41	38	74.5	355	2	O81J10	O81J10 bacillus ce
42	38	74.5	358	2	O8RDC2	O8RDC2 thermoaer
43	38	74.5	359	1	MRP_ECOLI	P21590 escherichia
44	38	74.5	369	2	O825C4	O825C4 salmonella
45	38	74.5	369	2	O8ZNN5	O8ZNN5 salmonella

DR PROSITE; PSS0853; FN3; 2.
 DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 1.
 FT NON_TER 756 756
 SQ SEQUENCE 756 AA; 8A9A63827BD69B6 CRC64;
 Query Match 100.0%; Score 51; DB 2; Length 756;
 Best local Similarity 100.0%; Pred. No. 1.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLILDVPPGV 10
 Db 244 TLILDVPPGV 253
 RESULT 2
 CD45_HUMAN STANDARD; PRT; 1304 AA.
 ID CD45_HUMAN
 AC P08575; Q16614; Q9H0Y6;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen) (7200).
 GN Name=PTPRC; Synonyms=CD45;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
 RC TISSUE=Lymphocytes;
 RA Screuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
 RT "Differential usage of three exons generates at least five different mRNAs encoding human leukocyte common antigens.";
 RL J. Exp. Med. 166:1548-1566 (1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
 RA Screuli M., Thomas M.L., Morton C.C., Trowbridge I.S.;
 RT "Structural variants of human T200 glycoprotein (leukocyte-common antigen).";
 RL EMBO J. 6:1251-1257 (1987).
 RN [3]
 RP SEQUENCE OF 191-1304 FROM N.A.
 RC TISSUE=Placenta;
 RA Hall L.R., Screuli M., Schlossman S.F., Saito H.;
 RT "Complete exon-intron organization of the human leukocyte common antigen (CD45) gene.";
 RL J. Immunol. 141:2781-2787 (1988).
 RN [4]
 RP FUNCTION.
 RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
 RT "The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186 (1988).
 RN [5]
 RP MUTAGENESIS.
 RA Screuli M., Krueger N.X., Thai T., Tang M., Saito H.;
 RT "Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";
 RL LAR. J. 9:2399-2407 (1990).
 CC -1- FUNCTION: Required for T-cell activation through the antigen receptor. The first PTPase domain has enzymatic activity, while the second one seems to affect the substrate specificity of the first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.
 CC -1- SUBUNIT: binds CANAB and PRKCSH (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: Named isoforms=2;
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=At least 8 isoforms are produced;
 CC Name=1;
 CC IsoId=P08575-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P08575-2; Sequence=VSP_007780;
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 1/6 subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD45 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/brow/cd/cd45.htm".
 CC -----
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 CC -----
 DR EMBL; Y00638; CAA68669.1; -;
 DR EMBL; Y00062; CAA68269.1; -;
 DR EMBL; M23492; AAD15273.2; -;
 DR EMBL; M23496; AAD15273.2; JOINED.
 DR EMBL; M23466; AAD15273.2; JOINED.
 DR EMBL; M23467; AAD15273.2; JOINED.
 DR EMBL; M23468; AAD15273.2; JOINED.
 DR EMBL; M23469; AAD15273.2; JOINED.
 DR EMBL; M23470; AAD15273.2; JOINED.
 DR EMBL; M23471; AAD15273.2; JOINED.
 DR EMBL; M23472; AAD15273.2; JOINED.
 DR EMBL; M23473; AAD15273.2; JOINED.
 DR EMBL; M23474; AAD15273.2; JOINED.
 DR EMBL; M23475; AAD15273.2; JOINED.
 DR EMBL; M23476; AAD15273.2; JOINED.
 DR EMBL; M23477; AAD15273.2; JOINED.
 DR EMBL; M23478; AAD15273.2; JOINED.
 DR EMBL; M23479; AAD15273.2; JOINED.
 DR EMBL; M23480; AAD15273.2; JOINED.
 DR EMBL; M23481; AAD15273.2; JOINED.
 DR EMBL; M23482; AAD15273.2; JOINED.
 DR EMBL; M23483; AAD15273.2; JOINED.
 DR EMBL; M23484; AAD15273.2; JOINED.
 DR EMBL; M23485; AAD15273.2; JOINED.
 DR EMBL; M23486; AAD15273.2; JOINED.
 DR EMBL; M23487; AAD15273.2; JOINED.
 DR EMBL; M23488; AAD15273.2; JOINED.
 DR EMBL; M23489; AAD15273.2; JOINED.
 DR EMBL; M23490; AAD15273.2; JOINED.
 DR EMBL; M23491; AAD15273.2; JOINED.
 DR PIR; A46546; A46546.
 DR HSSP; P18031; 1C88.
 DR Intract; P08575; -;
 DR GlycoSiteDB; P08575; -;
 DR GeneW; HGNC:9666; PTPRC.
 DR MIM; 151460; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR InterPro; IPR003961; FN_III-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_Pp.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR PROSITE; PSS0853; FN3; 2.
 DR PROSITE; PSS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.
KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1304
FT DOMAIN 24 575
FT TRANSMEM 575 597
FT DOMAIN 598 1304
FT DOMAIN 390 478
FT DOMAIN 482 570
FT DOMAIN 670 919
FT DOMAIN 961 1235
FT ACT_SITE 851 851
FT ACT_SITE 1167 1167
FT CARBOHYD 78 78
FT CARBOHYD 90 90
FT CARBOHYD 95 95
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 197 197
FT CARBOHYD 232 232
FT CARBOHYD 260 260
FT CARBOHYD 270 270
FT CARBOHYD 276 276
FT CARBOHYD 335 335
FT CARBOHYD 378 378
FT CARBOHYD 419 419
FT CARBOHYD 468 468
FT CARBOHYD 488 488
FT CARBOHYD 529 529
FT VARSLIC 32 192
FT MUTAGEN 851 851
FT CONFLICT 650 650
FT CONFLICT 1207 1207
SQ SEQUENCE 1304 AA; 147253 MW; A08FC2D6069A7F CRC64;
Query Match 100.0%; Score 51; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLILDVPGV 10
Db 292 TLILDVPGV 301
RESULT 3
O7M2R0 PRELIMINARY; PRT; 137 AA.
AC O7M2R0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE lectin, 205K, large granular lymphocyte.
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE
RA MEDLINE=93279333; PubMed=8504822;
RA Bezouska K., Krajhanzl A., Pospisil M., Kubrycht J., Stajner K.,
RA Falsberg J., Kocourek J.;
RT "Characterization of the high-affinity oligosaccharide-binding site of
RT the 205-kDa porcine large granular lymphocyte lectin, a member of the
RT leukocyte common antigen family.";
RL Eur. J. Biochem. 213:1303-1313(1993).
DR PIR; S32461; S32461.
SQ SEQUENCE 137 AA; 14936 MW; 84DABA4FBA700194 CRC64;
Query Match 92.2%; Score 47; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLILDVPGV 9
Db 47 TLILDVPGV 55
RESULT 4
O6ED62 PRELIMINARY; PRT; 1303 AA.
AC O6ED62;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD45.
OS Aotus nigriceps (black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
RT vs. human";
RT Tissue Antigens 64:165-172(2004).
RL EMBL; AY445816; AAS06901.1; -
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003595; PTFE motif.
DR InterPro; IPR000387; TYR_PTP.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y phosphatase; 2.
DR PRINTS; PR00700; PRTPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPc; 2.
DR SMART; SM00404; PTPc motif; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1303 AA; 146586 MW; 9BB023EBF4BC1165 CRC64;
Query Match 86.3%; Score 44; DB 2; Length 1303;
Best Local Similarity 90.0%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TLILDVPGV 10
Db 292 TLILDVPGV 301
RESULT 5
O6ED60 PRELIMINARY; PRT; 1290 AA.
AC O6ED60;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD45.
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Montoya G.E., Vernot J.P., Patatroyo M.E.;

RT "Comparative analysis of CD45 protein in primate context: owl monkeys
RT vs. human.".
RL Tissue Antigens 64:165-172(2004).
DR EMBL; A7445818; AAS06903.1; -.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; Tyr_Pp.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PRO0700; PRTYPHTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC_motif; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrobase.
KW Hydrobase.
SQ SEQUENCE 1290 AA; 145616 MW; 99EB10C75D932824 CRC64;

Query Match 84.3%; Score 43; DB 2; Length 1290;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLILDVPPGV 10
DB 283 TLILDVPPGV 292

RESULT 6
Q6QINI
ID Q6QINI PRELIMINARY; PRT; 72 AA.
AC Q6QINI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBT_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh11;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL; AY539691; AAS46946.1; -.
FT NON TER 1 72
FT NON TER 1 72
SQ SEQUENCE 72 AA; 8003 MW; 2EAC733A329D4E4 CRC64;

Query Match 80.4%; Score 41; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPP 8
DB 65 TLILDVPP 72

RESULT 7
Q93IY1
ID Q93IY1 PRELIMINARY; PRT; 880 AA.
AC Q93IY1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein SC05104.
GN ORFNames=SCBAC2861.30;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBT_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Challis H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kiese R., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz B., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorek A., Woodward J.R., Barrall B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)."
RL Nature 417:141-147(2002).
DR EMBL; AL939122; CAC44217.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR01932; P2C-like.
DR InterPro; IPR010822; SpoIIE.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF07228; SpoIIE; 1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00091; PAS; 2.
DR SMART; SM00331; P2C_Sig; 1.
DR TIGRFAMs; TIGR00229; sensory_box; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PS50112; PAS; 1.
KW Complete proteome; Hypothetical protein.
KM SEQUENCE 880 AA; 94778 MW; 4EB9867390CB436E CRC64;

Query Match 78.4%; Score 40; DB 2; Length 880;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLILDVPPGV 10
DB 646 TLILDVPPGV 654

RESULT 8
Q82IG2
ID Q82IG2 PRELIMINARY; PRT; 980 AA.
AC Q82IG2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SAV3185;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBT_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;

```

RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., T.,
RA Shinose M., Shiba T., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakai Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakai Y., Hattori M., Omura S.,
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
RD EMBL; AP005034; BAC70896.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; AtPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR010822; SpoIIE.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF07228; SpoIIE; 1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00091; PAS; 2.
DR SMART; SM00331; PP2C_SIG; 1.
DR TIGRFAMs; TIGR00229; sensory_box; 2.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PSS0112; PAS; 1.
DR PROSITE; PSS0112; PAS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 980 AA; 104505 MW; 25587847A78345C3 CRC64;

Query Match
Best Local Similarity 77.4%; Score 40; DB 2; Length 980;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLIDVPPGV 10
Db 746 LMLDVPFGM 754

RESULT 9
Q6QIM9 PRELIMINARY; PRT; 72 AA.
AC O6QIM9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OC NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msl11;
RA Filip L.C., Mundy N.I.,
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates."
RL Mol. Biol. Evol. 21:1504-1511(2004).
RD EMBL; AY539693; AAS46948.1; -.
RN NON_TER 1
RP SEQUENCE FROM N.A.

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FT NON TER 72
SQ SEQUENCE 72 AA; 8063 MW; 42AC733A3297AD52 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 2; Length 72;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLIDVPP 8
Db 65 TLIDVPP 72

RESULT 10
Q6QIM9 PRELIMINARY; PRT; 72 AA.
AC O6QIM9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OC NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msl11;
RA Filip L.C., Mundy N.I.,
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates."
RL Mol. Biol. Evol. 21:1504-1511(2004).
RD EMBL; AY539692; AAS46947.1; -.
RN NON_TER 1
FT NON TER 1
SQ SEQUENCE 72 AA; 8063 MW; 42AC733A3297AD52 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 2; Length 72;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLIDVPP 8
Db 65 TLIDVPP 72

RESULT 11
Q6AVH8 PRELIMINARY; PRT; 231 AA.
AC Q6AVH8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBA0079G12.6 (Hypothetical protein
DE OSUNBA0079J18.25).
GN Name=OSUNBA0079G12.6; Synonyms=OSUNBA0079J18.25;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Talcott T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsieh J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uteback T.T., Feldlyum T.V.,
RA Vang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.,
RT "Oryza sativa chromosome 3 BAC OSUNBA0079G12 genomic sequence."
RN Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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RA Buell R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton I.L., Teltrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadresh D.W., Tallon L.J., Koo H., Ziemann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldlyum T.V.,
 RA Yang Q.Q., Haas B.J., Sun B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.,
 RT "Oryza sativa chromosome 3 BAC OSUNBa0027018 genomic sequence."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC103550; AAT77885.1; -;
 DR EMBL; AC096689; AAT78795.1; -;
 DR InterPro; IPR006460; DUF_A_chal_3588.
 DR Pfam; PF04759; DUF617.1.
 KW Hypothetical protein.
 SQ SEQUENCE 231 AA; 24730 MW; CCFQFB7218499516 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 231;
 Best Local Similarity 66.7%; Pred. No. 63;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 L1LDPVPGV 10
 DB 103 L1LDPVPGV 111

RESULT 12
 Q83B30 PRELIMINARY; PRT; 306 AA.

ID Q83B30;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MTP protein, putative.
 GN OrderedLocustNames=CBU1689;
 OS Coxiella burnetii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Coxiellaceae; Coxiella.
 OX NCB1_TaxID=777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nine Mile phase I / RSA 493;
 RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
 RA Seshadri R., Paulsen I.T., Eisen U.A., Read T.D., Nelson K.E.,
 RA Nelson W.C., Ward N.L., Tettelin H., Davidson T.M., Beanan K.J.,
 RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
 RA Khouli H.M., Lee K.H., Carty H.A., Scanlan D., Heinen R.A.,
 RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.,
 RT "Complete genome sequence of the Q-fever pathogen, Coxiella burnetii."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
 DR EMBL; AEO16965; AAC091184.1; -;
 DR HSSP; O29562; 1HYQ.
 DR TIGR; CBU1689; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR000808; MTP.
 DR PROSITE; PS01215; MRP; 1.
 KW Complete proteome.
 SQ SEQUENCE 306 AA; 32537 MW; 28EBB2ECD9D993E5 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 306;
 Best Local Similarity 87.5%; Pred. No. 86;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 L1LDPVPGV 9
 DB 152 L1LDPVPGV 159

RESULT 13
 Q9KG72

ID Q9KG72 PRELIMINARY; PRT; 350 AA.

AC Q9KG72;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE ATP-binding MTP protein (Mtp/Nbp35 family).
 GN OrderedLocustNames=BH0240;
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCB1_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.,
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001507; BAB03959.1; -;
 DR FIR; H83679; H83679.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR002744; DUF59.
 DR InterPro; IPR000808; MTP.
 DR Pfam; PF01883; DUF59; 1.
 DR ProDom; PD005595; DUF59; 1.
 DR PROSITE; PS01215; MRP; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 350 AA; 37949 MW; 8CBCEB15467D5BCBF CRC64;

Query Match 76.5%; Score 39; DB 2; Length 350;
 Best Local Similarity 87.5%; Pred. No. 99;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 L1LDPVPGV 9
 DB 217 L1LDPVPGV 224

RESULT 14

ID Q99SAO PRELIMINARY; PRT; 354 AA.
 AC Q99SAO;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ATP-binding protein Mtp-like protein.
 GN OrderedLocustNames=SAV2165;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCB1_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iino J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hasegawa A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus."
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003364; BAB58327.1; -;
 DR PIR; A90012; A90012.
 DR GO; GO:0005786; C:signal recognition particle (sensu Eukaryota); IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0006614; P:SRP-dependent cotranslational protein-membr. .; IEA.

DR InterPro; IPR000897; SRP54.
 DR ProDom; PD000819; SRP54; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 354 AA; 38358 MM; 730E4D806920A691 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 354;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LILDVPPG 9
 ||||:||||
 Db 220 LILDLPFG 227

RESULT 15

Q7A0A1 PRELIMINARY; PRT; 354 AA.
 AC Q7A0A1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MW2092 protein.
 GN OrderedLocustNames=MW2092;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827 (2002).
 DR EMBL; AP004829; BAB95957.1; -
 DR GO; GO:0005786; C:signal recognition particle (sensu Eukaryota); IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0006614; P:SRP-dependent cotranslational protein-membr. . .; IEA.
 DR InterPro; IPR000897; SRP54.
 DR ProDom; PD000819; SRP54; 1.
 KW Complete proteome.
 SQ SEQUENCE 354 AA; 38358 MM; 730E4D806920A691 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 354;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LILDVPPG 9
 ||||:||||
 Db 220 LILDLPFG 227

Search completed: May 3, 2005, 06:00:36
 Job time : 52.5946 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-11

Perfect score: 51

Sequence: 1 ILVNHKFT 9

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	756	2 O6PUK7	O6PUK7 homo sapien
2	51	100.0	1304	2 CD45.HUMAN	P08575 homo sapien
3	41	80.4	564	2 Q7RWT2	Q7RWT2 plasmodium
4	39	76.5	208	2 Q88G11	Q88G11 pseudomonas
5	39	76.5	749	2 Q7Z391	Q7Z391 homo sapien
6	39	76.5	1103	2 Q6MZP4	Q6MZP4 homo sapien
7	39	76.5	2193	2 Q6MZM7	Q6MZM7 homo sapien
8	39	76.5	2240	2 Q68DP8	Q68DP8 homo sapien
9	39	76.5	2265	1 F1NC.BOVIN	P07359 bos taurus
10	39	76.5	2267	2 Q68DP9	Q68DP9 homo sapien
11	39	76.5	2296	2 Q6N0A6	Q6N0A6 homo sapien
12	39	76.5	2357	2 Q68DT4	Q68DT4 homo sapien
13	39	76.5	2386	1 F1NC.HUMAN	P02751 homo sapien
14	39	76.5	2444	2 Q6N0Z5	Q6N0Z5 homo sapien
15	39	76.5	2477	2 Q6MZU5	Q6MZU5 homo sapien
16	39	76.5	2477	2 Q6F0R3	Q6F0R3 mesoplasma
17	39	76.5	265	2 Q6BQ04	Q6BQ04 debaryomyce
18	39	76.5	390	2 Q7SAW7	Q7SAW7 ashyba goss
19	39	76.5	716	2 Q81900	Q81900 trypanosoma
20	39	76.5	980	1 BOB1.YEAST	P38041 saccharomyc
21	39	76.5	2162	2 Q81BH2	Q81BH2 plasmodium
22	39	76.5	3763	2 Q81T21	Q81T21 dictyosteli
23	39	76.5	107	2 Q6AKO7	Q6AKO7 desulfocale
24	39	76.5	202	2 Q7T3D0	Q7T3D0 brachydanio
25	39	76.5	358	1 T2H2.HABPA	P36433 haemophilus
26	39	76.5	399	2 Q83IX3	Q83IX3 enterococcu
27	39	76.5	1221	1 V143.NPVAC	P24307 autocorapha
28	39	76.5	1221	2 Q8B9G3	Q8B9G3 rachiplusia
29	39	76.5	1222	2 Q92455	Q92455 bombyx mori
30	39	76.5	1222	2 P90691	P90691 bombyx mori
31	39	76.5	72	2 Q76YV3	Q76YV3 bacterioph

ALIGNMENTS

RESULT 1	ID	Q6PUK7	PRELIMINARY	PRT	756 AA.
AC	O6PUK7				
DT	05-JUL-2004 (T-EMBLrel. 27, Created)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)				
DE	PTPRC protein (Fragment).				
GN	Name=PTPRC;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	(1)				
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RX	MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loeblano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,				
RA	Krzyvinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,				
RT	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
[2]					
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Primary B-Cells;				
RA	Strausberg R.;				
RA	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC014239; AA014239.1; -.				
DR	HSSP; P18031; IAAK.				
DR	GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.				
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.				
DR	InterPro; IPR003961; FN III.				
DR	InterPro; IPR008957; FN III-like.				
DR	InterPro; IPR000242; Tyr_PP.				
DR	Pfam; PF00041; fn3; 2.				
DR	Pfam; PF00102; Y_phosphatase; 1.				
DR	PRINTS; PR00700; PRYPPHTASE.				
DR	SMART; SM00060; FN3; 2.				
DR	SMART; SM00194; PTPC; 1.				

DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS50855; TYR_PHOSPHATASE_PTP; 1.
 FT NON_TER 756 756
 SQ SEQUENCE 756 AA; 85430 MW; 8A9A863827D65E6 CRC64;
 Query Match 100.0%; Score 51; DB 2; Length 756;
 Best local Similarity 100.0%; Pred. No. 0.61;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILYNNHKT 9
 DB 321 ILYNNHKT 329
 RESULT 2
 CD45_HUMAN STANDARD; PRT; 1304 AA.
 ID CD45_HUMAN
 AC P08575; Q16614; Q9H0Y6;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen) (T200).
 GN Name=PTPRC; Synonyms=CD45;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
 RC TISSUE=Lymphocytes;
 RA Striell M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
 RT "Differential usage of three exons generates at least five different mRNAs encoding human leukocyte common antigens.";
 RL J. Exp. Med. 166:1548-1566(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
 RC TISSUE=Lymphocytes;
 RA Ralph S.J., Thomas M.W., Morton C.C., Trowbridge I.S.;
 RT "Structural variants of human T200 glycoprotein (leukocyte-common antigen).";
 RL EMBO J. 6:1251-1257(1987).
 RN [3]
 RP SEQUENCE OF 191-1304 FROM N.A.
 RC TISSUE=Placenta;
 RA MEDLINE=89009812; PubMed=2971730; S.F., Saito H.;
 RT "Complete exon-intron organization of the human leukocyte common antigen (CD45) gene.";
 RL J. Immunol. 141:2781-2787(1988).
 RN [4]
 RP FUNCTION
 RA MEDLINE=89017162; PubMed=2845400;
 RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
 RT "The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
 RN [5]
 RP MUTAGENESIS.
 RA MEDLINE=90316093; PubMed=1695146;
 RA Striell M., Krueger N.X., Thai T., Tang M., Saito H.;
 RT "Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";
 RL EMBO J. 9:2399-2407(1990).
 CC -1- FUNCTION: Required for T-cell activation through the antigen receptor. The first PTPase domain has enzymatic activity, while the second one seems to affect the substrate specificity of the first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -1- SUBUNIT: Binds GANAB and PRKCSH (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=At least 8 isoforms are produced;
 CC Name=1;
 CC IsoId=P08575-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P08575-2; Sequence=VSP_007780;
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 1/6 subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD45 entry;
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
 CC -----
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 CC -----
 CC EMBL; Y00638; CAA68669.1; -;
 CC EMBL; Y00652; CAA68269.1; -;
 CC EMBL; M23492; AAD15273.2; -;
 CC EMBL; M23496; AAD15273.2; JOINED.
 CC EMBL; M23466; AAD15273.2; JOINED.
 CC EMBL; M23467; AAD15273.2; JOINED.
 CC EMBL; M23469; AAD15273.2; JOINED.
 CC EMBL; M23470; AAD15273.2; JOINED.
 CC EMBL; M23471; AAD15273.2; JOINED.
 CC EMBL; M23472; AAD15273.2; JOINED.
 CC EMBL; M23473; AAD15273.2; JOINED.
 CC EMBL; M23474; AAD15273.2; JOINED.
 CC EMBL; M23475; AAD15273.2; JOINED.
 CC EMBL; M23476; AAD15273.2; JOINED.
 CC EMBL; M23477; AAD15273.2; JOINED.
 CC EMBL; M23478; AAD15273.2; JOINED.
 CC EMBL; M23479; AAD15273.2; JOINED.
 CC EMBL; M23480; AAD15273.2; JOINED.
 CC EMBL; M23481; AAD15273.2; JOINED.
 CC EMBL; M23482; AAD15273.2; JOINED.
 CC EMBL; M23483; AAD15273.2; JOINED.
 CC EMBL; M23484; AAD15273.2; JOINED.
 CC EMBL; M23485; AAD15273.2; JOINED.
 CC EMBL; M23486; AAD15273.2; JOINED.
 CC EMBL; M23487; AAD15273.2; JOINED.
 CC EMBL; M23488; AAD15273.2; JOINED.
 CC EMBL; M23489; AAD15273.2; JOINED.
 CC EMBL; M23490; AAD15273.2; JOINED.
 CC EMBL; M23491; AAD15273.2; JOINED.
 CC PIR; A46546; A46546.
 CC HSSP; P18031; 1C88.
 CC InIntact; P08575; -;
 CC GlycoStatedB; P08575; -;
 CC Genew; HGNC:9666; PTPRC.
 CC MIM; 151460; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. .; TAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR000387; TYR_PP.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00102; Y_phosphatase; 2.
 CC PRINTS; PR00700; PRTYHPTASE.
 CC PROSITE; PS50853; FN3; 2.
 CC PROSITE; PS50833; TYR_PHOSPHATASE_1; 2.
 CC PROSITE; PS50856; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.
KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1304
FT DOMAIN 24 575
FT TRANSMEM 576 597
FT DOMAIN 598 1304
FT DOMAIN 390 478
FT DOMAIN 482 570
FT DOMAIN 670 919
FT DOMAIN 961 1235
FT ACT_SITE 851 851
FT ACT_SITE 1167 1167
FT CARBOHYD 78 78
FT CARBOHYD 90 90
FT CARBOHYD 95 95
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 197 197
FT CARBOHYD 232 232
FT CARBOHYD 260 260
FT CARBOHYD 270 270
FT CARBOHYD 276 276
FT CARBOHYD 335 335
FT CARBOHYD 378 378
FT CARBOHYD 419 419
FT CARBOHYD 468 468
FT CARBOHYD 488 488
FT CARBOHYD 529 529
FT VARSPIC 32 192
FT MTAGEN 851 851
FT CONFLICT 650 650
FT CONFLICT 1207 1207
SQ SEQUENCE 1304 AA; 147253 MW; A08FC22D609BAF7 CRC64;
Query Match Best Local Similarity 100.0%; Score 51; DB 1; Length 1304;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ILVNHKFT 9
Db 369 ILVNHKFT 377
RESULT 3
ID Q7RMT2 PRELIMINARY; PRT; 564 AA.
AC Q7RMT2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cysteine deaurylase.
GN Name=PY02096;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
NCBI_TaxID=73239;
RX PubMed=1368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguinoi S.V., Suh B.B., Kooji T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000573; EAA21516.1; -.
DR HSSP; Q9X218; 1EG5.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000192; AminoTran_V.
DR Pfam; PF00266; AminoTran_5; 1.
DR PROSITE; PS00595; AA TRANSFER CLASS 5; 1.
SQ SEQUENCE 564 AA; 63705 MW; 0A94F77AE297887C CRC64;
Query Match Best Local Similarity 80.4%; Score 41; DB 2; Length 564;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ILVNHKFT 9
Db 57 VCVNHKFTS 65
RESULT 4
ID Q88G11 PRELIMINARY; PRT; 208 AA.
AC Q88G11;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glutathione S-transferase family protein.
GN OrderedLocNames=PP3742;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
RX PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonos J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Knout H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzes A., Utebback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stejandic D., Hobeisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmls K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016788; AAN69337.1; -.
DR HSSP; P24472; 1GUK.
DR TIGR; PP3742; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR010987; GST_C_1like.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 208 AA; 24042 MW; F331A8CDAB21A3B7 CRC64;
Query Match Best Local Similarity 76.5%; Score 39; DB 2; Length 208;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ILVNHKFT 9
Db 98 MLFDNHKFT 106

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RESULT 5
ID Q72391 PRELIMINARY; PRT; 749 AA.
AC Q72391;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686B18150.
GN Name=DKFZp686B18150;
OS Homo sapiens (human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human colon endothel primary cell culture;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX53845; CAD9784.1; -.
DR HSSP; Q96K7; IPIR.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR0006209; EGF_1like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 2.
DR Pfam; PF00040; fn2; 2.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 9.
DR SMART; SM00059; FN2; 2.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 9.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR Hypothetical protein.
KW SEQUENCE 749 AA; 83524 MW; C8DDF97F3ED2F0DE CRC64;
SQ

Query Match 76.5%; Score 39; DB 2; Length 749;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYNNHKT 9
Db 517 LYNNHNYT 524

RESULT 6
ID Q6MZP4 PRELIMINARY; PRT; 1103 AA.
AC Q6MZP4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686K139 (Hypothetical protein DKFZp686F219)
DE (Fragment).
GN Name=DKFZp686K139; Synonyms=DKFZp686F219;
OS Homo sapiens (human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human cervix;
RA Ansoerge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX649182; CAE46200.1; -.
DR EMBL; BX640802; CAE45885.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 7.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 7.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 9.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 4.
DR Hypothetical protein.
KW NON_TER
SQ SEQUENCE 1103 AA; 122113 MW; 82FEC4CAF634AD56 CRC64;
FT
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DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 9.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 4.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 9.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 9.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 4.
DR Hypothetical protein.
KW NON_TER
SQ SEQUENCE 1103 AA; 122113 MW; 82FEC4CAF634AD56 CRC64;
FT

Query Match 76.5%; Score 39; DB 2; Length 1103;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYNNHKT 9
Db 514 LYNNHNYT 521

RESULT 7
ID Q6ZMW7 PRELIMINARY; PRT; 2193 AA.
AC Q6ZMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O12165 (Fragment).
GN Name=DKFZp686O12165;
OS Homo sapiens (human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP TISSUE=Human uterus endothel primary cell culture;
RC The German Human CDNA Consortium;
RA Lauber U., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640999; CAE46002.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd dehyd.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR0003962; FN_III_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 7.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 7.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 9.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 4.
DR Hypothetical protein.
KW
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FT NON TER 1 1
SQ SEQUENCE 2193 AA; 240641 MW; F876E93106540EF3 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 2193;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYNNHKT 9
DB 172 LYNNHNT 179

RESULT 8

068DP8 PRELIMINARY; PRT; 2240 AA.
ID 068DP8
AC 068DP8;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686H0342.
GN Name=DKFZp686H0342;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgama;
RG The German CDNA Consortium;
RA Otenaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CRR49317, CRR48172.1;
DR InterPro: IPR002086; Aldenyl_dehyd. dehyd.rog.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR000083; Fibrinctn.
DR InterPro: IPR003962; Fcrl1 subd.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000562; FN_Type_II.
DR Pfam: PF00039; fn1; 12.
DR Pfam: PF00040; fn2; 2.
DR Pfam: PF00041; fn3; 15.
DR PRINTS: PR00012; FNTYPEI.
DR PRINTS: PR00013; FNTYPEII.
DR PRINTS: PR00014; FNTYPEIII.
DR PRODOM: PD000995; FN_Type_II; 2.
DR SMART: SMO0058; FN1; 12.
DR SMART: SMO0059; FN2; 2.
DR SMART: SMO0060; FN3; 15.
DR PROSITE: PS00687; ALDEHYDE DEHYDR. GLU; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR PROSITE: PS01253; FIBRONECTIN_1; 10.
DR PROSITE: PS00023; FIBRONECTIN_2; 2.
KM Hypothetical protein.
SQ SEQUENCE 2240 AA; 246667 MW; 8FCD4F406F330621 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 2240;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYNNHKT 9
DB 425 LYNNHNT 432

RESULT 9

FINC_BOVIN STANDARD; PRT; 2265 AA.
ID 068DP8;
AC 068DP8;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Fibronectin (FN).
GN Name=FN1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin."
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
of internal homology."
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
fibronectin."
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
including collagen, fibrin, heparin, DNA, and actin. Fibronectins
are involved in cell adhesion, cell motility, opsonization, wound
healing, and maintenance of cell shape.
CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
variance, connected by 2 disulfide bonds near the carboxyl ends;
to a lesser extent homodimers.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced. Each of the "extra
domain" and the connecting strand 3 are present in some forms of
fibronectin and absent in others;
CC Name=1;
CC IsoId=P07589-1; Sequence=Displayed;
CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
forms), made by fibroblasts, epithelial and other cell types, is
deposited as fibrils in the extracellular matrix;
CC -1- PTM: Sulfated (By similarity).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 15 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: K00800; AAA30521.2; -;
DR PIR: A26452; FNBO.
DR HSSP: P08253; IKS0.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR000083; Fibrinctn.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000562; FN_Type_II.
DR InterPro: IPR003962; FN_III_subd.
DR Pfam: PF00039; fn1; 12.
DR Pfam: PF00040; fn2; 2.
DR Pfam: PF00041; fn3; 15.
DR PRINTS: PR00012; FNTYPEI.

DR PRINTS; PRO0013; FNTYPEII.
 DR PRINTS; PRO0014; FNTYPEIII.
 DR PRODOM; PS000995; FN_Type_II; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS00853; FN3; 15.
 DR Acute phase; Alternative splicing; Cell adhesion; Cell shape;
 KM Direct protein sequencing; Glycoprotein; Heparin-binding;
 KM Phosphorylation; Plasma; Pyroglutamate carboxylic acid; Repeat;
 KW Sulfation.
 FT MOD_RES 1 1
 FT DOMAIN 21 241 Pyroglutamate carboxylic acid.
 FT 577 277 Fibrin- and heparin-binding 1.
 FT DNA_BIND 876 1141 Collagen-binding.
 FT DOMAIN 1236 1509
 FT 1600 1870
 FT DOMAIN 1991 2216
 FT 19 59 Cell-attachment.
 FT DOMAIN 64 107 Heparin-binding 2.
 FT 108 151 Fibrin-binding 2.
 FT DOMAIN 153 197 Fibrin-binding 2.
 FT 198 242 Fibrin-binding 2.
 FT DOMAIN 275 314 Fibrin-binding 2.
 FT 314 373 Fibrin-binding 2.
 FT DOMAIN 374 438 Fibrin-binding 2.
 FT 437 480 Fibrin-binding 2.
 FT DOMAIN 485 527 Fibrin-binding 2.
 FT 528 571 Fibrin-binding 2.
 FT DOMAIN 576 668 Fibrin-binding 2.
 FT 689 778 Fibrin-binding 2.
 FT DOMAIN 780 867 Fibrin-binding 2.
 FT 877 964 Fibrin-binding 2.
 FT DOMAIN 965 1053 Fibrin-binding 2.
 FT 1056 1141 Fibrin-binding 2.
 FT DOMAIN 1142 1234 Fibrin-binding 2.
 FT 1235 1325 Fibrin-binding 2.
 FT DOMAIN 1326 1415 Fibrin-binding 2.
 FT 1416 1505 Fibrin-binding 2.
 FT DOMAIN 1510 1599 Fibrin-binding 2.
 FT 1602 1689 Fibrin-binding 2.
 FT DOMAIN 1692 1780 Fibrin-binding 2.
 FT 1781 1870 Fibrin-binding 2.
 FT DOMAIN 1871 1970 Fibrin-binding 2.
 FT 1979 2069 Fibrin-binding 2.
 FT DOMAIN 2083 2127 Fibrin-binding 2.
 FT 2128 2170 Fibrin-binding 2.
 FT DOMAIN 2172 2215 Fibrin-binding 2.
 FT SITE 1493 1495 Cell attachment site.
 FT DISULFID 21 47
 FT 45 56
 FT DISULFID 66 94
 FT 92 104
 FT DISULFID 110 138
 FT 136 148
 FT DISULFID 155 184
 FT 182 194
 FT DISULFID 200 229
 FT 227 239
 FT DISULFID 277 304
 FT 302 311
 FT DISULFID 329 355
 FT 343 370
 FT DISULFID 389 415
 FT 415 430
 FT DISULFID 439 467
 FT 465 477
 FT DISULFID 487 514
 FT 512 524
 FT DISULFID 530 558
 FT 556 568
 FT DISULFID 2085 2114
 FT 2112 2124

FT DISULFID 2130 2157
 FT 2155 2167
 FT DISULFID 2174 2200
 FT 2198 2209
 FT DISULFID 2246 2246
 FT 2250 2250
 FT DISULFID 2250 2250
 FT 845 845
 FT MOD_RES 850 850
 FT 389 389
 FT CARBOHYD 457 457
 FT 497 497
 FT CARBOHYD 511 511
 FT 846 846
 FT CARBOHYD 976 976
 FT 1213 1213
 FT CARBOHYD 1213 1213
 FT 1987 1987
 FT CARBOHYD 1943 1943
 FT 1944 1944
 FT MOD_RES 2263 2263
 FT 2265 2265
 FT SEQUENCE 2265 AA; 249557 MW; C2D21D486F498D5C CRC64;
 Qy 2 LYNHKEFT 9
 Db 394 LYNHNYT 401
 Query Match 76.5%; Score 39; DB 1; Length 2265;
 Best Local Similarity 75.0%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 10
 ID 068DP9 PRELIMINARY; PRT; 2267 AA.
 AC 068DP9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFZp666K08164.
 GN Name=DKFZp666K08164;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=uterus endothel;
 RG The German cDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR749316; CAH18171.1; -;
 DR InterPro; IPR002086; Aldehyd dehydrog.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000083; Fibrinectn.
 DR InterPro; IPR003962; Fibrinectn.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR000562; FN_Type_II.
 DR Pfam; PF00039; FN1; 12.
 DR Pfam; PF00040; FN2; 2.
 DR Pfam; PF00041; FN3; 16.
 DR PRINTS; PRO0012; FNTYPEI.
 DR PRINTS; PRO0013; FNTYPEII.
 DR PRINTS; PRO0014; FNTYPEIII.
 DR PRODOM; PS000995; FN_Type_II; 2.
 DR SMART; SM00058; FN1; 12.
 DR SMART; SM00059; FN2; 2.
 DR SMART; SM00060; FN3; 16.
 DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 2267 AA; 249358 MW; C4D124A038C323DF CRC64;

Query Match 76.5%; Score 39; DB 2; Length 2267;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYNNHKT 9
Db 425 LYNNHNT 432

RESULT 11

Q6N0A6 PRELIMINARY; PRT; 2296 AA.
ID Q6N0A6
AC Q6N0A6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Hypoetical protein DKFZp686M04163.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human uterus endochel primary cell culture;
RG The German Human cDNA Consortium;
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX40608; CAE5714.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd.dehydrog.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR005562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 15.
DR PRINTS; PRO0012; ENTYPET.
DR PRINTS; PRO0013; ENTYPET.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 15.
DR PROSITE; PS00687; ALDEHYDE DEHYDR. GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN 1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 15.
KW Hypoetical protein.
SQ SEQUENCE 2296 AA; 252761 MW; 9AB2D73CC0CED70 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 2296;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYNNHKT 9
Db 425 LYNNHNT 432

RESULT 12

Q6BDT4 PRELIMINARY; PRT; 2357 AA.
ID Q6BDT4
AC Q6BDT4;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Hypoetical protein DKFZp686F10164.
GN Name=DKFZp686F10164;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus endochel;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749281; CAH18136.1; -
DR InterPro; IPR002086; Aldehyd.dehydrog.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR00083; Fibrinctn1.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR005562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 15.
DR PRINTS; PRO0012; ENTYPET.
DR PRINTS; PRO0013; ENTYPET.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 15.
DR PROSITE; PS00687; ALDEHYDE DEHYDR. GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN 1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
KW Hypoetical protein.
SQ SEQUENCE 2357 AA; 259090 MW; BEA3990E27E532A CRC64;

Query Match 76.5%; Score 39; DB 2; Length 2357;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYNNHKT 9
Db 517 LYNNHNT 524

RESULT 13

FINC HUMAN STANDARD; PRT; 2386 AA.
ID F1NC HUMAN
AC P02751; O95609; O95610; O14312; O14325; O14326; Q86T27; Q81V18;
AC Q96KT7; Q96KP8; Q96KP9; Q9H1B8; Q9HAP3; Q9UMK2;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).
GN Name=FN1; Synonyms=FN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2).
RX MEDLINE=21600194; PubMed=11737888; DOI=10.1186/bcr125;
RA Schor S.L., Schor A.M.;
RT "Phenotypic and genetic alterations in mammary stroma: implications for tumour progression.";
RL Breast Cancer Res. 3:373-379 (2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3; 7 AND 10).
RC TISSUE=Cervix;
RA Ansojge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
RA Mewes H.-W., Weil B., Amid C., Osanger A., Fobo G., Han M.,
RA Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE=87030890; PubMed=3770189; DOI=10.1016/0014-5793(86)80029-1;
 RA Gutman A., Yamada K.M., Kornblith A.R.;
 RT "Human fibronectin is synthesized as a pre-propolypeptide.";
 RL FEBS Lett. 207:145-148(1986).
 RN [4]
 RP SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE=87175378; PubMed=3031656;
 RA Dean D.C., Bowlin C.L., Bourgeois S.;
 RT "Cloning and analysis of the promotor region of the human fibronectin gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).
 RN [5]
 RP SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).
 RX MEDLINE=85284965; PubMed=2992939;
 RA Kornblith A.R., Umezawa K., Vibbe-Pedersen K., Baralle F.E.;
 RT "Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";
 RL EMBO J. 4:1755-1759(1985).
 RN [6]
 RP SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1; 3; 8 AND 9).
 RX TISSUE=Peritoneal blood T-cell, and Umbilical vein endothelial cells;
 RA Godfrey H.P., Ebrahim A.A.;
 RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).
 RX MEDLINE=84272258; PubMed=6462919;
 RA Kornblith A.R., Vibbe-Pedersen K., Baralle F.E.;
 RT "Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";
 RL Nucleic Acids Res. 12:5853-5868(1984).
 RN [8]
 RP SEQUENCE OF 1232-1782 FROM N.A. (ISOFORM 7).
 RX MEDLINE=88233940; PubMed=3375063;
 RA Paolletta G., Henchcliffe C., Sebastiao G., Baralle F.E.;
 RT "Sequence analysis and in vivo expression show that alternative splicing of ED-B and ED-A regions of the human fibronectin gene are independent events.";
 RL Nucleic Acids Res. 16:3545-3557(1988).
 RN [9]
 RP SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).
 RX MEDLINE=88041070; PubMed=3478690;
 RA Gutman A., Kornblith A.R.;
 RT "Identification of a third region of cell-specific alternative splicing in human fibronectin mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7179-7182(1987).
 RN [10]
 RP SEQUENCE OF 1441-1548.
 RX MEDLINE=82265604; PubMed=7050098;
 RA Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
 RT "The cell attachment domain of fibronectin. Determination of the primary structure.";
 RL J. Biol. Chem. 257:9593-9597(1982).
 RN [11]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE=83290929; PubMed=6688419;
 RA Oldberg A., Linney E., Ruoslahti E.;
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell attachment domain in human fibronectin.";
 RL J. Biol. Chem. 258:10193-10196(1983).
 RN [12]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE=86111901; PubMed=3003095;
 RA Oldberg A., Ruoslahti E.;
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment domain.";
 RL J. Biol. Chem. 261:2113-2116(1986).
 RN [13]
 RP SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).
 RX MEDLINE=85280409; PubMed=2992573;
 RA Bernard M.P., Kolbe M., Weil D., Chu M.-L.;
 RT "Human cellular fibronectin: comparison of the carboxyl-terminal

RT portion with rat identifies primary structural domains separated by
 RT hypervariable regions.";
 RL Biochemistry 24:2698-2704(1985).
 RN [14]
 RP SEQUENCE OF 1712-1739 FROM N.A.
 RX MEDLINE=87026578; PubMed=3021206;
 RA Sekiguchi K., Klos A.M., Kurachi K., Yoshitake S., Hakomori S.;
 RT "Human liver fibronectin complementary DNAs: identification of two different messenger RNAs possibly encoding the alpha and beta subunits of plasma fibronectin.";
 RL Biochemistry 25:4936-4941(1986).
 RN [15]
 RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4; 5 AND 6).
 RX TISSUE=Cartilage;
 RX MEDLINE=22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;
 RA Parter A.E., Boulell J., Carr A., Maciewicz R.A.;
 RT "Novel cartilage-specific splice variants of fibronectin.";
 RL Osteoarthritis Cartilage 10:528-534(2002).
 RN [16]
 RP SEQUENCE OF 32-290.
 RX MEDLINE=84032463; PubMed=6630202;
 RA Garcia-Pardo A., Pearlstein E., Frangione B.;
 RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";
 RL J. Biol. Chem. 258:12670-12674(1983).
 RN [17]
 RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
 RX MEDLINE=87080265; PubMed=3024962;
 RA Owens R.J., Baralle F.E.;
 RT "Mapping the collagen-binding site of human fibronectin by expression in *Escherichia coli*.";
 RL EMBO J. 5:2825-2830(1986).
 RN [18]
 RP SULFATATION.
 RX MEDLINE=86042625; PubMed=2414772;
 RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
 RT "Tyrosine sulfation of proteins from the human hepatoma cell line Hep2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
 RN [19]
 RP O-GLYCOSYLATION OF THR-2064.
 RX MEDLINE=91190085; PubMed=2012601;
 RA Tresselt T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K., Shively J.E., Pande H.;
 RT "Human plasma fibronectin. Demonstration of structural differences between the A- and B-chains in the III CS region.";
 RL Biochem. J. 274:731-738(1991).
 RN [20]
 RP FIBLN1-BINDING SITE.
 RX MEDLINE=93015879; PubMed=1400330;
 RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K., Argaves W.S.;
 RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding region of fibronectin.";
 RL J. Biol. Chem. 267:20120-20125(1992).
 RN [21]
 RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
 RX MEDLINE=95081153; PubMed=7989369;
 RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
 RT "Further characterization of the NH2-terminal fibrin-binding site on fibronectin.";
 RL J. Biol. Chem. 269:31938-31945(1994).
 RN [22]
 RP INTERACTION WITH LGALS3BP.
 RX PubMed=9501082; DOI=10.1093/emboj/17.6.1606;
 RA Sasaki T., Brakheusch C., Engel J., Timpl R.;
 RT "Mac-2 binding protein is a cell-adhesive protein of the extracellular matrix which self-assembles into ring-like structures and binds beta1 integrins, collagens and fibronectin.";
 RL EMBO J. 17:1606-1613(1998).
 RN [23]
 RP STRUCTURE BY NMR OF 1447-1540.
 RX MEDLINE=92162710; PubMed=1311202;

RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,
RA Campbell I.D.;
RT "1H NMR assignment and secondary structure of the cell adhesion type
RT III module of fibronectin."
RL Biochemistry 31:2068-2073(1992).
RN [24]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=93046665; PubMed=1423622; DOI=10.1016/0092-8674(92)90600-H;
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT "The three-dimensional structure of the tenth type III module of
RT fibronectin: an insight into RGD-mediated interactions."
RL Cell 71:671-678(1992).
RN [25]
RP STRUCTURE BY NMR OF 182-275.
RX MEDLINE=94141923; PubMed=8308892;
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
RA Campbell I.D.;
RT "Solution structure of a pair of fibronectin type I modules with
RT fibrin binding activity."
RL J Mol. Biol. 235:1302-1311(1994).
RN [26]
RP STRUCTURE BY NMR OF 32-92.
RX MEDLINE=96069779; PubMed=7583666;
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;
RT "High-resolution structural studies of the factor XIIIa crosslinking
RT site and the first type I module of fibronectin."
RL Nc. Struct. Biol. 2:946-950(1995).
RN [27]

Query Match 76.5%; Score 39; DB 1; Length 2386;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYNNHKT 9
DB 425 LYNNHNYT 432

RESULT 14
Q6N025 PRELIMINARY; PRT; 2444 AA.
ID Q6N025;
AC Q6N025;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686M2451 (Fragment).
GN Name=DKFZp686M2451;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human endometrium carcinoma cell line;
RG The German Human cDNA Consortium;
RA Poustek A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amlid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640731; CAB45847.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd dehyd.rog.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR00083; Fibrinctn.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 16.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00059; FN1; 12.
DR SMART; SM00059; FN2; 2.

DR SMART; SM00060; FN3; 16.
DR PROSITE; PS00687; ALDEHYDE DEHYD. GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS50853; FN3; 16.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 2444 AA; 268676 MW; 71C5B8C56A84C7BC CRC64;

Query Match 76.5%; Score 39; DB 2; Length 2444;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYNNHKT 9
DB 514 LYNNHNYT 521

RESULT 15
Q6MZ05 PRELIMINARY; PRT; 2477 AA.
ID Q6MZ05;
AC Q6MZ05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O1166.
GN Name=DKFZp686O1166;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human endometrium carcinoma cell line;
RG The German Human cDNA Consortium;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amlid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640875; CAB45932.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd dehyd.rog.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR00083; Fibrinctn.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.

DR PROSITE; PS00687; ALDEHYDE DEHYD. GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS50853; FN3; 17.
KM Hypothetical protein.
SQ SEQUENCE 2477 AA; 272335 MW; D35B8D5C6B18207C CRC64;

Query Match 76.5%; Score 39; DB 2; Length 2477;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYNNHKT 9
DB 425 LYNNHNYT 432

Search completed: May 3, 2005, 06:01:08

Tue May 3 08:17:40 2005

us-10-003-983c-11.rup

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Job time : 63.1351 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:18:26 ; Search time 49 seconds
(without alignments)
71.038 Million cell updates/sec

Title: US-10-003-983C-11

Perfect score: 51

Sequence: 1 ILVNHKFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum March 0%
Maximum March 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	5 ABG31981	ABG31981 Human CD4
2	51	100.0	553	5 AAW35856	AAW35856 Human CD4
3	51	100.0	553	6 ABU07335	ABU07335 Human EST
4	51	100.0	641	4 AAM23689	AAM23689 Human EST
5	51	100.0	641	6 ABU07333	ABU07333 Human EST
6	51	100.0	664	4 AAM39262	AAM39262 Human pol
7	51	100.0	664	6 ABU07334	ABU07334 Human exp
8	51	100.0	960	8 ADQ39377	ADQ39377 Human exp
9	51	100.0	1114	6 ABU05246	ABU05246 Human exp
10	51	100.0	1114	6 ABU05239	ABU05239 Human exp
11	51	100.0	1143	6 ABU05240	ABU05240 Human exp
12	51	100.0	1143	6 ABU05245	ABU05245 Human exp
13	51	100.0	1143	7 ADL16232	ADL16232 Human pro
14	51	100.0	1143	8 ADQ18845	ADQ18845 Human sof
15	51	100.0	1192	8 ADR38747	ADR38747 Human kin
16	51	100.0	1219	8 ADQ39378	ADQ39378 Human myo
17	51	100.0	1256	8 ADM67187	ADM67187 Human adi
18	51	100.0	1256	8 ADP12966	ADP12966 Protein e
19	51	100.0	1258	8 ADQ39376	ADQ39376 Human myo
20	51	100.0	1267	8 ADQ39379	ADQ39379 Human myo
21	51	100.0	1304	6 ABU05243	ABU05243 Human exp
22	51	100.0	1304	6 ABU05241	ABU05241 Human exp
23	51	100.0	1304	6 ABU05244	ABU05244 Human exp
24	51	100.0	1304	7 ADL16230	ADL16230 Human pro
25	51	100.0	1304	7 ADP65158	ADP65158 Human pro

ALIGNMENTS

RESULT 1	ABG31981	standard; peptide; 9 AA.
AC	ABG31981;	
XX		
DT	05-NOV-2002	(first entry)
XX		
DE	Human CD45 HLA-binding peptide, huCD45/369.	
XX		
KW	Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;	
KW	antigen-presenting cell; APC; major histocompatibility complex; MHC;	
KW	antigen; allogenic; T cell receptor; TCR; cancer; tumour;	
KW	allogenic stem cell transplantation; CFU-GM; leukaemia;	
KW	colony forming unit-granulocyte macrophage; immunotherapeutic;	
XX	haematopoietic; malignant.	
OS	Homo sapiens.	
XX		
PN	W0200244207-A1.	
XX		
PD	06-JUN-2002.	
XX		
PF	30-NOV-2000; 2000MO-GB004566.	
XX		
PR	30-NOV-2000; 2000MO-GB004566.	
XX		
PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.	
XX		
PI	Stausen HU, Amrolia PU;	
DR	WPI; 2002-559413/64.	
XX		
PT	Novel peptide comprising leukocyte antigen binding peptide of human CD45	
PT	polypeptide, useful for producing activated cytotoxic T lymphocytes, for	
PT	killing cancerous cells e.g. leukemia.	
XX		
PS	Claim 2; Page 38; 56pp; English.	
XX		
CC	The invention discloses a peptide comprising the human leukocyte antigen	Adm67209 Human adi
CC	(HLA)-binding peptide of human CD45 polypeptide, its portion or variant,	Ab084455 Human can
CC	provided that the peptide is not the intact human CD45 polypeptide. The	Adq39380 Human myo
CC	peptides are useful for producing activated cytotoxic T lymphocyte (CTL)	Adq39375 Human myo
CC	in vitro which involves contacting the CTL with an antigen-presenting	Aam41048 Human pol
CC	cell, where its major histocompatibility complex (MHC) class I molecules	Abu05242 Human exp
CC	are loaded with the peptide, to activate, in an antigen specific manner,	Abp79870 N. gonorr
CC	where the CTL and the antigen presenting cell are allogenic with respect	Aaw62372 Antithrom
CC	to the class I MHC molecule that is presenting peptides of CD45. The	Abb06747 Human fib
		Abb06751 Collagen
		Abb08505 Antio act
		Abb07961 Modified
		Abb06750 Collagen-
		Aab08509 Hybrid of
		Abb07964 Human fib
		Abb07965 Human fib
		Aab08508 Hybrid of
		Adq39403 Human myo
		Adr67316 Human bla
		Adsl7489 Amino aci

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animals models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/369,
CC comprising an HLA-binding peptide of human CD45
XX
SQ Sequence 9 AA;
XX
Query Match 100.0%; Score 51; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILYNNHKFT 9
DB 1 ILYNNHKFT 9
XX
RESULT 2
AAW35856
ID AAW35856 standard; protein; 553 AA.
XX
AC AAW35856;
XX
DT 27-APR-1998 (first entry)
XX
DE Human CD45 for use in T lymphocyte veto molecule.
XX
KW Human; CD45; T lymphocyte veto molecule; chimeric molecule;
KW targeting polypeptide; suppression; immune response; treatment;
KW autoimmune disease; allergy; immunological disorder;
KW transplant rejection.
XX
OS Homo sapiens.
XX
PN WO9737687-A1.
XX
PD 16-OCT-1997.
XX
PF 10-APR-1997; 97WO-US005943.
XX
PR 10-APR-1996; 96US-00630172.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Staerz UD;
XX
DR WPI; 1997-512419/47.
XX
PT T lymphocyte veto molecule comprising response cell activating protein -
PT linked to molecule that targets stimulator cell marker, used for
PT selective suppression of immune response, e.g. prevention of graft
PT rejection or treatment of auto-immune disease.
XX
PS Claim 37; Page 70-72; 309pp; English.
XX
CC A novel T lymphocyte veto molecule is a chimeric molecule comprising a
CC protein, e.g. the present sequence, linked to a targeting polypeptide
CC that binds a molecule, which differentiates a host cell from a tissue
CC graft cell, or selectively targets a stimulator cell involved in the
CC autoimmune response. A veto molecule, in which the protein binds a

CC molecule that targets stimulator cells, can be used to suppress an immune
CC response and therefore treat autoimmune diseases, e.g. systemic lupus
CC erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
CC diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
CC thyroiditis, Addison's or Grave's diseases and rheumatoid carditis,
CC allergies and other immunological disorders. Where the protein binds a
CC molecule that differentiates graft and host cells, the veto molecule can
CC be used to reduce transplant rejection. The veto molecule provides
CC specific regulation of particular stimulator cells that can kill graft
CC cells or respond to autoantigens, but leave other stimulator cells
CC unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
CC affecting the other. The veto molecule can be administered locally to
CC minimise generalised immunosuppression
XX
SQ Sequence 553 AA;
XX
Query Match 100.0%; Score 51; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILYNNHKFT 9
DB 346 ILYNNHKFT 354
XX
RESULT 3
ABU07335
ID ABU07335 standard; protein; 553 AA.
XX
AC ABU07335;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2036.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2036; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 51; DB 6; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILNNHKFT 9
Db 346 ILNNHKFT 354

RESULT 4
AAW23689 standard; protein; 641 AA.
ID AAW23689;
AC AAW23689;
XX
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1214.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KM diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KM gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN MO200154477-A2.
XX
PD 02-AUG-2001.
XX
PP 25-JAN-2001; 2001MO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang U, Werhman T;
XX
XX WPI; 2001-476164/51.
DR N-PSDB; AAH98348.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
XX Claim 20; Page 875-876; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 51; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILNNHKFT 9
Db 210 ILNNHKFT 218

RESULT 5
ABU07333 standard; protein; 641 AA.
ID ABU07333;
AC ABU07333;
XX
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2034.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PP 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
PI
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 2034; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

```
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 664 AA;

Query Match          100.0%; Score 51; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILVNNHKFT 9
   |||||
Db 210 ILVNNHKFT 218

RESULT 6
AAM39262
ID AAM39262 standard; protein; 664 AA.
AC AAM39262;
XX
XX
DT 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2407.
XX
XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX MO200153312-A1.
XX
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US034263.
XX
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XR, Ren F, Wang D,
XX Wang Z, Wang J, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,
XX Zhou P, Goodrich R, Drianae RT;
XX
XX WPI; 2001-442253/47.
XX
XX N-PSDB; AAI58418.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 2407; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AAM38642-AA42213) with nootropic,
XX immunosuppressant and cyostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 664 AA;

Query Match          100.0%; Score 51; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILVNNHKFT 9
   |||||
Db 210 ILVNNHKFT 218

RESULT 7
ABU07334
ID ABU07334 standard; protein; 664 AA.
XX
XX ABU07334;
XX
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #2035.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002MO-US009671.
XX
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 2035; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
```


CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 664 AA;
Query Match 100.0%; Score 51; DB 6; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILYNNHKFT 9
Db 210 ILYNNHKFT 218
RESULT 8
ADQ39377
ID ADQ39377 standard; protein; 960 AA.
XX
AC ADQ39377;
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1040.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiac; gene therapy; human.
XX
OS Homo sapiens.
XX
PN MO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003MO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Iakubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PSDB; ADQ38549.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1040; 145bp; English.
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide
XX comprising an amino acid sequence given in the specification; an antibody
XX that specifically binds to the polypeptide or its antigen-binding
XX fragment; an amplified polynucleotide containing an SNP given in the
XX specification and which is between about 16 and 1000 nucleotides in
XX length; a kit for detecting an SNP in a nucleic acid, comprising the
XX polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 960 AA;
Query Match 100.0%; Score 51; DB 8; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILYNNHKFT 9
Db 25 ILYNNHKFT 33
RESULT 9
ABU05246
ID ABU05246 standard; protein; 1114 AA.
XX
AC ABU05246;
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1912.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1912; 134bp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;
XX
Query Match 100.0%; Score 51; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ILVNNHKFT 9
DB 179 ILVNNHKFT 187
XX
RESULT 10
ABU05239
ID ABU05239 standard; protein; 1114 AA.
XX
AC ABU05239;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1905.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR MPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1905; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;
XX
Query Match 100.0%; Score 51; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ILVNNHKFT 9
DB 179 ILVNNHKFT 187
XX
RESULT 11
ABU05240
ID ABU05240 standard; protein; 1143 AA.
XX
AC ABU05240;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1906.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR MPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 1143 AA;
Query Match 100.0%; Score 51; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILVNNHKFT 9
DB 208 ILVNNHKFT 216
RESULT 12
ABU05245
ID ABU05245 standard; protein; 1143 AA.
XX
AC ABU05245;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1911.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1911, 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 1143 AA;
Query Match 100.0%; Score 51; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILVNNHKFT 9
DB 208 ILVNNHKFT 216
RESULT 13
ADL16232
ID ADL16232 standard; protein; 1143 AA.
XX
AC ADL16232;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #27.
XX
KW cytostatic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signaling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
XX
PR 12-FEB-2003; 2003US-00366547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI (CEPT-) CEPTYR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-FSDB; ADL16231.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 81, 238pp; English.
XX
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (ii) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
CC dephosphorylation indicates that an active PTP is present. . No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly

Query Match 100.0%; Score 51; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNHKFT 9
Db 257 ILYNNHKFT 265

RESULT 16
ADQ39378
ID ADQ39378 standard; protein; 1219 AA.
XX

AC ADQ39378;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KW cardiant; gene therapy; human.

XX Homo sapiens.

XX WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

XX (APPL-) APPLERA CORP.

PI Cargill M, Devlin JI, Takubova O;

DR WPI; 2004-533949/51.

XX N-PSDB; ADQ38550.

PS Claim 10; SEQ ID NO 1041; 145bp; English.

CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has variant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-

CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX SQ Sequence 1219 AA;

Query Match 100.0%; Score 51; DB 8; Length 1219;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNHKFT 9
Db 284 ILYNNHKFT 292

RESULT 17
ADM67187
ID ADM67187 standard; protein; 1256 AA.
XX

AC ADM67187;

DT 03-JUN-2004 (first entry)

DE Human adipocyte specific PTPase receptor type C protein SeqID 541.

XX human; adipocyte specific; adipose tissue; anti-obesity;

KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;

KW adipogenesis; hypertension; cardiovascular disease; anorectic;

KW antidiabetic; hypotensive; PTPase receptor type C.

XX Homo sapiens.

XX WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

XX (HMGCE-) HMGCE INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

XX N-PSDB; ADM66908.

PS Disclosure; SEQ ID NO 541; 91bp; English.

CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C^{-/-}, ob/ob, or HMGI-C^{-/-} ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.

XX SQ Sequence 1256 AA;

Query Match 100.0%; Score 51; DB 8; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILVNNHKFT 9
 |||||
 DB 321 ILVNNHKFT 329

RESULT 18
 ID ADP12966
 ADP12966 standard; protein; 1256 AA.

XX AC ADP12966;
 XX DT 12-AUG-2004 (first entry)
 XX

DE Protein encoding reference mRNA sequence #51.

XX transplamt rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX

OS Homo sapiens.
 XX MO2004042346-AA2.
 XX

XX 21-MAY-2004.
 XX

XX 24-APR-2003; 2003WO-US012946.
 XX

XX 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX

XX MPI; 2004-400724/37.
 XX

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX

PS Claim 65; SEQ ID NO 2975; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection.
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein encoded by an mRNA sequence of the invention which show altered
 CC expression in renal transplantation and expression.

XX Sequence 1256 AA;

QY Query Match 100.0%; Score 51; DB 8; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILVNNHKFT 9
 |||||

DB 321 ILVNNHKFT 329

RESULT 19
 ID ADQ39376
 ADQ39376 standard; protein; 1258 AA.

XX AC ADQ39376;
 XX DT 18-NOV-2004 (first entry)
 XX

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiac; gene therapy, human.
 XX

OS Homo sapiens.
 XX MO2004058052-AA2.
 XX

XX 15-JUL-2004.
 XX

XX 22-DEC-2003; 2003WO-US040978.
 XX

XX 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0451335P.
 PR 30-APR-2003; 2003US-0466413P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX

XX (APPL-) APPLERA CORP.
 XX PA Cargill M, Devlin J, Iakoubova O;
 PI MPI; 2004-533949/51.
 XX

XX N-PSDB; ADQ38548.
 DR

PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX

XX Claim 10; SEQ ID NO 1039; 145pp; English.

XX The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiac activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1258 AA;

QY Query Match 100.0%; Score 51; DB 8; Length 1258;


```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;

Query Match          100.0%; Score 51; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNHKFT 9
   |||||
DB 369 ILYNNHKFT 377

RESULT 22
ABU05241
ID ABU05241 standard; protein; 1304 AA.
XX
AC ABU05241;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1907.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```

```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;

Query Match          100.0%; Score 51; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNHKFT 9
   |||||
DB 369 ILYNNHKFT 377

RESULT 23
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1910.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1910; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
```


CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
Query Match 100.0%; Score 51; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILYNNHKFT 9
| | | | | | | | | |
DB 369 ILYNNHKFT 377
RESULT 24
ADL16230
ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #26.
XX
KW cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
XX
PR 12-FEB-2003; 2003US-00366547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PA (CEPT-) CEPTYR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-PSDB; ADL16229.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
XX
XX Disclosure; SEQ ID NO 79; 238pp; English.
XX
PS The invention relates to a method for identifying a protein tyrosine
PS phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
XX invention.

SQ Sequence 1304 AA;
Query Match 100.0%; Score 51; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILYNNHKFT 9
| | | | | | | | | |
DB 369 ILYNNHKFT 377
RESULT 25
ADP65158
ID ADP65158 standard; protein; 1304 AA.
XX
AC ADP65158;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
XX
KW autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
OS Homo sapiens.
XX
PN WO2003072827-A1.
XX
PD 04-SEP-2003.
XX
PF 31-OCT-2002; 2002WO-US035433.
XX
PR 31-OCT-2001; 2001US-0336220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thornton SL;
XX
DR WPI; 2003-712740/67.
XX
DR GENBANK; NP_002829.
XX
PT diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
XX
XX Disclosure; Page; 56pp; English.
XX
PS The invention relates to a novel method for diagnosing and analyzing
PS autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an

CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritis. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.

XX Sequence 1304 AA;

XX Query Match 100.0%; Score 51; DB 7; Length 1304;

XX Best Local Similarity 100.0%; Pred. No. 1.5;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNHKFT 9

|||||

369 ILYNNHKFT 377

RESULT 26

ADM67209

ID ADM67209 standard; protein; 1304 AA.

XX ADM67209;

XX 03-JUN-2004 (first entry)

DE Human adipocyte specific leukocyte common antigen protein seqid 563.

XX human; adipocyte specific; adipose tissue; anti-obesity;

XX high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;

XX adipogenesis; hypertension; cardiovascular disease; anorectic;

XX anti-diabetic; hypotensive; leukocyte common antigen.

XX Homo sapiens.

XX WO2004011618-A2.

XX 05-FEB-2004.

XX 29-JUL-2003; 2003WO-US023684.

XX 29-JUL-2002; 2002US-0398785P.

XX 12-JUN-2003; 2003US-0478206P.

XX (HMGE-) HMGE INC.

XX Chada K, Chouinard R, Ashar H, Sayed AMD;

XX WPI; 2004-143846/14.

XX N-PSDB; ADM66930.

XX Identifying adipocyte specific genes, useful for treating obesity or

XX diabetes, and for identifying drug targets, by differential gene

XX expression analysis between adipose tissue or stromal vascular tissue of

XX mice of different genotypes.

XX Disclosure; SEQ ID NO 563; 91pp; English.

XX This invention relates to a novel method for identifying genes that are

XX over-expressed in adipose tissue and as such it provides targets for anti

XX -obesity pharmaceutical compositions. Specifically, it refers to a high

XX mobility group I-C protein (HMGI-C) that is associated with obesity and

XX is epistatic to leptin, furthermore, it refers to the ob gene where an

XX autosomal recessive trait is linked to obesity and diabetes. The present

XX invention describes performing differential gene expression analysis

XX between the white adipose tissue (WAT) or stromal vascular tissue (SVT)

XX of any two different mice selected from a group consisting of wild-type,

XX HMGI-C-/-, ob/ob, or HMGI-C-/- ob/ob genotype mice. Accordingly, using

XX this method novel nucleotides and the encoded proteins thereof were

XX identified that are adipocyte specific, and as such can be used for

XX preventing adipogenesis, diagnosing and treating diabetes, obesity,

XX hypertension and cardiovascular disease, as well as screening for

XX compounds that can modulate or prevent adipogenesis and treat diabetes or

XX obesity. These compositions exhibit anorectic, anti-diabetic and

CC hypotensive activities. This polypeptide sequence is a human homologue of

XX a murine adipocyte specific protein sequence of the invention.

XX Sequence 1304 AA;

XX Query Match 100.0%; Score 51; DB 8; Length 1304;

XX Best Local Similarity 100.0%; Pred. No. 1.5;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNHKFT 9

|||||

369 ILYNNHKFT 377

RESULT 27

AB084455

ID AB084455 standard; protein; 1304 AA.

XX AB084455;

XX 18-NOV-2004 (first entry)

DE Human cancer-associated protein HP13-011.2.

XX Human; cancer-associated protein; cytosolic; cancer; leukaemia;

XX lymphoma; CAP.

XX Homo sapiens.

XX WO2004074320-A2.

XX 02-SEP-2004.

XX 17-FEB-2004; 2004WO-US004730.

XX 14-FEB-2003; 2003US-00367094.

XX 14-MAR-2003; 2003US-00388838.

XX 15-APR-2003; 2003US-00417375.

XX 13-JUN-2003; 2003US-00461862.

XX 15-SEP-2003; 2003US-00663431.

XX 15-DEC-2003; 2003US-00737318.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Morris DW, Malandro MS;

XX WPI; 2004-652914/63.

XX N-PSDB; ABD32626.

XX New isolated cancer-associated polynucleotides and polypeptides useful

XX for diagnosing, preventing or treating cancers, especially lymphoma and

XX leukemia, or in screening for agents that modulate cancer.

XX claim 18; seqid 147; 310pp; English.

XX The invention relates to an isolated nucleic acid comprising at least 10

XX contiguous nucleotides of any of the 233 polynucleotide sequences given

XX in the specification, or its complement. The nucleic acids encode cancer-

XX associated proteins. Also included are an expression vector comprising

XX the isolated nucleic acid cited above, a host cell comprising the above

XX recombinant nucleic acid or expression vector, a microarray for detecting

XX a cancer-associated (CA) nucleic acid comprising at least one probe

XX comprising at least 10 contiguous nucleotides of any of the above-

XX mentioned nucleotide sequences, an isolated polypeptide (encoded within

XX an open reading frame of a CA sequence selected from any of the 95

XX polynucleotide sequences as mentioned in the specification, or its

XX complement), an isolated antibody, (or its antigen binding fragment) that

XX binds to the above polypeptide, a hybridoma that produces the above

XX monoclonal antibody, a pharmaceutical composition comprising the above

XX antibody and a pharmaceutical excipient, a kit for detecting cancer

XX cells (comprising the antibody cited above, methods for diagnosing cancer

XX or for detecting the presence or absence of cancer cells in an

XX individual, a method for inhibiting growth of cancer cells in an

CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
SQ Sequence 1304 AA;
QY
Db 1 ILYNNHKFT 9
ADQ39380 100.0%; Score 51; DB 8; Length 1304;
ID ADQ39380 standard; protein; 1304 AA.
XX
XX ADQ39380;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
XX Myocardial infarction; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
XX
XX 10-MAR-2003; 2003US-0453135P.
XX
XX 30-APR-2003; 2003US-0466412P.
XX
XX 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JF, Iakubova O;
XX
XX WPI, 2004-533949/51.
XX
XX N-PsDB; ADQ38552.
XX
XX
XX Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
XX
XX Claim 10; SEQ ID NO 1043; 145pp; English.
XX
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in

CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
SQ Sequence 1304 AA;
QY
Db 1 ILYNNHKFT 9
ADQ39375 100.0%; Score 51; DB 8; Length 1304;
ID ADQ39375 standard; protein; 1306 AA.
XX
XX ADQ39375;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
XX Myocardial infarction; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
XX
XX 10-MAR-2003; 2003US-0453135P.
XX
XX 30-APR-2003; 2003US-0466412P.
XX
XX 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JF, Iakubova O;
XX
XX WPI, 2004-533949/51.
XX
XX N-PsDB; ADQ38547.
XX
XX
XX Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
XX
XX Claim 10; SEQ ID NO 1038; 145pp; English.
XX
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 XX
 SQ Sequence 1306 AA;

Query Match 100.0%; Score 51; DB 8; Length 1306;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILVNNHKFT 9
 Db 371 ILVNNHKFT 379

Search completed: May 3, 2005, 07:31:37
 Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-11

Perfect score: 51

Sequence: 1 ILVNNHKFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	1304	1	A46546	leukocyte common a
2	39	76.5	2265	1	FNBO	fibronectin - bovi
3	39	76.5	2386	1	FNHU	fibronectin precu
4	38	74.5	980	1	S45444	BEM1 protein-bind
5	37	72.5	1221	1	HJNVAV	helicase (EC 3.6.1
6	37	72.5	1222	2	T41835	DNA helicase P143
7	36	70.6	371	2	G86851	permease [importe
8	36	70.6	395	2	F95179	aspartate aminotra
9	36	70.6	395	2	F98046	aspartate transami
10	36	70.6	716	2	S70398	zona pellucida gly
11	36	68.6	1218	2	A88429	protein C28A5.2 [i
12	35	68.6	149	2	F86380	protein F5A9.10 [i
13	35	68.6	216	2	H86380	protein F5A9.6 [im
14	35	68.6	287	2	A84041	sulfate ABC transp
15	35	68.6	313	2	A90097	hypothetical prote
16	35	68.6	394	2	G85829	O antigen polymera
17	35	68.6	394	2	D90984	O antigen polymera
18	35	68.6	469	2	B86381	probable anthranil
19	35	68.6	534	2	B96842	hypothetical prote
20	35	68.6	606	2	A99991	CD48 like protein
21	34	66.7	81	2	T28372	ORF MSV211 hypothe
22	34	66.7	117	2	A89964	hypothetical prote
23	34	66.7	170	2	C84997	heat shock protein
24	34	66.7	335	2	G27743	adhesin pagc.F13 p
25	34	66.7	341	2	T05764	hypothetical prote
26	34	66.7	438	2	F75290	conserved hypochet
27	34	66.7	439	2	A12957	L-seryl-tRNA(ser)
28	34	66.7	439	2	B98325	selenocysteine syn
29	34	66.7	551	2	T40812	probable thiamin b

30	34	66.7	606	2	T11060	NADH2 dehydrogenas
31	34	66.7	684	2	H82296	c-di-GMP phosphodi
32	34	66.7	1198	2	T20262	hypothetical prote
33	34	66.7	1203	2	C89217	protein C55A6.2 [i
34	34	66.7	1480	2	T21911	hypothetical prote
35	34	66.7	1483	2	T21914	hypothetical prote
36	34	66.7	1483	2	T21912	hypothetical prote
37	33	64.7	213	2	B81360	probable protein d
38	33	64.7	267	2	AG0947	probable Deor-fam1
39	33	64.7	298	2	E90550	conserved hypochet
40	33	64.7	339	2	S33560	hypothetical prote
41	33	64.7	340	2	C81596	conserved hypochet
42	33	64.7	340	2	D86552	CT391 hypothetical
43	33	64.7	340	2	G72072	ct391 hypothetical
44	33	64.7	380	2	S34964	rfc protein - Shig
45	33	64.7	409	2	T31662	hypothetical prote

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N/Contents: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 09-Jul-2004
C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
A/Title: Differential usage of three exons generates at least five different mRNAs enco
A/Reference number: A46546; MID:88061067; PMID:2824653
A/Accession: A46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.6/2
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-32,99-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.111 and clone LCA.260
A/Accession: C46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-31,193-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.1
R/Ralpin, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A/Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A/Reference number: A91066; MID:87275816; PMID:2956090
A/Accession: A29449
A/Molecule type: mRNA
A/Residues: 1-31,193-649,'L',651-869,'G',871-872,'A',874-1206,'P',1208-1304 <RAL>
A/Cross-references: GB:Y00062; MID:934275; PIDN:CAA68269.1; PID:934276
A/Experimental source: clones pHLC-1 and lambdaHLCL1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Teal, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A/Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative ;
A/Reference number: I57658; MID:9006468; PMID:2531281
A/Accession: I57658
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:g187020; PIDN:AAA59497.1; PID:g553521
C:Genetics:
A:Gene: GDB:PTPRC; CD45
A:Cross-references: GDB:119768; OMIM:151460
A:Map position: 1q31-1q32
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monester hyd
F:594-123/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:575-899/Domain: protein-tyrosine-phosphatase homology <PTP>
F:551/Active site: Cys (phosphocysteine intermediate) #status predicted
F:557/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 51; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNHFT 9
DB 369 ILYNNHFT 377

RESULT 2
F:NB0
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A26452; B21165; A23292
R:Skorsteingard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
Eur. J. Biochem. 161, 441-453, 1986
A:Title: Complete primary structure of bovine plasma fibronectin.
A:Reference number: A26452; MUID:87054047; PMID:3780752
A:Accession: A26452
A:Molecule type: protein
A:Residues: 1-2265 <SKO>
A:Cross-references: UNIPROT:P07589
R:Kornblith, A.R.; Vide-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A:Reference number: A21165; MUID:83221567; PMID:6304699
A:Accession: B21165
A:Molecule type: mRNA
A:Residues: 2170-2265 <KOR>
A:Cross-references: GB:X00800; NID:g163055; PIDN:AAA30521.2; PID:g5713323
R:Petersen, T.E.; Thogersen, H.C.; Skorsteingard, K.; Vide-Pedersen, K.; Sahl, P.; Sottrup
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
A:Title: Partial primary structure of bovine plasma fibronectin: three types of internal
A:Reference number: A23292; MUID:83117805; PMID:6218503
A:Accession: A23292
A:Molecule type: protein
A:Residues: 1-16, 'C', 18-20, 'S', 22-43, 44-463, 1367-1517, 1567-1673, 2062-2176, 'N', 2178-226
C:Comment: Cys-1201 and Cys-2015 have free sulphydryl groups.
C:Comment: The plasma fibronectin molecule consists of two chains, which are connected b
C:Comment: Fibronectins bind cell surfaces and various compounds including collagen, fib
aling, and maintenance of cell shape.
C:Comment: Plasma fibronectin is synthesized by hepatocytes.
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II rep
C:Keywords: acute phase; alternative splicing; collagen binding; duplication; extracellular
F:2174/Domain: fibrin and heparin binding <FBR>
F:2156/Domain: fibronectin type I repeat homology <1F1>
F:66-104/Domain: fibronectin type I repeat homology <1F2>
F:110-148/Domain: fibronectin type I repeat homology <1F3>
F:155-194/Domain: fibronectin type I repeat homology <1F4>
F:200-239/Domain: fibronectin type I repeat homology <1F5>
F:277-577/Domain: collagen binding <CBR>
F:777-311/Domain: fibronectin type I repeat homology <1F8>
F:329-370/Domain: fibronectin type II repeat homology <2F1>
F:389-430/Domain: fibronectin type II repeat homology <2F2>
F:439-477/Domain: fibronectin type I repeat homology <1F7>
F:487-524/Domain: fibronectin type I repeat homology <1F8>
F:530-568/Domain: fibronectin type I repeat homology <1F9>
F:578-661/Domain: fibronectin type II repeat homology <FN3A>
F:588-770/Domain: fibronectin type II repeat homology <FN3B>
F:779-860/Domain: fibronectin type III repeat homology <FN3C>

F:875-957/Domain: fibronectin type III repeat homology <FN3D>
F:965-1046/Domain: fibronectin type III repeat homology <FN3E>
F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>
F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>
F:1233-1318/Domain: fibronectin type III repeat homology <FN3H>
F:1328-1404/Domain: fibronectin type III repeat homology <FN3I>
F:1410-1507/Domain: cell attachment <CAD>
F:1416-1502/Domain: cell attachment <CAD>
F:1493-1495/Region: cell attachment (R-G-D) motif
F:1510-1592/Region: cell attachment (R-G-D) motif
F:1500-1870/Domain: heparin binding <HB2>
F:1600-1682/Domain: fibronectin type III repeat homology <FN3L>
F:1692-1773/Domain: fibronectin type III repeat homology <FN3M>
F:1781-1863/Domain: fibronectin type III repeat homology <FN3N>
F:1970-1972/Region: cell attachment (R-G-D) motif
F:1982-2062/Domain: fibronectin type III repeat homology <FN3O>
F:1985-2216/Domain: fibrin binding <FBR>
F:2085-2124/Domain: fibronectin type I repeat homology <1F10>
F:2130-2167/Domain: fibronectin type I repeat homology <1F11>
F:2174-2209/Domain: fibronectin type I repeat homology <1F12>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Cross-link: isopeptide (Gln) (interchain to lys N6-amino of fibrin) #status experime
F:21-47, 45-56, 66-94, 92-104, 110-138, 136-148, 155-184, 182-194, 200-225, 227-239, 277-304, 302-3
7, 2155-2167, 2174-2200, 2198-2209/Disulfide bonds: #status predicted
F:399, 497, 511, 846, 976, 1213, 1987/Binding site: carbohydrate (Asn) (covalent) #status expe
F:1205, 1692/Binding site: carbohydrate (Thr) (covalent) #status absent
F:1943, 1944/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:2246/Disulfide bonds: interchain (to 2250) #status predicted
F:2250/Disulfide bonds: interchain (to 2246) #status predicted
F:2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 76.5%; Score 39; DB 1; Length 2265;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ILYNNHFT 9
DB 394 ILYNNHFT 401

RESULT 3
F:NB0
C:Species: Homo sapiens (man)
C:Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A:Reference number: A26460; MUID:87175578; PMID:3031656
A:Accession: A26460
A:Molecule type: DNA
A:Residues: 1-49 <DEA>
A:Cross-references: UNIPROT:P0751; UNIPROT:Q14337; GB:M15801; NID:g182686; PIDN:AAA5337
R:Oldberg, A.; Ruoslahti, E.
J. Biol. Chem. 261, 2113-2116, 1986
A:Title: Evolution of the fibronectin gene.
A:Reference number: A26284; MUID:86111501; PMID:3003095
A:Accession: A26284
A:Molecule type: DNA
A:Residues: 1447-1540 <OLD>
A:Cross-references: GB:M12549; NID:g182688
A:Note: the authors translated the codon TTC for residue 1494 as Glu
R:Paolletta, G.; Reichliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A:Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S03917
A:Molecule type: DNA
A:Residues: 1594-1767, 'V', 1769-1783 <PAO>
A:Cross-references: EMBL:X07718; NID:g11402
A:Note: the authors translated the codon AAC for residue 1631 as Asp

R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A;Title: Donor and acceptor splice signals within an exon of the human fibronectin gene;
A;Reference number: A24854; MUID:87030929; PMID:3770201
A;Accession: A24854
A;Molecule type: DNA
A;Residues: 1992-2147 <VIB>
A;Cross-references: GB:X04530; NID:g31436
R;Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986
A;Title: Human fibronectin is synthesized as a pre-propolypeptide.
A;Reference number: A24476; MUID:87030890; PMID:3770189
A;Accession: A24476
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-14, 'Q', 16-38 <GUT>
R;Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
A;Title: Primary structure of human fibronectin: differential splicing may generate at l
A;Reference number: A91008; MUID:85284965; PMID:2992939
A;Accession: A91008
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 32-1344, 1346-2080, 2112-2386 <KOR>
A;Cross-references: GB:X02761
R;Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A;Reference number: A93529; MUID:84272258; PMID:6462939
A;Accession: A93529
A;Molecule type: mRNA
A;Residues: 973-2080, 2112-2386 <KO2>
A;Cross-references: GB:X00739
R;Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A;Reference number: A21011; MUID:83290929; PMID:6688418
A;Accession: A21011
A;Molecule type: mRNA
A;Residues: 1434-1537 <OI2>
A;Cross-references: GB:X0055; NID:g182680; PIDN:AAA52459.1; PID:g182683
R;Bernard, M.P.; Kolbe, M.; Well, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A;Reference number: A90495; MUID:85280403; PMID:2952573
A;Accession: A90495
A;Molecule type: mRNA
A;Residues: 1594-2386 <BER>
A;Cross-references: GB:M10905; NID:g182696; PIDN:AAA52462.1; PID:g182697
R;Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A;Reference number: A22245; MUID:85231203; PMID:2989004
A;Accession: A22245
A;Molecule type: mRNA
A;Residues: 1948-2067 <UME>
A;Cross-references: GB:M27569; NID:g182705; PIDN:AAA52465.1; PID:g182706
A;Accession: B22245
A;Molecule type: mRNA
A;Residues: 1975-1991, 2017-2039 <UM2>
A;Cross-references: GB:M27590
R;Sekiuchi, K.; Kloe, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A;Title: Human liver fibronectin complementary DNAs: identification of two different me
A;Reference number: 152394; MUID:87026578; PMID:3021206
A;Accession: 165273
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: mRNA
A;Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>
A;Cross-references: GB:M14060; NID:g182701; PIDN:AAA52464.1; PID:g182704
R;Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectins

A;Reference number: A21165; MUID:83221567; PMID:6304699
A;Accession: A21165
A;Molecule type: mRNA
A;Residues: 2291-2386 <KO3>
A;Cross-references: GB:X00799; NID:g182681; PIDN:AAA52460.1; PID:g182684
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A92398; MUID:84032463; PMID:6630202
A;Accession: A92398
A;Molecule type: protein
A;Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
R;Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A;Title: Further characterization of the binding of fibronectin to gelatin reveals the
A;Reference number: S34791; MUID:93312001; PMID:8323285
A;Accession: S34791
A;Molecule type: protein
A;Residues: 291-300, 551-560 <GAR2>
R;Giffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
A;Accession: A60904
A;Molecule type: protein
A;Residues: 293-301 <GAR>
R;Calaycay, J.; Fandé, H.; Lee, T.; Borai, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12336-12341, 1985
A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human p
A;Reference number: A23901; MUID:86008277; PMID:3900070
A;Accession: A23901
A;Molecule type: protein
A;Residues: 616-677, 'Q', 679-703, 'PT', <CAL>
R;Pierchbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A;Title: The cell attachment domain of fibronectin. Determination of the primary structu
A;Reference number: A92386; MUID:82265604; PMID:7050098
A;Accession: A92386
A;Molecule type: protein
A;Residues: 1441-1548 <PIE>
A;Note: residues 1524-1527 are responsible for the cell-binding activity
R;Garcia-Pardo, A.; Rosagnolo, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa do
A;Reference number: A32517; MUID:87241275; PMID:3593230
A;Accession: A32517
A;Molecule type: protein
A;Residues: 1589-1630, 'T', 1722-2058 <GAR3>
R;Tresselt, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pan
Biochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the
A;Reference number: S14357; MUID:91190085; PMID:2012601
A;Accession: S14357
A;Molecule type: protein
A;Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TR3>
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-da
A;Reference number: A23891; MUID:85261459; PMID:4019516
A;Accession: A23891
A;Molecule type: protein
A;Residues: 2071-2080, 2112-2356 <GAR4>
C;Comment: The extra domain and connecting strand 3 are subject to developmental and ti
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins
action, and transformation.
C;Genetics:
A;Gene: GDB:FNI
A;Cross-references: GDB:119135; OMIM:135600
A;Map position: 2q34-2q34
A;Intons: 49/3, 1266/1, 1357/1, 1447/1, 1487/1, 1541/1, 1631/1, 1721/1, 1991/1, 2145/1
C;Superfamily: fibronectin, fibronectin type I repeat homology; fibronectin type II rep
C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplica
F;1-26/Domain: signal sequence #status predicted <SIG>

F/27-31/Domain: propeptide #status predicted <PRO>
 F/32-2386/Product: fibronectin #status experimental <MAT>
 F/32-272/Domain: fibrin and heparin binding <FRH>
 F/32-87/Domain: fibronectin type I repeat homology <1F1>
 F/37-135/Domain: fibronectin type I repeat homology <1F2>
 F/41-179/Domain: fibronectin type I repeat homology <1F3>
 F/186-225/Domain: fibronectin type I repeat homology <1F4>
 F/231-270/Domain: fibronectin type I repeat homology <1F5>
 F/308-608/Domain: collagen binding <CBR>
 F/308-342/Domain: fibronectin type I repeat homology <1F6>
 F/360-401/Domain: fibronectin type II repeat homology <2F1>
 F/420-461/Domain: fibronectin type II repeat homology <2F2>
 F/470-508/Domain: fibronectin type I repeat homology <1F7>
 F/518-555/Domain: fibronectin type I repeat homology <1F8>
 F/561-599/Domain: fibronectin type I repeat homology <1F9>
 F/609-692/Domain: fibronectin type III repeat homology <3FA>
 F/616-706/Domain: heparin binding <HPB>
 F/719-801/Domain: fibronectin type III repeat homology <3FB>
 F/810-891/Domain: fibronectin type III repeat homology <3FC>
 F/906-988/Domain: fibronectin type III repeat homology <3FD>
 F/996-1077/Domain: fibronectin type III repeat homology <3FE>
 F/1086-1164/Domain: fibronectin type III repeat homology <3FF>
 F/1173-1258/Domain: fibronectin type III repeat homology <3FG>
 F/1266-1349/Domain: fibronectin type III repeat homology <3FH>

Query Match 76.5%; Score 39; DB 1; Length 2386;
 Best Local Similarity 75.0%; Pred. No. 79;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYNNHKT 9
 Db 425 LYNNHKT 432

RESULT 4
 S4544
 BEM1 protein-binding protein BOB1 - Yeast (Saccharomyces cerevisiae)
 N/Alternate names: protein YBL0717; protein YBL085W
 C/Species: Saccharomyces cerevisiae
 C/Date: 09-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C/Accession: S45444; S45421; S45826; S59218
 R/Bender, A.; Bender, L.; Kokojan, V.
 submitted to the EMBL Data Library, April 1994
 A/Description: Yeast Bob1p (Bem1p-binding protein) binds to the SH3 domain-containing pr
 A/Reference number: S45444
 A/Accession: S45444
 A/Molecule type: DNA
 A/Residues: 1-980 <BEN>
 A/Cross-references: UNIPROT:P38041; EMBL:L31406; NID:9829041; PIDN:AB08439.1; PID:94664
 R/Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
 submitted to the EMBL Data Library, May 1994
 A/Description: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces ce
 A/Reference number: S45387
 A/Accession: S45387
 A/Reference number: S45421
 A/Molecule type: DNA
 A/Residues: 1-980 <OBE>
 A/Cross-references: EMBL:X79489; NID:9496661; PIDN:CAA56021.1; PID:9496694
 R/Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
 submitted to the Protein Sequence Database, August 1994
 A/Reference number: S45816
 A/Accession: S45826
 A/Molecule type: DNA
 A/Residues: 1-980 <DOM>
 A/Cross-references: EMBL:Z35846; NID:9536137; PIDN:CAA84906.1; PID:9536138; GSPDB:GN0000
 R/Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
 Yeast 11, 1103-1112, 1995
 A/Title: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevis
 A/Reference number: S59184; MUID:96076635; PMID:7502586
 A/Accession: S59218
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-980 <DBW>
 A/Cross-references: EMBL:X79489; NID:9496661; PIDN:CAA56021.1; PID:9496694

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
 C/Genetics: SGD:BOB1; BOB1; MIPS:YBL085W
 A/Genes: SGD:BOB1; BOB1; MIPS:YBL085W
 A/Cross-references: MIPS:YBL085W; SGD:S0000181
 A/Map position: 2L
 C/Superfamily: BEM1 protein-binding protein BOB1, pleckstrin repeat homology; SAM homolo
 F/20-72/Domain: SH3 homology <SH3>
 F/225-291/Domain: SAM homology <SAM>

Query Match 74.5%; Score 38; DB 1; Length 980;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILYNNHKT 9
 Db 515 ILYNNHKT 523

RESULT 5
 HUNVAV
 helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus
 C/Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C/Accession: A38499; H72861
 R/Lu, A.; Carstens, E.B.
 Virology 181, 336-347, 1991
 A/Title: Nucleotide sequence of a gene essential for viral DNA replication in the baculo
 A/Reference number: A38499; MUID:91134998; PMID:1994581
 A/Accession: A38499
 A/Molecule type: DNA
 A/Residues: 1-1221 <LUN>
 A/Cross-references: UNIPROT:P24307; EMBL:M57687
 R/Myers, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
 Virology 202, 586-605, 1994
 A/Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
 A/Reference number: A72850; MUID:94303173; PMID:8030224
 A/Accession: H72861
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-125, 'F', 127-1148, 'F', 1150-1221 <AYR>
 A/Cross-references: GB:L22858; NID:9510708; PIDN:AAA66725.1; PID:9559164
 C/Genetics:
 A/Genes: Ac-helicase
 C/Superfamily: AcMNPV helicase
 C/Keywords: Arp. DNA binding; DNA repair; DNA replication; hydrolase; nucleotide binding
 F/917-924/Region: nucleotide-binding motif A (P-loop)

Query Match 72.5%; Score 37; DB 1; Length 1221;
 Best Local Similarity 75.0%; Pred. No. 92;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILYNNHKT 8
 Db 1029 ILYNNHKT 1036

RESULT 6
 T41835
 DNA helicase P143 orf95 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
 C/Species: Bombyx mori nuclear polyhedrosis virus, BmsNPV
 A/Variety: isolate T3
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T41835
 R/Gomi, S.; Majima, K.; Maeda, S.
 J. Gen. Virol. 80, 1323-1337, 1999
 A/Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
 A/Reference number: Z22020; MUID:99281911; PMID:10355780
 A/Accession: T41835
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-1222 <KAW>
 A/Cross-references: UNIPROT:O92455; EMBL:I33180; NID:93745835; PIDN:AAC63764.1; PID:9374
 A/Experimental source: isolate T3


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C:Superfamily: AcNMPV helicase

Query Match      72.5%; Score 37; DB 2; Length 1222;
Best Local Similarity 75.0%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILVNNHKE 8
    |||||
Db 1030 LVYNNHKE 1037

RESULT 7
G86851
pennase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86851
R:Bolotin, A.; Winkler, P.; Mager, S.; Jallou, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-371 <STO>
A:Cross-references: UNIPROT:Q9CEM2; GB:AE005176; PID:g12724842; PIDN:AAK05913.1; GSPDB:
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ysa1B

Query Match      70.6%; Score 36; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNNHK 7
    |||||
Db 357 LVNNHK 362

RESULT 8
F95179
aspartate aminotransferase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95179
R:Jettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: F95179
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <KIR>
A:Cross-references: UNIPROT:Q97PQ9; GB:AE005672; PIDN:AAK75631.1; PID:g14973033; GSPDB:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI544
C:Superfamily: aspartate transaminase

Query Match      70.6%; Score 36; DB 2; Length 395;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILVNNHKE 9
    ::|||
Db 209 LVYNNHKE 217

RESULT 9
F98046

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aspartate transaminase (EC 2.6.1.1) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: F98046
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98046
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <KIR>
A:Cross-references: UNIPROT:Q8DP26; GB:AE007317; PIDN:AAI0203.1; PID:g15459050; GSPDB:
C:Genetics:
A:Gene: aspB
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match      70.6%; Score 36; DB 2; Length 395;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILVNNHKE 9
    ::|||
Db 209 LVYNNHKE 217

RESULT 10
S70398
zona pellucida glycoprotein A - cat
C:Species: Felis silvestris catus (domestic cat)
C>Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: S70398
R:Harris, J.D.; Hibler, D.W.; Fontenot, G.K.; Hsu, K.T.; Yurewicz, E.C.; Sacco, A.G.
DNA Seq. 4, 361-393, 1994
A>Title: Cloning and characterization of zona pellucida genes and cDNAs from a variety
A:Reference number: S70396; MUID:95143578; PMID:7841460
A:Accession: S70398
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-716 <HAR>
A:Cross-references: UNIPROT:P47984; EMBL:U05776; NID:9458268; PIDN:AAA74388.1; PID:9458
C:Superfamily: sperm-binding glycoprotein P2; ZP domain homology
F:370-630/Domain: ZP domain homology <ZPH>

Query Match      70.6%; Score 36; DB 2; Length 716;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILVNNHKE 9
    |||||
Db 208 ILFDNHKIT 216

RESULT 11
A88429
protein C28A5.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A88429
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_el.
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A:Accession: A88429
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1218 <STO>

```

A:Cross-references: UNIPROT:Q18270; GB:chr_III; PIDN:CAAB3597.1; PID:G3874514; GSPDB:GN0
C:Genetics:
A:Gene: C28A5.2
A:/Map position: 3
C:/Superfamily: Caenorhabditis elegans C28A5.1 protein (clone C28A5)

Query Match
Best Local Similarity 70.6%; Score 36; DB 2; Length 1218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ILYNNH 9
DB 1139 NNHKT 1144

RESULT 12
F86380
protein F5A9.10 [imported] - Arabidopsis thaliana
C:/Species: Arabidopsis thaliana (mouse-ear cress)
C:/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:/Accession: F86380
R:/theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
Nansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Linn, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, I.; Rowley, D.; Sakano, H.
A:/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:/Reference number: A86141; MUID:21016719; PMID:11130712
A:/Accession: F86380
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-149 <STO>
A:/Cross-references: UNIPROT:Q9FXK6; GB:AB005172; NID:G9945074; PIDN:AAG03111.1; GSPDB:GN
C:/Genetics:
A:/Gene: F5A9.10
A:/Map position: 1

Query Match
Best Local Similarity 68.6%; Score 35; DB 2; Length 149;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNH 6
DB 44 ILYNNH 49

RESULT 13
H86380
Protein F5A9.6 [imported] - Arabidopsis thaliana
C:/Species: Arabidopsis thaliana (mouse-ear cress)
C:/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:/Accession: H86380; C86380
R:/theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
Nansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Linn, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:/Reference number: A86141; MUID:21016719; PMID:11130712
A:/Accession: H86380

A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-216 <STO>
A:/Cross-references: UNIPROT:Q9FEF7; GB:AB005172; NID:G9945072; PIDN:AAG03109.1; GSPDB:GN
A:/Accession: C86380

A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-216 <STO>
A:/Cross-references: GB:AB005172; NID:G9945078; PIDN:AAG03115.1; GSPDB:GN00141
C:/Genetics:
A:/Gene: F5A9.6; F5A9.16
A:/Map position: 1

Query Match
Best Local Similarity 68.6%; Score 35; DB 2; Length 216;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILYNNH 6
DB 44 ILYNNH 49

RESULT 14
A84041
suifate ABC transporter (permease) cyw [imported] - Bacillus halodurans (strain C-125)
C:/Species: Bacillus halodurans
C:/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:/Accession: A84041
R:/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:/Reference number: A83650; MUID:20512582; PMID:11058132
A:/Accession: A84041
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-287 <STO>
A:/Cross-references: UNIPROT:Q9K877; GB:AP001517; GB:BA000004; NID:G10175500; PIDN:BA068
C:/Genetics:
A:/Gene: cyw
C:/Superfamily: maltose transport protein malG

Query Match
Best Local Similarity 68.6%; Score 35; DB 2; Length 287;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILYNNHKT 9
DB 245 ILYNNHKT 253

RESULT 15
A90097
hypothetical protein orf313 [imported] - Guillardia theta nucleomorph
C:/Species: nucleomorph Guillardia theta
A:/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:/Accession: A90097
R:/Poullas, S.; Zaurer, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A:/Title: The highly reduced genome of an enslaved algal nucleus.
A:/Reference number: A90082; MUID:11323671; PMID:11323671
A:/Accession: A90097

A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-313 <DOU>
A:/Cross-references: UNIPROT:Q9BRP3; GB:AF165818; NID:G13794529; PIDN:AAK39904.1; GSPDB:G
C:/Genetics:
A:/Gene: orf313
A:/Map position: 1
A:/genome: nucleomorph
C:/Keywords: nucleomorph

Query Match
Best Local Similarity 68.6%; Score 35; DB 2; Length 313;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ILYNNHKT 8

Tue May 3 08:17:40 2005

us-10-003-983c-11.rpr

Page 7

Db : |||| |
214 IYNNHNF 220

Search completed: May 3, 2005, 06:16:51
Job time : 31.6892 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-12

Perfect score: 50

Sequence: 1 ILPDYDNRV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: Dir1: *
3: Dir2: *
4: Dir3: *
5: Dir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	50	100.0	1273	1	TDRILT	leukocyte common a
2	50	100.0	1291	1	A28334	protein-tyrosine-p
3	50	100.0	1304	1	A46546	leukocyte common a
4	46	92.0	711	2	T23738	probable protein-c
5	45	90.0	1200	2	T43148	protein-tyrosine-p
6	45	90.0	1237	2	A54080	protein-tyrosine-p
7	44	88.0	680	2	JC8052	protein-tyrosine-p
8	44	88.0	699	2	UC6132	protein-tyrosine-p
9	44	88.0	700	1	S12053	protein-tyrosine-p
10	41	82.0	405	2	S68250	protein-tyrosine-p
11	41	82.0	405	2	I49372	protein-tyrosine-p
12	41	82.0	1187	1	A53661	protein-tyrosine-p
13	41	82.0	1188	1	A57064	protein-tyrosine-p
14	41	82.0	1216	2	S60613	protein-tyrosine-p
15	41	82.0	1226	2	JC7503	protein-tyrosine-p
16	40	80.0	183	2	F72676	hypothetical prote
17	40	80.0	796	1	JC1285	protein-tyrosine-p
18	40	80.0	802	1	A36055	protein-tyrosine-p
19	40	80.0	829	1	A47373	protein-tyrosine-p
20	40	80.0	832	2	JC8051	protein-tyrosine-p
21	39	78.0	841	2	A43254	protein-tyrosine-p
22	39	78.0	1118	1	A49724	protein-tyrosine-p
23	39	78.0	1462	1	B36182	protein-tyrosine-p
24	39	78.0	1711	1	A55148	protein-tyrosine-p
25	38	76.0	363	2	B86248	protein T2318.11
26	38	76.0	990	2	T14756	hypothetical prote
27	38	76.0	1494	2	T14355	protein-tyrosine-p
28	38	76.0	1583	2	S59644	sister chromatid c
29	37	74.0	161	2	F70916	hypothetical prote

30	37	74.0	218	2	F86896	hypothetical prote
31	37	74.0	316	2	T42949	hypothetical prote
32	37	74.0	337	2	T25210	hypothetical prote
33	37	74.0	431	2	E89829	conserved hypochet
34	37	74.0	771	2	T49160	hypothetical prote
35	37	74.0	1088	2	S39261	VPI protein - porc
36	36	72.0	382	1	S48748	protein-tyrosine-p
37	36	72.0	395	2	T20724	hypothetical prote
38	36	72.0	449	2	B69398	hypothetical prote
39	36	72.0	583	2	S17671	protein-tyrosine-p
40	36	72.0	595	1	A44390	protein-tyrosine-p
41	36	72.0	595	1	S20825	protein-tyrosine-p
42	36	72.0	750	2	S67100	protein-tyrosine-p
43	36	72.0	773	1	JH0609	protein-tyrosine-p
44	36	72.0	775	2	S55345	protein-tyrosine-p
45	36	72.0	780	1	JC1368	protein-tyrosine-p

ALIGNMENTS

RESULT 1
TDRILT
leukocyte common antigen precursor, splice form 4 - rat
N:Alternate names: CD45; L-CA; Ly-5; T200
N:Contents: leukocyte common antigen precursor, splice form 1; leukocyte common antigen
.1.3.48)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Dec-1986 #sequence revision 05-May-2000 #ext change 09-Jul-2004
C:Accession: A29450; B29450; C29450; D29450; A60241; A02247; I54569; A45854
R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
EMBL J. 6, 1259-1264, 1987
A>Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) i.
A:Reference number: A91067; MUID:87275817; PMID:2440674
A:Accession: A29450
A:Molecule type: mRNA
A:Residues: 20-30,163-218 <BAR1>
A:Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:g205153; GB:Y00065; GB:K0
A:Experimental source: splice form 1
A>Note: the translation in GenBank entry RATTLCAL, PIDN:AAA41518.1, PID:g205154, release
A:Molecule type: B29450
A:Accession: B29450
A:Molecule type: mRNA
A:Residues: 19-30,122-218 <BAR2>
A:Cross-references: GB:M25821; GB:M24611; NID:g205155; PIDN:AAA41519.1; PID:g205156; GB
A:Experimental source: splice form 2
A:Accession: C29450
A:Molecule type: C29450
A:Residues: 20-30,73-121,163-218 <BAR3>
A:Cross-references: GB:M25822; GB:M24611; NID:g205157; PIDN:AAA41520.1; PID:g205158; GB
A:Experimental source: splice form 3
A:Accession: D29450
A:Molecule type: mRNA
A:Residues: 28-218 <BAR4>
A:Cross-references: GB:M25823; GB:M24611; NID:g205159; PIDN:AAA41521.1; PID:g205160; GB
A:Experimental source: splice form 4
A>Note: the sequence in GenBank entry RATTLCALV, release 113.0, has the codon AGG for 56
R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
Adv. Exp. Med. Biol. 237, 3-7, 1988
A>Title: The leukocyte-common antigen (L-CA) family.
A:Reference number: A60241; MUID:89319817; PMID:2878200
A:Accession: A60241
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-161 <BAR5>
R:Thomas, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
Cell 41, 83-93, 1985
A>Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans c
A:Reference number: A02247; MUID:85201651; PMID:3158393
A:Accession: A02247
A:Molecule type: mRNA
A:Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>
A:Cross-references: GB:M10072; GB:M81859; NID:g205140; PIDN:AAA41513.1; PID:g205143
A>Note: the translation in GenBank entry RATTLCAL, release 113.0, begins at non-initiator

A>Note: parts of this sequence were determined by protein sequencing
 R:McCall, M.N.; Shotton, D.M.; Barclay, A.N.
 Immunology 76, 310-317, 1992
 A>Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
 A:Reference number: 154569; PMID:92340120; PMID:1378817
 A:Accession: 154569
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-30, 163-180 <MC>
 A:Cross-references: GB:S40716; NID:g252015; PIDN:AA22648.1; PID:g252016
 R:Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A>Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are deriv
 A:Reference number: A45854; PMID:89233293; PMID:252368
 A:Accession: A45854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JAC>
 A:Cross-references: GB:M18347; GB:M18348; GB:M18349
 C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; phosphoric
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1273/Product: leukocyte common antigen precursor, splice form 4 #status predicted <
 F:24-546/Domain: extracellular #status predicted <EXT>
 F:24-30, 122-1273/Product: leukocyte common antigen, splice form 2 #status predicted <MAT
 F:24-30, 122-1273/Product: leukocyte common antigen, splice form 1 #status predicted <MAT
 F:24-30, 163-1273/Product: leukocyte common antigen, splice form 3 #status predicted
 F:547-568/Domain: transmembrane #status predicted <TM>
 F:565-1206/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:569-870/Domain: intracellular #status predicted <INT>
 F:569-870/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:622, 142, 153, 164, 178, 200, 245, 271, 282, 327, 371, 374, 502/Binding site: carbohydrate (Aen) (C
 F:822/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:828/Binding site: substrate phosphate (Arg) #status predicted
 F:1063/Binding site: carbohydrate (Aen) (covalent) #status absent

Query Match 100.0%; Score 50; DB 1; Length 1273;
 Best local Similarity 100.0%; Pred. No. 0.36;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPEYDNRV 9
 |||||
 Db 655 ILPEYDNRV 663

RESULT 2
 A28334
 protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
 N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
 N:Contains: protein-tyrosine-phosphatase (T-cell variant)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #ext. change 09-Jul-2004
 C:Accession: A28334; A29381; A61180; A60933; A35522; A29075; I54450; A28335; A23329; I57
 R:Thomas, M.L.; Reynolds, P.J.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
 A>Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
 A:Reference number: A28334; PMID:87260986; PMID:255416
 A:Accession: A28334
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1291 <THO>
 A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
 A>Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
 A:Reference number: A29381; PMID:86313686; PMID:2944116
 A:Accession: A29381
 A:Molecule type: mRNA
 A:Residues: 1-30, 170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, 'A:
 A:Cross-references: GB:M14342; NID:g198914; PIDN:AAA39458.1; PID:g198915
 R:Li, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A>Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by

A:Reference number: A61180; PMID:92032882; PMID:1932742
 A:Accession: A61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 730-838 <YIA>
 R:Gonzalez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
 Immunogenetics 25, 263-266, 1987
 A>Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
 A:Reference number: A60933; PMID:87192931; PMID:3570377
 A:Accession: A60933
 A:Molecule type: protein
 A:Residues: 'R', 289-298; 329, 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375; 595-608; 638-649; 669-
 R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
 J. Biol. Chem. 264, 6220-6229, 1989
 A>Title: Sequence conservation in potential regulatory regions of the mouse and human le
 A:Reference number: A33522; PMID:89197920; PMID:2522930
 A:Accession: A33522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <JOH>
 A:Cross-references: GB:M22456; NID:g198755; PIDN:AA46374.1; PID:g554185; GB:J04640; GB:
 R:Raschke, W.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
 A>Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
 A:Reference number: A29075; PMID:87092355; PMID:2946186
 A:Accession: A29075
 A:Molecule type: mRNA
 A:Residues: 961-1291 <RAS>
 A:Cross-references: GB:M15174; NID:g201105; PIDN:AAA40161.1; PID:g201106
 R:Tung, J.
 Immunogenetics 28, 271-277, 1988
 A>Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
 A:Reference number: I54450; PMID:8830145; PMID:3417340
 A:Accession: I54450
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 32-73 <RES>
 A:Cross-references: GB:M23241; NID:g340850; PIDN:AAA39460.1; PID:g548174
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A>Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishin
 A:Reference number: A28335; PMID:87260987; PMID:3037546
 A:Accession: A28335
 A:Molecule type: mRNA
 A:Residues: 1-30, 74-226 <SA2>
 A:Cross-references: GB:M14342
 R:Shen, F.W.; Saga, Y.; Altman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
 A:Reference number: A23329; PMID:86042665; PMID:3864163
 A:Accession: A23329
 A:Molecule type: mRNA
 A:Residues: 10-30, 170-263 <SHR>
 A:Cross-references: GB:M11934; NID:g198919; PIDN:AAA39461.1; PID:g198920
 R:Saga, Y.; Tung, J.
 Mol. Cell. Biol. 8, 4889-4895, 1988
 A>Title: Organization of the Ly-5 Gene.
 A:Reference number: I57644; PMID:89096862; PMID:3211131
 A:Accession: I57644
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 'MT', 1-22 <RE2>
 A:Cross-references: GB:M23354; NID:g340890; PIDN:AAA39462.1; PID:g554192
 C:Genetics:
 A:Gene: Ly-5
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MAT
 F:24-664/Domain: extracellular #status predicted <EXT>
 F:24-30, 170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicte
 F:565-586/Domain: transmembrane #status predicted <TM>
 F:583-1223/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:587-1291/Domain: intracellular #status predicted <INT>

F:664-888/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: c
 F:840/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:846/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 50; DB 1; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPDYNNRV 9
 Db 673 ILPDYNNRV 681

RESULT 3

A46546
 Leukocyte common antigen long splice form precursor - human
 N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprotein
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A46546; B46546; A29449; B29449; I57658
 R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Salto, H.
 J. Exp. Med. 166, 1548-1566, 1987
 A/Title: Differential usage of three exons generates at least five different mRNAs encod
 A/Reference number: A46546; MUID:88061067; PMID:2824653
 A/Accession: A46546
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1304 <STR>
 A/Cross-references: UNIPROT:P08575; GB:Y00638
 A/Experimental source: clone LCA.6/2
 A/Accession: B46546
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-32, 99-264 <STR>
 A/Cross-references: GB:Y00638
 A/Experimental source: clone LCA.111 and clone LCA.260
 A/Accession: C46546
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-31, 193-264 <STR>
 A/Cross-references: GB:Y00638
 A/Experimental source: clone LCA.1
 R/Kalish, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
 EMBO J. 6, 1251-1257, 1987
 A/Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
 A/Reference number: A91066; MUID:87275816; PMID:2956090
 A/Accession: A29449
 A/Molecule type: mRNA
 A/Residues: 1-31, 193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
 A/Cross-references: GB:Y0062; NID:G34275; PIDN:CA68269.1; PID:G34276
 A/Experimental source: clones pLHC-1 and lambdaHMG1
 A/Accession: B29449
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 32-192 <RA2>
 A/Experimental source: clone HLC-2
 R/Teal, A.Y.; Streuli, M.; Salto, H.
 Mol. Cell. Biol. 9, 4550-4555, 1989
 A/Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative B
 A/Reference number: I57658; MUID:9006468; PMID:2531281
 A/Accession: I57658
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 146-192 <RES>
 A/Cross-references: GB:M29253; NID:G187020; PIDN:AAA59497.1; PID:G553521
 C/Genetics:
 A/Gene: GDB:PTPRC; CD45
 A/Cross-references: GDB:119768; OMIM:151460
 A/Map position: 1q31-q32
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homo
 C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 50; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPDYNNRV 9
 Db 684 ILPDYNNRV 692

RESULT 4

T23738
 Probable protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type precursor - Caenorha
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T23738; T24902
 R/Burton, J.
 Submitted to the EMBL Data Library, October 1995
 A/Reference number: Z19791
 A/Accession: T23738
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-711 <MIL>
 A/Cross-references: UNIPROT:Q21527; EMBL:Z66523; PIDN:CAA91417.1; GSPDB:GN00020; CESP:T
 A/Experimental source: clone M05D6
 R/Lighting, J.
 Submitted to the EMBL Data Library, October 1995
 A/Reference number: Z19950
 A/Accession: T24902
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-711 <M12>
 A/Cross-references: EMBL:Z66524; PIDN:CAA91422.1; GSPDB:GN00020; CESP:T13H5.1
 A/Experimental source: clone T13H5
 C/Genetics:
 A/Gene: CESP:T13H5.1
 A/Map position: 2
 A/Intons: 9/2; 25/1; 63/3; 89/3; 119/3; 165/3; 259/2; 316/3; 355/3; 389/1; 413/3; 459/
 C/Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common anti
 C/Keywords: phosphoric monoester hydrolase
 Query Match 92.0%; Score 46; DB 2; Length 711;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPDYNNRV 9
 Db 92 LPDYNNRV 99

RESULT 5

T43148
 Probable protein-tyrosine-phosphatase (EC 3.1.3.48) - horn shark
 N/Alternate names: CD45 homolog
 C/Species: Heterodontus francisci (horn shark)
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T43148
 R/Okumura, M.; Matthews, R.J.; Robb, B.; Bork, P.; Thomas, M.L.
 Submitted to the EMBL Data Library, August 1995
 A/Reference number: Z23117
 A/Accession: T43148
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1200 <OKU>
 A/Cross-references: UNIPROT:Q21054; EMBL:U14750; NID:G1304393; PID:G1335805; PIDN:AA01
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homo
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata

Query Match 90.0%; Score 45; DB 2; Length 1200;

Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9
|||||:
Db 584 ILPYDNRV 592

RESULT 6

AS4080
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C/Accession: A54080; 150592
R/Range: K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
J. Biol. Chem. 269, 14056-14063, 1994
A/Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in
A/Reference number: A54080; MID:94245724; PMID:8188686
A/Accession: A54080
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1237 <FAN>
A/Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:9510510; PID:CAA79972.1; PID:95105
C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:510-834/Domain: protein-tyrosine-phosphatase homology <PTP>
F:786/Active site: Cys (phosphocysteine intermediate) #status predicted
F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 90.0%; Score 45; DB 2; Length 1237;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9
|||||:
Db 619 ILPYDNRV 627

RESULT 7

JC8052
protein tyrosine phosphatase epsilon - Japanese medaka
C/Species: Oryzias latipes (Japanese medaka)
C/Date: 09-May-2004 #sequence_revision 09-May-2004 #text_change 09-May-2004
C/Accession: JC8052
R/Okubo, K., and Aida, K.
Biochem. Biophys. Res. Commun. 312, 531-536, 2003
A/Title: Gonadotropin-releasing hormone gene products downregulate the expression of the
A/Reference number: JC8051; PMID: 14680798
A/Accession: JC8052
A/Molecule type: mRNA
A/Residues: 1-680 <OKU>
A/Cross-references: DDBJ:AB094509
A/Experimental source: (Brain)
C/Comment: This protein is capable of both driving neuromodulatory effects of gonadotrop
ifying potassium channel.
C/Genetics:
A/Gene: pyp epsilon
C/Keywords: Brain; gonadotropin-releasing hormone; protein tyrosine phosphatase

Query Match 88.0%; Score 44; DB 2; Length 680;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9
|||||:
Db 444 ILPYDNRV 452

RESULT 8

JC6132
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - mouse
N/Alternate names: phosphotyrosine phosphatase; protein-tyrosine-phosphate phosphohydroly

C/Species: Mus musculus (house mouse)
C/Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C/Accession: JC6132

R/Schmidt, A.; Rutledge, S.J.; Endo, N.; Opas, E.E.; Tanaka, H.; Wesolowski, G.; Leu, C
Proc. Natl. Acad. Sci. U.S.A. 93, 3068-3073, 1996
A/Title: Protein-tyrosine phosphatase activity regulates osteoclast formation and functi
A/Reference number: JC6132; MID:96181534; PMID:8610169
A/Contents: bone marrow cell
A/Accession: JC6132

A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-699 <SCH>
A/Cross-references: UNIPROT:O61042; GB:U40280; NID:91373052; PID:AA802190.1; PID:913730
C/Comment: This enzyme plays an important role in osteoclast formation and function in t
hosphonate action.
C/Genetics:

A/Gene: pyp
C/Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antig
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros
F:77-697/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:158-382/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:334/Active site: Cys (phosphocysteine intermediate) #status predicted
F:340/Binding site: substrate phosphate (Arg) #status predicted
F:629/Active site: Cys (phosphocysteine intermediate) #status predicted
F:635/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.0%; Score 44; DB 2; Length 699;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9
|||||:
Db 459 ILPYDNRV 467

RESULT 9

S12053
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - human
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S12053
R/Krueger, N.X.; Screlli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A/Title: Structural diversity and evolution of human receptor-like protein tyrosine phos
A/Reference number: S12049; MID:91006018; PMID:2170109
A/Accession: S12053

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-700 <KRU>
A/Cross-references: UNIPROT:P23469; GB:X54134; NID:935791; PID:CAA38069.1; PID:935792
C/Genetics:
A/Gene: GDB:PTPRB
A/Cross-references: GDB:131385; OMIM:600926
A/Map position: 10q26-10q26
C/Function:

A/Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate
C/Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antig
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot
F:1-15/Domain: signal sequence #status predicted <Sig>
F:20-700/Product: protein-tyrosine-phosphatase, receptor type epsilon #status predicted
F:47-63/Domain: transmembrane #status predicted <TM>
F:78-698/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:159-383/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:335/Active site: Cys (phosphocysteine intermediate) #status predicted
F:341/Binding site: substrate phosphate (Arg) #status predicted
F:630/Active site: Cys (phosphocysteine intermediate) #status predicted
F:636/Binding site: substrate phosphate (Arg) #status predicted

Query Match 88.0%; Score 44; DB 1; Length 700;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9


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Db      460  |||:|||||
        |||PDNRY 468

RESULT 10
568250
protein-tyrosine-phosphatase (EC 3.1.3.48) - rabbit
M:Alternate names: phosphotyrosyl phosphatase
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: 568250
R:Mu. L.W.; Baylink, D.J.; Lau, K.H.W.
Biochem. J. 316, 515-523, 1996
A:Title: Molecular cloning and expression of a unique rabbit osteoclastic phosphotyrosyl
A:Reference number: 568250; MUID:96257745; PMID:8687395
A:Accession: 568250
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-405 <WU>
A:Cross-references: UNIPROT:Q29500; EMBL:U32587; NID:g1304388; PIDN:AB16824.1; PID:g1304
C:Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repeat
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
P:151-373/Domain: protein-tyrosine-phosphatase homology <RP1>
P:325/Active site: Cys (phosphocysteine intermediate) #status predicted
P:331/Binding site: substrate phosphate (Arg) #status predicted

Query Match      82.0%; Score 41; DB 2; Length 405;
Best Local Similarity 77.8%; Pred. No. 5.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      1  ILPYDNYR 9
        |||:|||||
        |||PDNRY 9
Db      160  ILPYDFSrv 168

RESULT 11
149372
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O - mouse (fragment)
M:Alternate names: GLEPP1; glomerular epithelial protein 1
N:Contains: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphatase
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: 149372; 149373; 149374
R:Pisley, F.J.; Lee, P.S.W.; Dominguez, M.G.; Einstein, D.B.; Stanley, E.R.
J. Biol. Chem. 270, 27339-27347, 1995
A:Title: A heteromeric protein tyrosine phosphatase, PTPphi, is regulated by CSF-1 in
A:Reference number: 149372; MUID:96070847; PMID:7592997
A:Accession: 149372
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-405 <RB5>
A:Cross-references: UNIPROT:Q60998; EMBL:U37465; NID:g1063639; PIDN:ACS2311.1; PID:g1063642
A:Accession: 149373
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-65,94-405 <RB2>
A:Cross-references: EMBL:U37466; NID:g1063641; PIDN:ACS2312.1; PID:g1063642
A:Accession: 149374
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 113-405 <RB3>
A:Cross-references: EMBL:U37467; NID:g1063643; PIDN:ACS2313.1; PID:g1063644
C:Comment: Expression of the various forms is tissue specific. GLEPP1 is expressed in kidney
cytosolic form is expressed at very low levels in macrophages.
C:Genetics:
A:Gene: PTPphi
A:Map position: 6q
C:Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repeat
C:Keywords: alternative initiators; alternative splicing; brain; cardiac muscle; glycoprotein
ne-specific phosphatase
P:1-405/Product: protein tyrosine phosphatase phi, long form #status predicted <PHL>
P:1-65,94-405/Product: protein tyrosine phosphatase phi, short form #status predicted <PHS>
P:9-33/Domain: transmembrane #status predicted <TMN>

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F.334-405/Domain: intracellular #status predicted <INT>
F.113-405/Product: protein tyrosine phosphatase phi, cytosolic form #status predicted <F.113-373/Domain: protein tyrosine phosphatase phi, cytosolic form>
F.115-373/Domain: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphat
N/Contents: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphat
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 07-Oct-1994 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C/Accession: A53661
R/Thomas, P.E.; Wharram, B.L.; Goyal, M.; Wiggins, J.E.; Holzman, L.B.; Wiggins, R.C.
J/Biol. Chem. 269, 19953-19962, 1994
A/Title: GLEPP1, a renal glomerular epithelial cell (podocyte) membrane protein-tyrosin
A/Reference number: A53661; MUID:94327545; PMID:7519601
A/Accession: A53661
A/Molecule type: mRNA
A/Residues: 1-1187 <THO>
A/Cross-references: UNIPROT:Q28613; GB:U09490; NID:9529411; PID:AAA61709.1; PID:952941
A/Note: authors translated the codon GGC for residue 1101 as Gln
C/Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repe
C/Keywords: glycoprotein; kidney; phosphoprotein; phosphoric monoester hydrolase; recep
F.1-39/Domain: signal sequence #status predicted <SIG>
F.30-816/Domain: extracellular #status predicted <EXT>
F.30-115/Domain: fibronectin type III repeat homology #status atypical <FN3A>
F.116-209/Domain: fibronectin type III repeat homology #status atypical <FN3B>
F.328-415/Domain: fibronectin type III repeat homology <FN3D>
F.451-519/Domain: fibronectin type III repeat homology <FN3E>
F.528-625/Domain: fibronectin type III repeat homology <FN3F>
F.630-713/Domain: fibronectin type III repeat homology <FN3G>
F.721-810/Domain: fibronectin type III repeat homology <FN3H>
F.811-1187/Product: protein tyrosine phosphatase phi, long form #status predicted <PHL
F.811-875,876-1187/Product: protein tyrosine phosphatase phi, short form #status predic
F.819-883/Domain: transmembrane #status predicted <TMN>
F.884-1187/Domain: intracellular #status predicted <INT>
F.901-1187/Product: protein tyrosine phosphatase phi, cytosolic form #status predicted
F.933-1155/Domain: protein-tyrosine-phosphatase homology <PTP>
F.75,154,189,201,227,277,286,333,359,460,489,699,711,732,789/Binding site: carboxylate
F.1107/Active site: Cys (phosphocysteine intermediate) #status predicted
F.1113/Binding site: substrate phosphate (Arg) #status predicted

Query Match      82.0%; Score 41; DB 2; Length 405;
Best Local Similarity 77.8%; Pred. No. 5.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILPDYNNR 9      |||||:|
Db      160  ILPDPSRV 168

RESULT 12
A53661
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O precursor - rabbit
N/Alternate names: GLEPP1; glomerular epithelial protein 1
N/Contents: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphat
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 07-Oct-1994 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C/Accession: A53661
R/Thomas, P.E.; Wharram, B.L.; Goyal, M.; Wiggins, J.E.; Holzman, L.B.; Wiggins, R.C.
J/Biol. Chem. 269, 19953-19962, 1994
A/Title: GLEPP1, a renal glomerular epithelial cell (podocyte) membrane protein-tyrosin
A/Reference number: A53661; MUID:94327545; PMID:7519601
A/Accession: A53661
A/Molecule type: mRNA
A/Residues: 1-1187 <THO>
A/Cross-references: UNIPROT:Q28613; GB:U09490; NID:9529411; PID:AAA61709.1; PID:952941
A/Note: authors translated the codon GGC for residue 1101 as Gln
C/Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repe
C/Keywords: glycoprotein; kidney; phosphoprotein; phosphoric monoester hydrolase; recep
F.1-39/Domain: signal sequence #status predicted <SIG>
F.30-816/Domain: extracellular #status predicted <EXT>
F.30-115/Domain: fibronectin type III repeat homology #status atypical <FN3A>
F.116-209/Domain: fibronectin type III repeat homology #status atypical <FN3B>
F.328-415/Domain: fibronectin type III repeat homology <FN3D>
F.451-519/Domain: fibronectin type III repeat homology <FN3E>
F.528-625/Domain: fibronectin type III repeat homology <FN3F>
F.630-713/Domain: fibronectin type III repeat homology <FN3G>
F.721-810/Domain: fibronectin type III repeat homology <FN3H>
F.811-1187/Product: protein tyrosine phosphatase phi, long form #status predicted <PHL
F.811-875,876-1187/Product: protein tyrosine phosphatase phi, short form #status predic
F.819-883/Domain: transmembrane #status predicted <TMN>
F.884-1187/Domain: intracellular #status predicted <INT>
F.901-1187/Product: protein tyrosine phosphatase phi, cytosolic form #status predicted
F.933-1155/Domain: protein-tyrosine-phosphatase homology <PTP>
F.75,154,189,201,227,277,286,333,359,460,489,699,711,732,789/Binding site: carboxylate
F.1107/Active site: Cys (phosphocysteine intermediate) #status predicted
F.1113/Binding site: substrate phosphate (Arg) #status predicted

Query Match      82.0%; Score 41; DB 1; Length 1187;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILPDYNNR 9      |||||:|
Db      942  ILPDPSRV 950

RESULT 13
A57064
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O precursor - human
N/Alternate names: GLEPP1; glomerular epithelial protein 1
N/Contents: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphat
C/Species: Homo sapiens (man)
C/Date: 03-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
C/Accession: A57064
R/Wiggins, R.C.; Wiggins, J.E.; Goyal, M.; Wharram, B.L.; Thomas, P.E.
J/Biol. Chem. 27, 174-181, 1995
A/Title: Molecular cloning of cDNAs encoding human GLEPP1, a membrane protein tyrosine p

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ne to human chromosome 12p12-p13.

A/Reference number: A57064; MUID:95394455; PMID:7665166

A/Accession: A57064

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1188 <WIG>

A/Cross-references: GB:U20489; NID:9885925; PIND:AAA82892.1; PID:9885926

A/Genetics:

A/Gene: GDB:PTPRO

A/Cross-references: GDB:454477; OMIM:600579

A/Map position: 12p13.3-12p13.1

C/Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repeat

C/Keywords: glycoprotein; kidney; phosphoprotein; phosphoric monoester hydrolase; recep

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-819/Domain: extracellular #status predicted <EXT>

F/30-109/Domain: fibronectin type III repeat homology #status atypical <FN3A>

F/116-202/Domain: fibronectin type III repeat homology #status atypical <FN3B>

F/329-409/Domain: fibronectin type III repeat homology <FN3D>

F/432-520/Domain: fibronectin type III repeat homology <FN3F>

F/529-619/Domain: fibronectin type III repeat homology <FN3G>

F/631-714/Domain: fibronectin type III repeat homology <FN3H>

F/722-804/Domain: fibronectin type III repeat homology <FN3I>

F/812-1188/Domain: protein tyrosine phosphatase phi, long form #status predicted <PHIL>

F/812-876,877-1188/Domain: protein tyrosine phosphatase phi, short form #status predicted

F/820-844/Domain: intracellular #status predicted <INT>

F/845-1188/Domain: intracellular #status predicted <INT>

F/902-1188/Domain: protein tyrosine phosphatase phi, cytosolic form #status predicted <

F/934-1156/Domain: protein-tyrosine-phosphatase homology <PTPL>

F/75,154,189,201,227,278,323,324,370,461,490,700,712,733,790/Binding site: carbohydr

F/1108/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1114/Binding site: substrate phosphate (Arg) #status predicted

Query Match 82.0%; Score 41; DB 1; Length 1188;

Best Local Similarity 77.8%; Pred. No. 17;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9

Db 943 ILPYDNRV 951

RESULT 14

S60613

Protein-tyrosine-phosphatase (EC 3.1.3.48) U2 precursor - human

C/Species: Homo sapiens (man)

C/Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S60613

R/Seimiyu, H.; Sawabe, T.; Inazawa, J.; Tsunuo, T.

Oncogene 10, 1731-1738, 1995

A/Title: Cloning, expression and chromosomal localization of a novel gene for protein ty

A/Reference number: S60613; MUID:95273089; PMID:7753550

A/Accession: S60613

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1216 <SEI>

A/Cross-references: UNIPROT:Q16827; EMBL:Z48541; NID:9963058; PIND:CAA8425.1; PID:99630

C/Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III rep

C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat

F/529-626/Domain: fibronectin type III repeat homology <3FR>

F/962-1184/Domain: protein-tyrosine-phosphatase homology <PTPL>

F/1136/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1142/Binding site: substrate phosphate (Arg) #status predicted

Query Match 82.0%; Score 41; DB 2; Length 1216;

Best Local Similarity 77.8%; Pred. No. 17;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9

Db 971 ILPYDNRV 979

RESULT 15

JC7503

Protein-tyrosine-phosphatase (EC 3.1.3.48), a receptor-type - mouse

N/Alternate names: phosphotyrosine phosphatase, a receptor-type

C/Species: Mus musculus (house mouse)

C/Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004

C/Accession: JC7503

R/Tomomori, T.; Seki, N.; Suzuki, Y.; Shimizu, T.; Nagata, H.; Konno, A.; Shirasawa, T.

Biochem. Biophys. Res. Commun. 276, 974-981, 2000

A/Title: Isolation and characterization of murine orthologue of PTP-BK.

A/Reference number: JC7503

A/Contents: Brain

A/Accession: JC7503

A/Molecule type: mRNA

A/Residues: 1-1226 <TOM>

A/Cross-references: UNIPROT:Q9ERM5; GB:AF295638

C/Comment: This enzyme, specifically expressed in brains and kidneys, functions in phos

C/Genetics:

A/Gene: PTP-BK

A/Map position: 6

C/Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repe

C/Keywords: brain; glycolysis; kidney; phosphoric monoester hydrolase

Query Match 82.0%; Score 41; DB 2; Length 1226;

Best Local Similarity 77.8%; Pred. No. 17;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9

Db 981 ILPYDNRV 989

Search completed: May 3, 2005, 06:16:55
Job time : 10.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:35:47 ; Search time 43 seconds
(without alignments)
80.950 Million cell updates/sec

Title: US-10-003-983C-12

Perfect score: 50

Sequence: 1 ILPDYXRV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	5 ABG31982	ABG31982 Human CD4
2	50	100.0	235	8 ADJ92680	Adj92680 Human leu
3	50	100.0	248	7 ADD22988	Add22988 Human pro
4	50	100.0	253	4 AAB59374	Aab59374 Murine pr
5	50	100.0	309	4 AAG78272	Aag78272 Mouse CD4
6	50	100.0	641	4 AAM23689	Aam23689 Human EST
7	50	100.0	641	6 ABU07333	Abu07333 Human exp
8	50	100.0	664	4 AAM39262	Aam39262 Human pol
9	50	100.0	664	6 ABU07334	Abu07334 Human exp
10	50	100.0	764	8 ABO84454	AbO84454 Human can
11	50	100.0	960	8 ADQ39377	Adq39377 Human myo
12	50	100.0	962	7 ADL16236	Adl16236 Rat prote
13	50	100.0	1114	6 ABU05246	Abu05246 Human exp
14	50	100.0	1114	6 ABU05239	Abu05239 Human exp
15	50	100.0	1143	6 ABU05240	Abu05240 Human exp
16	50	100.0	1143	6 ABU05245	Abu05245 Human exp
17	50	100.0	1143	7 ADL16232	Adl16232 Human pro
18	50	100.0	1143	8 ADQ18845	AdQ18845 Human pro
19	50	100.0	1149	4 AAM41048	Aam41048 Human pro
20	50	100.0	1149	6 ABU05242	Abu05242 Human pol
21	50	100.0	1157	8 ABO84453	AbO84453 Mouse can
22	50	100.0	1192	8 ADR39747	Adr39747 Human kin
23	50	100.0	1219	8 ADQ39378	Adq39378 Human myo
24	50	100.0	1256	8 ADM67187	Adm67187 Human adi
25	50	100.0	1256	8 ADP12966	Adp12966 Protein e

ALIGNMENTS

26	50	100.0	1258	8 ADQ39376	Adq39376 Human myo
27	50	100.0	1267	8 ADQ39379	Adq39379 Human myo
28	50	100.0	1281	7 ADL16234	Adl16234 Mouse pro
29	50	100.0	1304	6 ABU05243	Abu05243 Human exp
30	50	100.0	1304	6 ABU05241	Abu05241 Human exp
31	50	100.0	1304	6 ABU05244	Abu05244 Human exp
32	50	100.0	1304	7 ADL16230	Adl16230 Human pro
33	50	100.0	1304	7 ADP65158	Adp65158 Human pro
34	50	100.0	1304	8 ADM67209	Adm67209 Human adi
35	50	100.0	1304	8 ABO84455	AbO84455 Human can
36	50	100.0	1304	8 ADQ39380	Adq39380 Human myo
37	50	100.0	1306	8 ADQ39375	Adq39375 Human myo
38	50	100.0	1343	8 ADM67208	Adm67208 Murine ad
39	47	94.0	260	8 ADJ92685	Adj92685 Human leu
40	47	94.0	273	7 ADD22989	Add22989 Human pro
41	45	90.0	146	8 ADE28298	Ade28298 Human KPP
42	45	90.0	180	6 ABU08106	Abu08106 Human kin
43	45	90.0	692	2 AAY28653	Aay28653 Human Cyt
44	45	90.0	750	8 ABM83659	Abm83659 Human dia
45	45	90.0	799	4 AAG78623	Aag78623 Human tyr

RESULT 1
ABG31982
ID ABG31982 standard; peptide; 9 AA.
AC
XX ABG31982;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CD45 HLA-binding peptide, huCD45/684.
XX
XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
XX
XX antigen-presenting cell; APC; major histocompatibility complex; MHC;
XX
XX antigen; allogenic; T cell receptor; TCR; cancer; tumour;
XX
XX allogenic stem cell transplantation; CFU-GM; leukaemia;
XX
XX colony forming unit-granulocyte macrophage; immunotherapeutic;
XX
XX haematopoietic; malignant.
OS
XX Homo sapiens.
XX
XX PN WC0200244207-A1.
XX
XX PD 06-JUN-2002.
XX
XX PF 30-NOV-2000, 2000WO-GB004566.
XX
XX PR 30-NOV-2000, 2000WO-GB004566.
XX
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX PI Straus HJ, Amrolia PJ;
XX
XX DR WPI, 2002-599413/64.
XX
XX PT Novel peptide comprising leukocyte antigen binding peptide of human CD45
XX
XX PT polypeptide, useful for producing activated cytotoxic T lymphocytes, for
XX
XX PT killing cancerous cells e.g. leukemia.
XX
XX PS Claim 2, Page 38, 56pp; English.
XX
XX

The invention discloses a peptide comprising the human leukocyte antigen (HLA)-binding peptide of human CD45 polypeptide, its portion or variant, provided that the peptide is not the intact human CD45 polypeptide. The peptides are useful for producing activated cytotoxic T lymphocyte (CTL) in vitro which involves contacting the CTL with an antigen-presenting cell, where its major histocompatibility complex (MHC) class I molecules are loaded with the peptide, to activate, in an antigen specific manner, CC where the CTL and the antigen presenting cell are allogenic with respect CC to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
 CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
 CC for killing, and in the manufacture of a medicament for, target cells
 CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
 CC recognising cells expressing the CD45 peptides, is useful for killing
 CC target cells (cancer cells) in a patient which involves obtaining CTLs
 CC from the patient, introducing into the CTLs the polynucleotide encoding
 CC the TCR and then introducing the cells thus produced into the patient who
 CC has undergone an allogeneic stem cell transplantation. Tumour reactive
 CC CTLs have been shown to mediate tumour regression in animals models by
 CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
 CC colony formation. The cancer is leukaemia which expresses the CD45
 CC polypeptide. The method is useful as an immunotherapeutic for treating a
 CC patient with haematopoietic malignancy or to target and kill cells which
 CC express the CD45 polypeptide. The advantage this method provides is that
 CC the CTLs destroy the malignant haematopoietic cells but not the
 CC transplanted cells. The sequence presented is the peptide, huCD45/684,
 CC comprising an HLA-binding peptide of human CD45

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9
 1 ILPYDYNRV 9

RESULT 2
 ADJ92680
 ID ADJ92680 standard; protein; 235 AA.

AC ADJ92680;
 DT 06-MAY-2004 (first entry)

XX Human leukocyte common antigen (LCA) phosphatase domain (PD) 1.

KM Receptor-tyrosine protein tyrosine phosphatase; RPTP;
 KM phosphotyrosine phosphatase; cancer; diabetes; human;
 KM leukocyte common antigen; LCA; phosphatase domain; PD.

OS Homo sapiens.

PN US662905-B1.

PD 27-JAN-2004.

PF 29-MAR-1999; 99US-00280597.

PR 11-JUL-1990; 90US-00551270.

PR 26-FEB-1991; 91US-00654188.

PR 10-FEB-1993; 93US-00015985.

PR 23-MAY-1995; 95US-00448288.

PA (UTNY) UNIV NEW YORK STATE.

PI Schlessinger J, Sap JM;

DR WPI; 2004-118574/12.

PT Identifying a compound that modulates the phosphotyrosine phosphatase
 PT activity of a polypeptide by incubating the compound with the
 PT polypeptide, which is in pure form, in a membrane preparation or in a
 PT whole cell.

PS Example; SEQ ID NO 5; 52pp; English.

CC The invention relates to receptor-tyrosine protein tyrosine phosphatase
 CC (RPTP) and its corresponding nucleic acid. The invention also relates to
 CC a method for identifying a compound that modulates the phosphotyrosine

CC phosphatase activity. The method is useful for identifying a compound
 CC that modulates the phosphotyrosine phosphatase activity of a polypeptide
 CC and for identifying susceptibility to cancer, diabetes or other diseases
 CC associated with alterations in cellular phosphotyrosine metabolism. The
 CC present sequence is human leukocyte common antigen (LCA) phosphatase
 CC domain (PD) 1. This sequence is used to illustrate the method of the
 CC invention.

XX
 SQ Sequence 235 AA;

Query Match 100.0%; Score 50; DB 8; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9
 1 ILPYDYNRV 9

RESULT 3
 ADD22988
 ID ADD22988 standard; protein; 248 AA.

AC ADD22988;

DT 15-JAN-2004 (first entry)

DE Human protein tyrosine phosphatase, CD45-D1.

KM Human; enzyme; protein tyrosine phosphatase; PTPH1; cytosolic;
 KM gene therapy; retroviral vector; phosphotyrosine; pp60 (V-src);
 KM breast cancer; leukaemia; CD45-D1.

OS Homo sapiens.

PN US2003113294-A1.

PD 19-JUN-2003.

PF 12-NOV-2002; 2002US-00293231.

PR 14-MAR-1990; 90US-00494036.

PR 01-MAR-1991; 91US-00663579.

PR 16-ANG-1993; 93US-00107420.

PR 04-DEC-1996; 96US-00759536.

PR 22-JAN-1999; 99US-00235251.

PR 03-MAY-2001; 2001US-00848294.

PA (COLD-) COLD SPRING HARBOR LAB.

PI Tonks NK;

DR WPI; 2003-810871/76.

PT New isolated RNA encoding protein tyrosine phosphatase designated as
 PT PTPH1 useful for treating malignancies such as breast cancer, leukemia.

PS disclosure; Fig 4B; 12pp; English.

CC The invention relates to an isolated RNA encoding a protein tyrosine
 CC phosphatase designated as PTPH1 appearing as ADD22982. Also included is a
 CC retroviral vector comprising the RNA. The RNA is useful for treating or
 CC preventing a condition in which abnormally high levels of phosphotyrosine
 CC occur in a mammalian cell (which involves introducing into the mammalian
 CC cell and agent which comprises DNA or RNA encoding all or a portion of a
 CC PTPH1, under conditions sufficient to express PTPH1 where the polypeptide
 CC can catalyse dephosphorylation of tyrosyl residues that are
 CC phosphorylated through action of a protein tyrosine kinase. The RNA is
 CC also useful for reversing a malignant phenotype of a mammalian cell which
 CC is associated with tyrosyl phosphorylation catalysed by a protein
 CC tyrosine kinase. The DNA or RNA is delivered via a recombinant retrovirus
 CC or a recombinant vaccinia virus. At least one tyrosyl residue that is
 CC dephosphorylated by the protein tyrosine phosphatase polypeptide can be

PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dymnac RA, Zhang U, Weirman T;
XX
XX WPI; 2001-476164/51.
DR N-PSDB; AAH98348.
XX
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX
XX antipodles and research use.
XX
XX Claim 20; Page 875-876; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
XX Sequence 641 AA;
SQ

Query Match 100.0%; Score 50; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9
DB 525 ILPYDYNRV 533

RESULT 7
ABU07333
ID ABU07333 standard; protein; 641 AA.
XX
XX AC ABU07333;
XX
XX DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2034.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX
XX PR 21-MAY-2001; 2001US-0292544P.
XX
XX PR 08-AUG-2001; 2001US-0310801P.
XX
XX PR 01-OCT-2001; 2001US-0326370P.
XX
XX PR 04-DEC-2001; 2001US-0336780P.
XX
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX PA (ZYCO-) ZYCO INC.
XX
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX

DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX

PS Example 2; SEQ ID NO 2034; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 641 AA;

Query Match 100.0%; Score 50; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9
DB 525 ILPYDYNRV 533

RESULT 8
AAM39262
ID AAM39262 standard; protein; 664 AA.
XX
XX AC AAM39262;
XX
XX DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2407.
XX
XX Human; nocitropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200153312-A1.
XX
XX PD 26-JUL-2001.
XX
XX PF 26-DEC-2000; 2000WO-US034263.
XX
XX PR 23-DEC-1999; 99US-00471275.
XX
XX PR 21-JAN-2000; 2000US-00488725.
XX
XX PR 25-APR-2000; 2000US-00552317.
XX
XX PR 20-JUN-2000; 2000US-00598042.
XX
XX PR 19-JUL-2000; 2000US-00620312.
XX
XX PR 03-AUG-2000; 2000US-00653450.
XX
XX PR 14-SEP-2000; 2000US-00662191.
XX
XX PR 19-OCT-2000; 2000US-00693036.
XX
XX PR 29-NOV-2000; 2000US-00727344.
XX

PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
XX
DR N-PSDB; AAI58418.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2407; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA158642-AA1642213) with nucleotopic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 664 AA;
XX
Query Match 100.0%; Score 50; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ILPPDYNRV 9
XX
Db 525 ILPPDYNRV 533
XX
RESULT 9
ABU07334
ID ABU07334 standard; protein; 664 AA.
XX
AC ABU07334;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2035.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX

XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2035; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 664 AA;
XX
Query Match 100.0%; Score 50; DB 6; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ILPPDYNRV 9
XX
Db 525 ILPPDYNRV 533
XX
RESULT 10
ABO84454
ID ABO84454 standard; protein; 764 AA.
XX
AC ABO84454;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HPI3-011.1.
XX
KW Human; cancer-associated protein; cytoskeletal; cancer; leukaemia;
KW lymphoma; GAP.
XX
OS Homo sapiens.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX

DR MPI: 2004-652914/63.
 DR N-PSDB; ABD32625.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS claim 18; seqid 145; 310pp; English.
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://ipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 764 AA;
 CC
 Query Match 100.0%; Score 50; DB 8; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDYNRV 9
 DB 144 ILPYDYNRV 152

RESULT 11
 ADQ39377
 ID ADQ39377 standard; protein; 960 AA.
 XX
 AC ADQ39377;
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1040.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiact; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN MO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003MO-US040978.

XX
 PR 20-DEC-2002; 2002US-0434772P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin UT, Iakubova O;
 PT MPI: 2004-533949/51.
 DR N-PSDB; ADQ38549.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 PS Claim 10; SEQ ID NO 1040; 145pp; English.
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiact activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 SQ Sequence 960 AA;
 CC
 Query Match 100.0%; Score 50; DB 8; Length 960;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDYNRV 9
 DB 340 ILPYDYNRV 348

RESULT 12
 ADL16236
 ID ADL16236 standard; protein; 962 AA.
 XX
 AC ADL16236;
 DT 06-MAY-2004 (first entry)
 XX
 DE Rat protein tyrosine phosphatase #7.
 XX
 KW cytostatic; immunosuppressive; antiallergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signaling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.


```

XX OS Rattus norvegicus.
XX EN WO2003068984-A2.
XX PD 21-AUG-2003.
XX PF 13-FEB-2003; 2003MO-EP001446.
XX PR 13-FEB-2002; 2002JUS-0356810P.
XX PR 12-FEB-2003; 2003JUS-00366547.
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PA (CEPT-) CEPTIR INC.
XX PT Tonks NK, Tzu-Ching M, Cool DE;
XX DR WPI; 2003-712572/67.
XX DR N-PSDB; ADL16235.
XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX PT screening for specific modulators, potential agents for treating e.g.
XX PT cancer or autoimmune disease.
XX PS Disclosure; SEQ ID NO 85; 238bp; English.
XX CC The invention relates to a method for identifying a protein tyrosine
XX CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX CC subjecting a sample, including a cell that contains at least one PTP, to
XX CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX CC anaerobically, in presence of a sulphydryl-reactive agent (II) that
XX CC irreversibly modifies the thiol group of an invariant Cys in the active
XX CC site of PTP; and (iii) determining, under reducing conditions, the level
XX CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
XX CC dephosphorylation indicates that an active PTP is present. . No details
XX CC of tests for these activities are given. The method is used to identify
XX CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX CC are involved. These agents are potentially useful, in human or veterinary
XX CC medicine, for treating abnormal cell proliferation or growth (cancer);
XX CC guest vs. host disease; autoimmune diseases; allergy or other
XX CC immunosuppressed states; metabolic disorders and cell-cycle
XX CC abnormalities. This sequence represents one of the PTP enzyme of the
XX CC invention.
XX SQ Sequence 962 AA;
XX
Query Match 100.0%; Score 50; DB 7; Length 962;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILPYDYNRV 9
Db 344 ILPYDYNRV 352

```

```

RESULT 13
ABU05246
ID ABU05246 standard; protein; 1114 AA.
XX
AC ABU05246;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1912.
XX

```

```

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; WBC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.

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XX XX WO200278524-A2.
XX PN 10-OCT-2002.
XX PD 28-MAR-2002; 2002MO-US009671.
XX PF 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002JUS-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PA Chicx RM, Tomlinson AJ, Urban RG;
XX PI WPI; 2003-040607/03.
XX DR
XX XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX XX cytoskeletal proteins, receptors or transcription factors), useful for
XX XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX XX leukemia.
XX PS Example 2; SEQ ID NO 1912; 134bp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1114 AA;
XX
Query Match 100.0%; Score 50; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILPYDYNRV 9
Db 494 ILPYDYNRV 502

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RESULT 14
ABU05239
ID ABU05239 standard; protein; 1114 AA.
XX
AC ABU05239;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1905.
XX

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XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; WBC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.

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```
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1905; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;
XX
Query Match 100.0%; Score 50; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILPYDYNRV 9
DB 494 ILPYDYNRV 502
XX
RESULT 15
ABU05240
ID ABU05240 standard; protein; 1143 AA.
XX
AC ABU05240;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1906.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
```

```
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;
XX
Query Match 100.0%; Score 50; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILPYDYNRV 9
DB 523 ILPYDYNRV 531
XX
RESULT 16
ABU05245
ID ABU05245 standard; protein; 1143 AA.
XX
AC ABU05245;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1911.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
```

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XX  WO200278524-A2.
PN  10-OCT-2002.
PD  28-MAR-2002; 2002WO-US009671.
XX  28-MAR-2001; 2001US-0279495P.
XX  21-MAY-2001; 2001US-0292544P.
PR  08-AUG-2001; 2001US-0310801P.
PR  01-OCT-2001; 2001US-0326370P.
PR  04-DEC-2001; 2001US-0336780P.
PR  20-FEB-2002; 2002US-0358985P.
XX  (ZYCO-) ZYCOs INC.
PA  Chicz RM, Tomlinson AJ, Urban RG;
PI  WPI; 2003-040607/03.
XX  New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT  cytoskeletal proteins, receptors or transcription factors), useful for
PT  treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT  leukemia.
XX  Example 2; SEQ ID NO 1911; 134pp; English.
XX  The invention describes a purified polypeptide, which comprises a
CC  fragment of a kinase, phosphatase, protease, protease inhibitor,
CC  transporter, cytoskeletal protein, receptor or transcription factor. The
CC  polypeptide is useful as an immunogenic composition for eliciting in a
CC  mammal an immunogenic response directed against any of the purified
CC  polypeptide. The purified polypeptide, or the antibody that binds to this
CC  polypeptide, is useful for treating cancer. The polypeptide is also
CC  useful for identifying compounds that binds to a naturally processed
CC  class I or class II MHC-binding polypeptide. The polypeptides and
CC  polynucleotides are particularly useful for treating or preventing
CC  myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC  lymphoma or leukaemia. These are also useful for screening agents for
CC  treating the above mentioned diseases. This sequence represents an
CC  expressed protein tag (EPT) isolated from human tissue for translational
CC  profiling. Note: This sequence does not appear in the printed
CC  specification but was obtained in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX  Sequence 1143 AA:
SQ
Query Match 100.0%; Score 50; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILPYDYNRV 9
Db 523 ILPYDYNRV 531

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RESULT 17
ADL16232
ID ADL16232 standard; protein; 1143 AA.
XX
AC ADL16232;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #27.
XX
XX cytosolic; immunosuppressive; anti-allergic;
KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KM inducible signalling pathway; cell proliferation; cancer;
KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KM cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.

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XX  WO2003068984-A2.
PN  21-AUG-2003.
PD  13-FEB-2003; 2003WO-EP001446.
XX  13-FEB-2002; 2002US-0356810P.
PR  12-FEB-2003; 2003US-00366547.
XX  (COLD-) COLD SPRING HARBOR LAB.
PA  (CEPT-) CEPTYR INC.
XX  Tonks NK, Tzu-Ching M, Cool DE;
PI  WPI; 2003-712572/67.
XX  N-PSDB; ADL16231.
XX  Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT  screening for specific modulators, potential agents for treating e.g.
PT  cancer or autoimmune disease.
XX  Disclosure; SEQ ID NO 81; 238pp; English.
XX  The invention relates to a method for identifying a protein tyrosine
CC  phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC  subjecting a sample, including a cell that contains at least one PTP, to
CC  conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC  anaerobically, in presence of a sulphydryl-reactive agent (II) that
CC  irreversibly modifies the thiol group of an invariant Cys in the active
CC  site of PTP; and (iii) determining, under reducing conditions, the level
CC  of dephosphorylation caused by PTP, of a labelled substrate (III), where
CC  dephosphorylation indicates that an active PTP is present. No details
CC  of tests for these activities are given. The method is used to identify
CC  reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC  modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC  are involved. These agents are potentially useful, in human or veterinary
CC  medicine, for treating abnormal cell proliferation or growth (cancer);
CC  guest vs. host disease; autoimmune diseases; allergy or other
CC  immunosuppressed states; metabolic disorders and cell-cycle
CC  abnormalities. This sequence represents one of the PTP enzyme of the
CC  invention.
XX  Sequence 1143 AA:
SQ
Query Match 100.0%; Score 50; DB 7; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILPYDYNRV 9
Db 523 ILPYDYNRV 531

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RESULT 18
ADQ18845
ID ADQ18845 standard; protein; 1143 AA.
XX
AC ADQ18845;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
XX
XX soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
KM WO2004048938-A2.
PN 10-JUN-2004.
PD 26-NOV-2003; 2003WO-US038193.
PF

```

XX 26-NOV-2002; 2002US-0429739P.
PR (PROT-) PROTEIN DESIGN LABS INC.
XX Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 1664; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1143 AA;

```

Query Match 100.0%; Score 50; DB 8; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.77; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0;

```

QY 1 ILPYDYNRV 9
   |||||
Db 523 ILPYDYNRV 531

```

RESULT 19
ID AAM41048
XX AAM41048 standard; protein; 1149 AA.
AC AAM41048;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5979.
XX
KM Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KM leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.

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PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Dmanac RT;
XX WPI; 2001-442253/47.
XX
DR N-PSDB; AA160204.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5979; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AAM42213) with noctropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1149 AA;

```

Query Match 100.0%; Score 50; DB 4; Length 1149;
Best Local Similarity 100.0%; Pred. No. 0.78; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0;

```

QY 1 ILPYDYNRV 9
   |||||
Db 528 ILPYDYNRV 536

```

RESULT 20
ID ABU05242
XX ABU05242 standard; protein; 1149 AA.
AC ABU05242;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1908.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 XX Chicz RM, Tomlinson AJ, Urban RG;
 XX WPI; 2003-040607/03.
 DR
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 PS
 XX Example 2; SEQ ID NO 1908; 134pp; English.
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1149 AA;
 Query Match 100.0%; Score 50; DB 6; Length 1149;
 Best Local Similarity 100.0%; Pred. No. 0.78;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9
 |||||
 Db 528 ILPYDYNRV 536

RESULT 21
 AB084453 standard; protein; 1157 AA.
 XX
 AC AB084453;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Mouse cancer-associated protein MP13-011.1.
 XX
 KM Mouse; cancer-associated protein; cytoskeletal; cancer; leukaemia;
 KM lymphoma; CAP.
 XX
 OS Mus musculus.
 XX
 PN WO2004074320-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-0038838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.

XX
 PI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABD32623.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 PS
 XX disclosure; seqid 142; 310pp; English.

CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1157 AA;
 Query Match 100.0%; Score 50; DB 8; Length 1157;
 Best Local Similarity 100.0%; Pred. No. 0.78;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9
 |||||
 Db 539 ILPYDYNRV 547

RESULT 22
 ADR39747 standard; protein; 1192 AA.
 XX
 AC ADR39747;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
 XX
 KM human; kinase and phosphatase protein; KPP; enzyme; cytoskeletal;
 KM antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
 KM cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
 KM thymimetic; gene therapy; cell proliferative disorder; cancer;
 KM atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
 KM stroke; immune disorder; inflammatory disorder; AIDS; allergy;
 KM developmental disorder; Hypothyroidism; Cushing's syndrome; infection;

KM KPP-20.
 OS Homo sapiens.
 XX
 XX WO2004074453-A2.
 PN
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005092.
 XX
 PR 20-FEB-2003; 2003US-0449059P.
 XX
 PR 19-MAR-2003; 2003US-0456932P.
 XX
 PR 28-MAR-2003; 2003US-0458844P.
 XX
 PR 09-APR-2003; 2003US-0461678P.
 XX
 PR 17-APR-2003; 2003US-0463937P.
 XX
 PA (INCYTE) INCYTE CORP.
 XX
 PI Ramkumar J, Marguis JP, Swarnakar A, Chawla NK, Tran UK,
 PI Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
 PI Jackson AA, Yang J, Corvrad AE;
 XX
 DR WPI; 2004-635568/61.
 DR N-PSDB; ADR39793.
 XX
 PT New human kinases and phosphatases (Kpp) for diagnosing, treating and
 PT preventing diseases or conditions associated with aberrant Kpp expression
 PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
 XX
 PS Claim 1; SEQ ID NO 20; 299pp; English.
 XX
 CC The present sequence represents the human kinase and phosphatase protein
 CC (Kpp), designated KPP-20. The human Kpp sequences from the present
 CC invention have cytostatic, antitumorocytotoxic, anticonvulsant,
 CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
 CC antiinflammatory and thymimetic activities, and can be used in gene
 CC therapy. The human Kpp proteins and polynucleotides can be used in
 CC diagnosing, treating and preventing diseases or conditions associated
 CC with the decreased expression or overexpression of Kpp, such as cell
 CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
 CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
 CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
 CC disorders, or infections. They can also be used in assessing the effects
 CC of exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of Kpp. The Kpp or its fragments are useful in screening
 CC compounds for effectiveness as agonist or antagonist of the polypeptides,
 CC or in altering the expression of the target polynucleotide and compounds
 CC that specifically bind to or modulate the activity of the polypeptide.
 XX
 SQ Sequence 1192 AA;
 Query Match 100.0%; Score 50; DB 8; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 0.81; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDYNRV 9
 Db 572 ILPYDYNRV 580
 RESULT 23
 ADQ39378
 ID ADQ39378 standard; protein: 1219 AA.
 XX
 AC ADQ39378;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human.
 XX

OS Homo sapiens.
 XX
 XX WO2004058052-A2.
 PN
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 XX
 PR 10-MAR-2003; 2003US-0453135P.
 XX
 PR 30-APR-2003; 2003US-0466412P.
 XX
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL) APPLERA CORP.
 XX
 PI Cargill M, Devlin UT, Iakubova O;
 PI WPI; 2004-533949/51.
 DR N-PSDB; ADQ38550.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1041; 145pp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1219 AA;
 Query Match 100.0%; Score 50; DB 8; Length 1219;
 Best Local Similarity 100.0%; Pred. No. 0.83; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDYNRV 9
 Db 599 ILPYDYNRV 607
 RESULT 24
 ADM67187
 ID ADM67187 standard; protein: 1256 AA.
 XX
 AC ADM67187;
 XX
 DT 03-JUN-2004 (first entry)
 XX

DE Human adipocyte specific PTPase receptor type C protein SeqID 541.
XX
XX human; adipocyte specific; adipose tissue; anti-obesity;
KM high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
XX antidiabetic; hypotensive; PTPase receptor type C.
OS
XX Homo sapiens.
XX
XX WO2004011618-A2.
XX
XX PD 05-FEB-2004.
XX
XX PF 29-JUL-2003; 2003WO-US023684.
XX
XX PR 29-JUL-2002; 2002US-0398785P.
XX PR 12-JUN-2003; 2003US-0478206P.
XX
XX PA (HMG-) HMG- INC.
XX
XX PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX WPI; 2004-143846/14.
XX DR N-PSDB; ADM66908.
XX
XX PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
XX PS Disclosure; SEQ ID NO 541; 91dp; English.
XX
XX CC This invention relates to a novel method for identifying genes that are
XX over-expressed in adipose tissue and as such it provides targets for anti-
XX -obesity pharmaceutical compositions. Specifically, it refers to a high
XX mobility group I-C protein (HMGI-C) that is associated with obesity and
XX is epistatic to leptin, furthermore, it refers to the ob gene where an
XX autosomal recessive trait is linked to obesity and diabetes. The present
XX invention describes performing differential gene expression analysis
XX between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
XX of any two different mice selected from a group consisting of wild-type,
XX HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
XX this method novel nucleotides and the encoded proteins thereof were
XX identified that are adipocyte specific, and as such can be used for
XX preventing adipogenesis, diagnosing and treating diabetes, obesity,
XX hypertension and cardiovascular disease, as well as screening for
XX compounds that can modulate or prevent adipogenesis and treat diabetes or
XX obesity. These compositions exhibit anorectic, antidiabetic and
XX hypotensive activities. This polypeptide sequence is a human homologue of
XX a murine adipocyte specific protein sequence of the invention.
XX
XX SQ Sequence 1256 AA;
XX
XX Query Match 100.0%; Score 50; DB 8; Length 1256;
XX Best Local Similarity 100.0%; Pred. No. 0.86;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ILPYDYNRV 9
XX |||||
XX AC ADP12966 644
XX
XX DB 636 ILPYDYNRV 644
XX
XX RESULT 25
XX ADP12966 standard; protein; 1256 AA.
XX
XX AC ADP12966;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Protein encoding reference mRNA sequence #51.
XX
XX KM transplant rejection; immune system; rheumatoid arthritis; lupus;

KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
XX OS Homo sapiens.
XX
XX PN WO2004042346-A2.
XX
XX PD 21-MAY-2004.
XX
XX PF 24-APR-2003; 2003WO-US012946.
XX
XX XX 24-APR-2002; 2002US-00131831.
XX PR 20-DEC-2002; 2002US-00325899.
XX
XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX PI Rosenberg S;
XX DR WPI; 2004-40724/37.
XX
XX PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX PT rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX
XX PS Claim 65; SEQ ID NO 2975; 1762dp; English.
XX
XX CC The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprising detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection, in an
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX protein encoded by an mRNA sequence of the invention which show altered
XX expression in renal transplantation and expression.
XX
XX SQ Sequence 1256 AA;
XX
XX Query Match 100.0%; Score 50; DB 8; Length 1256;
XX Best Local Similarity 100.0%; Pred. No. 0.86;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ILPYDYNRV 9
XX |||||
XX AC ADQ39376 644
XX
XX DB 636 ILPYDYNRV 644
XX
XX RESULT 26
XX ADQ39376 standard; protein; 1258 AA.
XX
XX ID ADQ39376
XX
XX AC ADQ39376;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
XX
XX KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KM cardiac; gene therapy; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004058052-A2.
XX
XX PD 15-JUL-2004.
XX
XX PF 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JT, Iakubova O;
 DR MPI; 2004-533949/51.
 DR N-PSDB; ADQ38548.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1039; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiact activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 XX
 SQ Sequence 1258 AA;
 CC
 CC Query Match 100.0%; Score 50; DB 8; Length 1258;
 CC Best Local Similarity 100.0%; Pred. No. 0.86; Indels 0; Gaps 0;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 ILPYDYNRV 9
 Db 638 ILPYDYNRV 646
 XX
 AC ADQ39379;
 XX
 AC ADQ39379;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
 XX
 KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 XX cardiact; gene therapy; human.
 XX
 OS Homo sapiens.
 XX

PN MO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JT, Iakubova O;
 DR MPI; 2004-533949/51.
 DR N-PSDB; ADQ38551.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1042; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiact activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 XX
 SQ Sequence 1267 AA;
 CC
 CC Query Match 100.0%; Score 50; DB 8; Length 1267;
 CC Best Local Similarity 100.0%; Pred. No. 0.87; Indels 0; Gaps 0;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 ILPYDYNRV 9
 Db 647 ILPYDYNRV 655
 XX
 AC ADL16234;
 XX
 AC ADL16234;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Mouse protein tyrosine phosphatase #7.
 XX

KW cytosolic; immunosuppressive; antiallergic;
KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX Mus musculus.
XX OS
XX PN WO2003068984-A2.
XX PD
XX 21-AUG-2003.
XX PF
XX 13-FEB-2003; 2003WO-EP001446.
XX PR
XX 13-FEB-2002; 2002US-0356810P.
XX PR 12-FEB-2003; 2003US-00366547.
XX PA
XX (COLD-) COLD SPRING HARBOR LAB.
XX (CEPT-) CEPTVR INC.
XX PI
XX Tonks NK, Tzu-Ching M, Cool DE;
XX WPI; 2003-712572/67.
XX DR
XX N-PSDB; ADL16233.
XX PT
XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX screening for specific modulators, potential agents for treating e.g.
XX cancer or autoimmune disease.
XX PS
XX Disclosure; SEQ ID NO 83; 238pp; English.
XX CC
XX The invention relates to a method for identifying a protein tyrosine
XX phosphatase (PTP) that is reversibly oxidized in a cell by: (i) PTP, to
XX subjecting a sample, including a cell that contains at least one PTP, to
XX conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX anaerobically, in presence of a sulhydryl-reactive agent (II) that
XX irreversibly modifies the thiol group of an invariant Cys in the active
XX site of PTP; and (iii) determining, under reducing conditions, the level
XX of dephosphorylation, caused by PTP, of a labelled substrate (III), where
XX dephosphorylation indicates that an active PTP is present. . No details
XX of tests for these activities are given. The method is used to identify
XX reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX are involved. These agents are potentially useful, in human or veterinary
XX medicine, for treating abnormal cell proliferation or growth (cancer);
XX guest vs. host disease; autoimmune diseases; allergy or other
XX immunosuppressed states; metabolic disorders and cell-cycle
XX abnormalities. This sequence represents one of the PTP enzyme of the
XX invention.
XX CC
XX SQ Sequence 1291 AA;
XX
XX Query Match 100.0%; Score 50; DB 7; Length 1291;
XX Best Local Similarity 100.0%; Pred. No. 0.89;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9
Db 673 ILPYDYNRV 681

RESULT 29

ABU05243
ID ABU05243 standard; protein; 1304 AA.

XX AC ABU05243;
XX XX

DT 29-JAN-2003 (first entry)
XX XX

DE Human expressed protein tag (EPT) #1909.
XX XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX OS
XX PN WO200278524-A2.
XX PD
XX 10-OCT-2002.
XX PF
XX 28-MAR-2002; 2002WO-US009671.
XX PR
XX 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA
XX (ZYCO-) ZYCO INC.
XX XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX PT
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS
XX Example 2; SEQ ID NO 1909; 134pp; English.
XX CC
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 1304 AA;
XX

QY 1 ILPYDYNRV 9
Db 684 ILPYDYNRV 692

RESULT 30

ABU05241
ID ABU05241 standard; protein; 1304 AA.

XX AC ABU05241;
XX XX

DT 29-JAN-2003 (first entry)
XX XX

DE Human expressed protein tag (EPT) #1907.
XX XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 50; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ILPYDYNRV 9
DB 684 ILPYDYNRV 692

RESULT 31
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1910.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1910; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 50; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ILPYDYNRV 9
DB 684 ILPYDYNRV 692

RESULT 32
ADL16230
ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #26.
XX
KW cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;

KW inducible signalling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 XX Homo sapiens.
 XX OS
 XX PN WO2003068984-A2.
 XX
 XX PD 21-AUG-2003.
 XX
 XX PF 13-FEB-2003; 2003WO-EP001446.
 XX
 XX PR 13-FEB-2002; 2002US-0356810P.
 XX PR 12-FEB-2003; 2003US-00366547.
 XX
 XX PA (COLD-) COLD SPRING HARBOR LAB.
 XX PA (CEPT-) CEPTYR INC.
 XX
 XX PI Tonks NK, Tzu-Ching M, Cool DE;
 XX
 XX WPI; 2003-712572/67.
 XX DR N-PSDB; ADL16229.
 XX
 XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX
 XX PS Disclosure; SEQ ID NO 79; 238pp; English.
 XX
 XX CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulhydryl-reactive agent (II) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
 CC dephosphorylation indicates that an active PTP is present. . No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 XX
 XX SQ Sequence 1304 AA;
 XX
 XX Query Match 100.0%; Score 50; DB 7; Length 1304;
 XX Best Local Similarity 100.0%; Pred. No. 0.9;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX
 XX OS Homo sapiens.
 XX PN WO2003072827-A1.
 XX
 XX PD 04-SEP-2003.
 XX
 XX PF 31-OCT-2002; 2002WO-US035433.
 XX
 XX PR 31-OCT-2001; 2001US-0336220P.
 XX
 XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 XX PI Hirsch R, Thornton SL;
 XX
 XX WPI; 2003-712740/67.
 XX DR GENBANK; NP_002829.
 XX
 XX PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 XX PS Disclosure; Page; 56pp; English.
 XX
 XX CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analysis of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antiout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.
 XX
 XX SQ Sequence 1304 AA;
 XX
 XX Query Match 100.0%; Score 50; DB 7; Length 1304;
 XX Best Local Similarity 100.0%; Pred. No. 0.9;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33
 ADP65158
 ID ADP65158 standard; protein; 1304 AA.
 XX
 XX AC ADP65158;
 XX
 XX DT 12-AUG-2004 (first entry)
 XX
 XX DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
 XX
 XX KW autoimmune disease; arthritis; gene expression analysis;
 XX KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antiout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;

RESULT 34
 ADM67209
 ID ADM67209 standard; protein; 1304 AA.
 XX
 XX AC ADM67209;
 XX
 XX DT 03-JUN-2004 (first entry)
 XX

DE Human adipocyte specific leukocyte common antigen protein seqid 563.
 XX human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; leukocyte common antigen.
 XX Homo sapiens.
 OS
 PN WO2004011618-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 29-JUL-2003; 2003WO-US023684.
 XX
 PR 29-JUL-2002; 2002US-0398785P.
 XX
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMGE-) HMGNE INC.
 XX
 PI Chada K, Chouinard R, Ashar H, Sayed AMD;
 XX
 DR WPI; 2004-143846/14.
 DR N-PSDB; ADM66930.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 PS Disclosure; SEQ ID NO 563; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 XX
 SQ Sequence 1304 AA;
 Query Match 100.0%; Score 50; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDYNRV 9
 Db 684 ILPYDYNRV 692
 RESULT 35
 AB084455
 ID AB084455 standard; protein; 1304 AA.
 XX
 AC AB084455;
 XX
 XX
 DT 18-NOV-2004 (first entry)
 DE Human cancer-associated protein HPI3-011.2.
 XX
 XX Human; cancer-associated protein; cytosstatic; cancer; leukaemia;

KM Lymphoma; CAP.
 XX
 OS Homo sapiens.
 XX
 PN WO2004074320-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 XX
 PR 14-MAR-2003; 2003US-0038838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 XX
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABD32626.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS claim 18; seqid 147; 310pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1304 AA;
 Query Match 100.0%; Score 50; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILPYDYNRV 9
 Db 684 ILPYDYNRV 692

RESULT 36
ADQ39380
ID ADQ39380 standard; protein; 1304 AA.
XX
AC ADQ39380;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiac; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLEA CORP.
XX
PI Cargill M, Devlin JJ, Iakubova O;
XX
DR WPI: 2004-533949/51.
DR N-PSDB; ADQ38552.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1043; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 50; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDNRV 9
DB 684 ILPYDNRV 692
RESULT 37
ADQ39375
ID ADQ39375 standard; protein; 1306 AA.
XX
AC ADQ39375;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiac; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLEA CORP.
XX
PI Cargill M, Devlin JJ, Iakubova O;
XX
DR WPI: 2004-533949/51.
DR N-PSDB; ADQ38547.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1038; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX

SQ Sequence 1306 AA;

Query Match 100.0%; Score 50; DB 8; Length 1306;

Best Local Similarity 100.0%; Pred. No. 0.9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9

Db 686 ILPYDYNRV 694

RESULT 38

ADM67208

ID ADM67208 standard; protein; 1343 AA.

AC ADM67208;

DT 03-JUN-2004 (first entry)

DE Murine adipocyte specific leukocyte common antigen protein SegID 562.

KM murine; mouse; adipocyte specific; adipose tissue; anti-obesity;

KM high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;

KM adipogenesis; hypertension; cardiovascular disease; anorectic;

KM antidiabetic; hypotensive; leukocyte common antigen.

OS Mus musculus.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMGE-) HMGNE INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66929.

XX Identifying adipocyte specific genes, useful for treating obesity or

PT diabetes; and for identifying drug targets, by differential gene

PT expression analysis between adipose tissue or stromal vascular tissue of

PT mice of different genotypes.

PS Disclosure; SEQ ID NO 562; 91pp; English.

XX This invention relates to a novel method for identifying genes that are

CC over-expressed in adipose tissue and as such it provides targets for anti

CC -obesity pharmaceutical compositions. Specifically, it refers to a high

CC mobility group I-C protein (HMGI-C) that is associated with obesity and

CC is epistatic to leptin, furthermore, it refers to the ob gene where an

CC autosomal recessive trait is linked to obesity and diabetes. The present

CC invention describes performing differential gene expression analysis

CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)

CC of any two different mice selected from a group consisting of wild-type,

CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using

CC this method novel nucleotides and the encoded proteins thereof were

CC identified that are adipocyte specific, and as such can be used for

CC preventing adipogenesis, diagnosing and treating diabetes, obesity,

CC hypertension and cardiovascular disease, as well as screening for

CC compounds that can modulate or prevent adipogenesis and treat diabetes or

CC obesity. These compositions exhibit anorectic, antidiabetic and

CC hypotensive activities. This polypeptide sequence is a murine adipocyte

CC specific protein sequence of the invention.

XX Sequence 1343 AA;

SQ

Best Local Similarity 100.0%; Pred. No. 0.93;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILPYDYNRV 9

Db 673 ILPYDYNRV 681

Search completed: May 3, 2005, 07:41:53

Job time : 52 secs

Query Match 100.0%; Score 50; DB 8; Length 1343;

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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds
(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-13
Perfect score: 44
Sequence: 1 YILIHQALV 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	44	100.0	1237	2 A54080	protein-tyrosine-p
2	44	100.0	1273	1 TDRIT	leukocyte common a
3	44	100.0	1291	1 A28334	protein-tyrosine-p
4	44	100.0	1304	1 A46546	leukocyte common a
5	41	93.2	1200	2 T43148	probable protein-t
6	37	84.1	467	2 T40513	yeast erol homolog
7	34	77.3	335	2 AG0489	probable iron tran
8	34	77.3	806	2 AB1015	glycerol-3-phospha
9	34	77.3	810	2 D64090	glycerol-3-phospha
10	34	77.3	825	2 AC0039	glycerol-3-phospha
11	34	77.3	827	1 XUECAG	glycerol-3-phospha
12	34	77.3	827	2 H91256	glycerol-3-phospha
13	34	77.3	827	2 D66097	glycerol-3-phospha
14	33	75.0	327	2 S73304	hypothetical prote
15	33	75.0	464	2 AG2769	cytochrome P450 cy
16	33	75.0	464	2 H97549	cytochrome P450 hy
17	33	75.0	540	2 B41325	heat shock protein
18	33	75.0	582	2 A57068	protein-tyrosine-p
19	33	75.0	613	2 T16885	hypothetical prote
20	33	75.0	1290	2 A56493	leucocyte common a
21	33	75.0	1301	1 A41622	protein-tyrosine-p
22	33	75.0	1897	1 TDRIT	leukocyte antigen-
23	33	75.0	1898	2 S46216	leukocyte antigen-
24	32	72.7	324	2 A97919	3-oxoacyl-(acyl)-ca
25	32	72.7	324	2 C95048	3-oxoacyl-(acyl)-ca
26	32	72.7	326	2 T15194	hypothetical prote
27	32	72.7	537	2 G2576	hypothetical prote
28	32	72.7	579	2 B86565	oligopeptide perme
29	32	72.7	579	2 C72059	peptide ABC transp

30	32	72.7	1231	2 S53089	protein-tyrosine-p
31	32	72.7	1422	2 T42636	protein-tyrosine-p
32	32	72.7	1442	1 B48148	protein-tyrosine-p
33	32	72.7	1445	1 A48148	protein-tyrosine-p
34	32	72.7	1557	2 D41214	protein-tyrosine-p
35	32	72.7	1630	2 C41214	protein-tyrosine-p
36	32	72.7	1691	1 D54689	protein-tyrosine-p
37	32	72.7	1894	2 C54689	protein-tyrosine-p
38	32	72.7	1912	2 A56178	protein-tyrosine-p
39	31	70.5	268	2 F87487	ribosomal protein
40	31	70.5	352	2 T42744	hypothetical prote
41	31	70.5	358	2 AB2041	hypothetical prote
42	31	70.5	369	2 T38428	hypothetical oxido
43	31	70.5	431	2 T06019	hypothetical prote
44	31	70.5	433	2 C86694	glycerol-3-phospha
45	31	70.5	458	2 S56816	GTPase-activating

ALIGNMENTS

RESULT 1

A54080
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #ext_change 09-Jul-2004
C:Accession: A54080; I50592
R:Yang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
J. Biol. Chem. 269, 14056-14063, 1994
A:Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in
A:Reference number: A54080; MUID:94245724; PMID:818686
A:Accession: A54080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1237 <F&N>
A:Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:9510510; PID:CAA79972.1; PID:9510
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homo
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <FIR>
F:610-834/Domain: protein-tyrosine-phosphatase homology <FIR>
F:786/Active site: Cys (phosphocysteine intermediate) #status predicted
F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 44; DB 2; Length 1237;

Best Local Similarity 100.0%; Pred. No. 0.68; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YILIHQALV 9
Db 835 YILIHQALV 843

RESULT 2

TDRIT
leukocyte common antigen precursor, splice form 4 - rat

N:Alternate names: CD45; L-CA; Ly-5; T200

N:Contents: leukocyte common antigen precursor, splice form 1; leukocyte common antigen

.1.3.48)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 04-Dec-1986 #sequence_revision 05-May-2000 #ext_change 09-Jul-2004

C:Accession: A29450; B29450; C29450; D29450; A60241; A02247; I54569; A45854

R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.

EMBL J. 6, 1259-1264, 1987

A:Title: Lymphocyte specific heterogeneity in the rat leukocyte common antigen (T200) 1

A:Reference number: A91067; MUID:87275817; PMID:2440674

A:Accession: A29450

A:Molecule type: mRNA

A:Residues: 20-30, 163-218 <B&R1>

A:Cross-references: UNIPROT:Q64224; GB:M25820; GB:M24611; NID:9205153; GB:Y00065; GB:KO

A:Experimental source: splice form 1

A>Note: the translation in GenBank entry RATLCAI, PID:AAA41518.1, PID:9205154, release

A:Accession: B29450

A:Molecule type: mRNA

A:Residues: 19-30,122-218 <BAR2>
 A:Cross-references: GB:M25821; GB:M24611; NID:g205155; PIDN:AAA41519.1; PID:g205156; GB:
 A:Experimental source: splice form 2
 A:Accession: C29450
 A:Molecule type: mRNA
 A:Residues: 20-30,73-121,163-218 <BAR3>
 A:Cross-references: GB:M25822; GB:M24611; NID:g205157; PIDN:AAA41520.1; PID:g205158; GB:
 A:Experimental source: splice form 3
 A:Accession: D29450
 A:Molecule type: mRNA
 A:Residues: 28-218 <BAR4>
 A:Cross-references: GB:M25823; GB:M24611; NID:g205159; PIDN:AAA41521.1; PID:g205160; GB:
 A:Experimental source: splice form 4
 A:Note: the sequence in GenBank entry R4TLCALV, release 113.0, has the codon AGG for 56-
 R:Barclay, A.N.; Jackson, D.I.; Willis, A.C.; Williams, A.F.
 Adv. Exp. Med. Biol. 237, 3-7, 1988
 A:Title: The leukocyte-common antigen (L-CA) family.
 A:Reference number: A60241; PMID:89319817; PMID:2978200
 A:Accession: A60241
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 30-161 <BAR5>
 R:Thomsen, M.L.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
 Cell 41, 83-93, 1985
 A:Title: Evidence from cDNA clones that the rat leukocyte-common antigen (T200) spans th
 A:Reference number: A02247; PMID:85201691; PMID:3158393
 A:Accession: A02247
 A:Molecule type: mRNA
 A:Residues: 187-189, 'K', 191-192, 'K', 208-1273 <THO>
 A:Cross-references: GB:M10072; GB:M81859; NID:g205140; PIDN:AAA41513.1; PID:g205143
 A:Note: the translation in GenBank entry R4TLCAL, release 113.0, begins at non-initiatio
 R:McCall, M.N.; Shotton, D.M.; Barclay, A.N.
 Immunology 76, 310-317, 1992
 A:Title: Expression of soluble isoforms of rat CD45. Analysis by electron microscopy and
 A:Reference number: I54569; PMID:92340120; PMID:1378817
 A:Accession: I54569
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 130,163-180 <MC>
 A:Cross-references: GB:940716; NID:g252015; PIDN:AA822648.1; PID:g252016
 R:Jackson, D.I.; Barclay, A.N.
 Immunogenetics 29, 281-287, 1989
 A:Title: The extra segments of sequence in rat leukocyte common antigen (L-CA) are deriv
 A:Reference number: A45854; PMID:89232323; PMID:2523868
 A:Accession: A45854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 24-227, 'H', 229-305, 'Y', 307-310 <JAC>
 A:Cross-references: GB:M18347; GB:M18348; GB:M18349
 C:Comment: This glycoprotein is found on lymphoid and myeloid cell surfaces.
 C:Keywords: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 F:1-23/DNA:in: signal sequence #status predicted <SIG>
 F:1-23/Produce: leukocyte common antigen precursor; splice form 4 #status predicted <
 F:24-56/DNA:in: extracellular #status predicted <EXT>
 F:24-30,122-1273/Produce: leukocyte common antigen, splice form 2 #status predicted <MA
 F:24-30,73-121,163-218/Produce: leukocyte common antigen, splice form 1 #status predicte
 F:547-568/DNA:in: transmembrane #status predicted <TM>
 F:545-1206/DNA:in: leukocyte common antigen cytosolic domain homology <LAC>
 F:569-1273/DNA:in: intracellular #status predicted <INT>
 F:646-870/DNA:in: protein-tyrosine-phosphatase homology <PTP>
 F:62,142,153,164,178,200,245,271,282,327,373,374,502/Binding site: carbohydrate (Aa
 F:522/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:528/Binding site: substrate phosphate (Arg) #status predicted
 F:1063/Binding site: carbohydrate (Aa) (covalent) #status absent

Query Match 100.0%; Score 44; DB 1; Length 1273;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YILIHQALV 9

DB 871 YILIHQALV 879

RESULT 3
 A28334
 protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
 N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
 N:Contains: protein-tyrosine-phosphatase (T-cell variant)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C:Accession: A28334; A29381; A61180; A60993; A33522; A29075; I54450; A28335; A23329; I57
 R:Thomsen, M.L.; Reynolds, P.J.; Chan, A.; Ben-Nerish, Y.; Trowbridge, I.S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
 A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
 A:Reference number: A28334; PMID:87260986; PMID:2955416
 A:Accession: A28334
 A:Molecule type: mRNA
 A:Residues: 1-1291 <THO>
 A:Cross-references: UNIPROT:P06800; UNIPROT:061814; UNIPROT:061815; UNIPROT:061813; GB:M
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
 A:Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
 A:Reference number: A29381; PMID:86313686; PMID:2944116
 A:Accession: A29381
 A:Molecule type: mRNA
 A:Residues: 1-30,170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, '
 A:Cross-references: GB:M13342; NID:g198914; PIDN:AAA39458.1; PID:g198915
 R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
 A:Reference number: A61180; PMID:92032882; PMID:1932742
 A:Accession: A61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 730-838 <YIA>
 R:Gomez, L.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
 Immunogenetics 25, 263-266, 1987
 A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
 A:Reference number: A60933; PMID:87192331; PMID:3570377
 A:Accession: A60933
 A:Molecule type: protein
 A:Residues: 'R', 289-298; 329, 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375; 595-608; 638-649; 669-
 R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
 J. Biol. Chem. 264, 6220-6229, 1989
 A:Title: Sequence conservation in potential regulatory regions of the mouse and human le
 A:Reference number: A33522; PMID:89197920; PMID:2522930
 A:Accession: A33522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <JON>
 A:Cross-references: GB:M24456; NID:g198755; PIDN:AA846374.1; PID:g554185; GB:J04640; GB:
 R:Raschke, W.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
 A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
 A:Reference number: A29075; PMID:8709235; PMID:2948186
 A:Accession: A29075
 A:Molecule type: mRNA
 A:Residues: 961-1291 <RAS>
 A:Cross-references: GB:M15174; NID:g201105; PIDN:AAA40161.1; PID:g201106
 R:Tung, J.
 Immunogenetics 28, 271-277, 1988
 A:Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
 A:Reference number: I54450; PMID:86330145; PMID:3417340
 A:Accession: I54450
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 32-73 <RES>
 A:Cross-references: GB:M23241; NID:g340850; PIDN:AAA39460.1; PID:g548174
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A:Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishin
 A:Reference number: A28335; PMID:87260987; PMID:3037546

A/Accession: A28335
 A/Molecule type: mRNA
 A/Residues: 1-30,74-226 <SR2>
 A/Cross-references: GB:M1432
 R/Shen, F.W.; Sage, Y.; Litman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
 A/Reference number: A23329; MUID:8604265; PMID:3864163
 A/Accession: A23329
 A/Molecule type: mRNA
 A/Residues: 10-30,170-263 <SHE>
 A/Cross-references: GB:M1934; NID:g198919; PIDN:AAA39461.1; PID:g198920
 R/Saga, Y.; Tung, J.
 Mol. Cell. Biol. 8, 4889-4895, 1988
 A/Title: Organization of the ly-5 Gene
 A/Reference number: 157644; MUID:8906862; PMID:3211131
 A/Accession: 157644
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 'MT', 1-22 <RE2>
 A/Cross-references: GB:M2354; NID:g340890; PIDN:AAA39462.1; PID:g554192
 C/Genetics:
 A/Gene: ly-5
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MAT>
 F:24-566/Domain: extracellular #status predicted <EXT>
 F:24-30,170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicte
 F:555-586/Domain: transmembrane #status predicted <TM>
 F:553-1223/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:587-1291/Domain: intracellular #status predicted <INT>
 F:664-888/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: c
 F:840/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:846/Binding site: substrate phosphate (Arg) #status predicted

 Query Match 100.0%; Score 44; DB 1; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YIIHQALV 9
 Db 889 YIIHQALV 897

 RESULT 4
 A46546
 leukocyte common antigen long splice form precursor - human
 N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type C; T200 glycoprotei
 N/Contents: leukocyte common antigen intermediate splice form; leukocyte common antigen
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C/Accession: A46546; B46546; A29449; B29449; 157658
 R/Streuli, M.; Hall, L.R.; Sage, Y.; Schlossman, S.F.; Saito, H.
 J. Exp. Med. 166, 1548-1566, 1987
 A/Title: Differential usage of three exons generates at least five different mRNAs encod
 A/Reference number: A46546; MUID:88061067; PMID:2824653
 A/Accession: A46546
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1304 <STR>
 A/Cross-references: UNIPROT:P08575; GB:Y00638
 A/Experimental source: clone LCA.6/2
 A/Accession: B46546
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-32,99-264 <ST2>
 A/Cross-references: GB:Y00638
 A/Experimental source: clone LCA.111 and clone LCA.260
 A/Accession: C46546
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-31,193-264 <ST3>

A/Cross-references: GB:Y00638
 A/Experimental source: clone LCA.1
 R/Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
 EMBO J. 6, 1251-1257, 1987
 A/Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
 A/Reference number: A91066; MUID:87275816; PMID:2956090
 A/Accession: A29449
 A/Molecule type: mRNA
 A/Residues: 1-31,193-649,'U',651-869,'G',871-872,'A',874-1206,'P',1208-1304 <RAL>
 A/Cross-references: GB:Y0062; NID:g34275; PIDN:CAA68269.1; PID:g34276
 A/Experimental source: clones pHLc-1 and lambdaHLc1
 A/Accession: B29449
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 32-192 <RA2>
 A/Experimental source: clone HLC-2
 R/Tsai, A.Y.; Streuli, M.; Saito, H.
 Mol. Cell. Biol. 9, 4550-4555, 1989
 A/Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative
 A/Reference number: 157658; MUID:90066468; PMID:2531261
 A/Accession: 157658
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 146-192 <RES>
 A/Cross-references: GB:M29253; NID:g187020; PIDN:AAA59497.1; PID:g553521
 C/Genetics:
 A/Gene: GDB:PRRC; CD45
 A/Cross-references: GDB:119768; OMIM:151460
 A/Map position: 1q31-1q32
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hy
 F:54-123/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:857/Binding site: substrate phosphate (Arg) #status predicted

 Query Match 100.0%; Score 44; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YIIHQALV 9
 Db 900 YIIHQALV 908

 RESULT 5
 T43148
 probable protein-tyrosine-phosphatase (EC 3.1.3.48) - horn shark
 N/Alternate names: CD45 homolog
 C/Species: Heterodontus francisci (horn shark)
 C/Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 09-Jul-2004
 C/Accession: T43148
 R/Okumura, M.; Matthews, R.J.; Robb, B.; Bork, P.; Thomas, M.L.
 Submitted to the EMBL Data Library, August 1995
 A/Reference number: Z22317
 A/Accession: T43148
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1200 <OKU>
 A/Cross-references: UNIPROT:Q91054; EMBL:U34750; NID:g1304393; PID:g1335805; PIDN:AA011
 C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 93.2%; Score 41; DB 2; Length 1200;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YIIHQALV 9
 Db 800 YIIHQALV 808

 RESULT 6

T40513
Yeast erol homolog - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T40513
R/Gilliam, R.; Rajandram, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Submitted to the EMBL Data Library, September 1998
A/Reference number: Z21933
A/Accession: T40513
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-467 <GWI>
A/Cross-references: UNIPROT:O74401; EMBL:AL031534; PIDD:CAA20736.1; GSPDB:GN00067; SPDB:
A/Experimental source: strain 972h-; coamid c4P6
C/Genetics:
A/Gene: SPDB:SPBC4P6.16c
A/Map position: 2

Query Match 84.1%; Score 37; DB 2; Length 467;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps -0;

QY 1 YLIIHQALV 9
|:|:|:|:|
Db 270 YLIIHQALV 278

RESULT 7
AC0489
Probable iron transport permease YPO4024 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC0489
R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, J.
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AG0489
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-335 <KUR>
A/Cross-references: UNIPROT:Q8ZAO2; GB:AL590842; PIDD:CA093483.1; PTD:G15981928; GSPDB:C
C/Genetics:
A/Gene: YPO4024

Query Match 77.3%; Score 34; DB 2; Length 335;
Best Local Similarity 55.6%; Pred. No. 21;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLIIHQALV 9
|:|:|:|:|
Db 52 YLIIHQALV 60

RESULT 8
AB1015
Glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - Salmonella enterica subsp. enteri
C/Species: Salmonella enterica subsp. enterica serovar Typh
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
C/Accession: AB1015
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Mout, S.; O'Gea, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AB1015
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-806 <PAR>
A/Cross-references: GB:AL513382; PIDD:CAD09219.1; PTD:G16505223; GSPDB:GN00176
C/Genetics:
A/Gene: STY4431
C/Superfamily: Glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acylt
C/Keywords: acyltransferase; coenzyme A

Query Match 77.3%; Score 34; DB 2; Length 806;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YLIIHQALV 9
|:|:|:|:|
Db 317 YLIIHQALV 325

RESULT 9
D64090
Glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - Haemophilus influenzae (strain Rd
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
C/Accession: D64090
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: D64090
A/Molecule type: DNA
A/Status: nucleic acid sequence not shown; translation not shown
A/Residues: 1-810 <TIG>
A/Cross-references: UNIPROT:P44857; GB:U32758; GB:L42023; NID:G1573747; PIDD:ACC22406.1;
C/Superfamily: Glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acylt
C/Keywords: acyltransferase; coenzyme A; membrane protein; phospholipid biosynthesis

Query Match 77.3%; Score 34; DB 2; Length 810;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YLIIHQALV 9
|:|:|:|:|
Db 317 YLIIHQALV 325

RESULT 10
AC0039
Glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) [imported] - Yersinia pestis (strai
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 16-Aug-2004
C/Accession: AC0039
R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, J.
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AC0039
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-825 <KUR>
A/Cross-references: UNIPROT:Q8Z018; GB:AL590842; PIDD:CA09174.1; PTD:G15978413; GSPDB:G
C/Genetics:
A/Gene: p18B
C/Superfamily: Glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acylt
C/Keywords: acyltransferase; coenzyme A

Query Match 77.3%; Score 34; DB 2; Length 825;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YLIIHQALV 9

Db 316 YVLYHQGLV 324

RESULT 11

XUECAG

glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - Escherichia coli (strain K-12)

C/Species: Escherichia coli

C/Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Aug-2004

C/Accession: A00565; C42956; H65211

R/Lightner, V.A.; Bell, R.W.; Modrich, P.

J. Biol. Chem. 258, 10856-10861, 1983

A/Title: The DNA sequences encoding plb and dgk loci of Escherichia coli.

A/Reference number: A92393; MUID:83291031; PMID:6309817

A/Accession: A00565

A/Molecule type: DNA

A/Residues: 1-827 <LIG>

A/Cross-references: UNIPROT:P00482

A/Note: this sequence was partially confirmed by protein sequencing

R/Nichols, B.P.; Green, J.M.

J. Bacteriol. 174, 5309-5316, 1992

A/Title: Cloning and sequencing of Escherichia coli ubc and purification of chorismate

A/Reference number: A42956; MUID:92355505; PMID:1644758

A/Accession: C42956

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 805-827 <NIC>

A/Note: sequence extracted from NCBI backbone (NCBIN:110475, NCBI:P110483)

R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: H65211

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-827 <BLAT>

A/Cross-references: GB:AE000477; GB:U00096; NID:92367338; PIDN:AACT7011.1; PID:G1790474;

A/Experimental source: strain K-12, substrain MG1655

C/Genetics:

A/Gene: plbB

A/Map position: 92 min

C/Function:

A/Description: this membrane-bound enzyme catalyzes the first step in de novo phospholip

cid; it may also function in the regulation of membrane biogenesis

A/Pathway: phospholipid biosynthesis

C/Superfamily: Glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acylt

C/Keywords: acyltransferase; coenzyme A; membrane protein; phospholipid biosynthesis

Query Match

Best Local Similarity 66.7%; Pred. No. 56;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 337 YVLYHQGLV 345

QY 1 YVLYHQGLV 9

H91256

glycerol-3-phosphate acyltransferase [imported] - Escherichia coli (strain O157:H7, sub

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Jun-2003

C/Accession: H91256

R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

Gawawa, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A/Reference number: A9629; MUID:21156231; PMID:11258796

A/Accession: H91256

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-827 <HAY>

A/Cross-references: GB:BA000007; PIDN:BA838447.1; PID:G13364501; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain RIMD 0509952

C/Genetics:

A/Gene: EGS5024

C/Superfamily: glycerol-3-phosphate O-acyltransferase

Query Match

Best Local Similarity 77.3%; Score 34; DB 2; Length 827;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 337 YVLYHQGLV 345

QY 1 YVLYHQGLV 9

Db 337 YVLYHQGLV 345

RESULT 13

D86097

glycerol-3-phosphate acyltransferase [imported] - Escherichia coli (strain O157:H7, sub

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004

C/Accession: D86097

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayne

iller, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: D86097

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-827 <STO>

A/Cross-references: GB:AE005174; NID:G12518990; PIDN:AA659240.1; GSPDB:GN00145; UWGP:251

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: plbB

C/Superfamily: Glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acylt

Query Match

Best Local Similarity 77.3%; Score 34; DB 2; Length 827;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 337 YVLYHQGLV 345

QY 1 YVLYHQGLV 9

Db 337 YVLYHQGLV 345

RESULT 14

S73304

hypothetical protein 327 - red alga (Porphyra purpurea) chloroplast

C/Species: chloroplast Porphyra purpurea

C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C/Accession: S73304

R/Reich, M.; Munholland, J.

Plant Mol. Biol. Rep. 13, 333-335, 1995

A/Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.

A/Reference number: S73108

A/Accession: S73304

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-327 <REI>

A/Cross-references: UNIPROT:P51383; EMBL:U38804; NID:G1276652; PID:G1276649

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

C/Genetics:

A/Gene: chloroplast

C/Keywords: chloroplast

Query Match

Best Local Similarity 75.0%; Score 33; DB 2; Length 327;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 244 FILIHQDLI 252

QY 1 YVLYHQGLV 9

RESULT 15

AG2769
cytochrome P450 cys (imported) - Agrobacterium tumefaciens (strain C58, Dupont)
C:/Species: Agrobacterium tumefaciens
C:/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:/Accession: AG2769
R:/Wood, D.W.; Serubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A:/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:/Reference number: AB2577, MUID:21608550, PMID:11743193
A:/Accession: AG2769
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-464 <RUR>
A:/Cross-references: UNIPROT:Q8UPF1; GB:AE008688; PID:AAU42573.1; PID:GI7739998; GSPDB:G
A:/Experimental source: strain C58 (Dupont)
C:/Genetics:
A:/Gene: cys
A:/Map position: circular chromosome
C:/Superfamily: Bacillus halodurans cytochrome P450 BH0579; cytochrome P450 homology
C:/Keywords: heme; iron; metalloprotein
P/405/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 2 ILTHOALV 9
Best Local Similarity 75.0%; Score 33; DB 2; Length 464;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 65 VLTREALV 72

Search completed: May 3, 2005, 06:17:02
Job time : 13.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-13

Perfect score: 44

Sequence: 1 YILHQAIV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	878	2	Q8C607
2	44	100.0	962	2	Q6L2D3
3	44	100.0	1152	1	CD45_MOUSE
4	44	100.0	1237	2	Q91976
5	44	100.0	1255	1	CD45_RAT
6	44	100.0	1290	2	Q6ED60
7	44	100.0	1291	2	Q6ED62
8	44	100.0	1303	2	Q6ED61
9	44	100.0	1303	2	Q6ED62
10	44	100.0	1304	1	CD45_HUMAN
11	44	100.0	1343	2	Q64730
12	41	93.2	1200	2	Q91054
13	41	93.2	1245	2	Q918F0
14	41	93.2	1246	2	Q918F1
15	37	84.1	467	1	ERL1_SCHPO
16	37	84.1	907	2	Q8MY41
17	37	84.1	1100	2	Q8MY45
18	37	84.1	1187	2	Q8MY42
19	37	84.1	1202	2	Q8MY43
20	37	84.1	1216	2	Q91BD8
21	37	84.1	1222	2	Q8MY44
22	37	84.1	1285	2	Q6UNF4
23	36	81.8	736	1	KUP2_BIFLO
24	36	81.8	1384	2	Q7USX6
25	35	79.5	497	2	Q91B98
26	35	79.5	730	2	Q7OCM4
27	35	79.5	832	2	Q90S47
28	35	79.5	1457	2	Q61RM3
29	35	79.5	2271	2	Q91909
30	34	77.3	294	1	GLUB_CORGF
31	34	77.3	295	1	GLUB_CORGL

32	34	77.3	314	2	Q8C210	Q8C210
33	34	77.3	335	2	Q664B2	Q664B2
34	34	77.3	335	2	Q82A02	Q82A02
35	34	77.3	341	2	Q74Q53	Q74Q53
36	34	77.3	468	2	Q91BA5	Q91BA5
37	34	77.3	508	2	Q90YJ5	Q90YJ5
38	34	77.3	806	1	PLSB_ECO57	P58137
39	34	77.3	806	1	PLSB_ECO57	P58137
40	34	77.3	806	1	PLSB_SALTI	P00482
41	34	77.3	806	1	PLSB_SALTY	P00482
42	34	77.3	809	1	PLSB_PASWU	Q9C1N7
43	34	77.3	810	1	PLSB_HAEIN	P44857
44	34	77.3	818	1	PLSB_PHOIL	Q7MB37
45	34	77.3	823	2	Q65UK8	Q65UK8

ALIGNMENTS

RESULT 1

Q8C607 PRELIMINARY, PRT, 878 AA.

AC Q8C607;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230015G23 product:protein tyrosine DE phosphatase, receptor type, C, full insert sequence. (fragment).
GN Name=Ptpdc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RL "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RL "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RA The FANTOM Consortium;
RX "The RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M., Sumi N., Iihii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubara M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurahara H., Kawai J., Kojima Y., Kondo S., Kono M., Konda M., Koya S.,
 RA Kurahara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishii K., Nomura K., Numazaki R., Ono M., Onisato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashita S., Takeda Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK054056; BAC35638.1; -.
 DR HSSP: P18052; 1YFO.
 DR MGD: MGJ:97810; PpPrc.
 DR GO: GO:0009897; C:external side of plasma membrane; IDA.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0005515; F:protein binding; IPT.
 DR GO: GO:00030183; F:B-cell differentiation; IMP.
 DR GO: GO:0042100; F:B-cell proliferation; IMP.
 DR GO: GO:0030217; P:T-cell differentiation; IMP.
 DR GO: GO:0042098; P:T-cell proliferation; IMP.
 DR GO: GO:0046552; P:thymocyte differentiation; IMP.
 DR InterPro: IPR003961; FN_III-like.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00041; fn3; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRYHPHTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPc; 1.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase; Receptor.
 FT NON_TER 878 878
 SQ SEQUENCE 878 AA; 99891 MW; 19E5FCD7909D4CA6 CRC64;
 Query Match 100.0%; Score 44; DB 2; Length 878;
 Best Local Similarity 100.0%; Pred. No. 2.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YLIIHQALV 9
 Db 752 YLIIHQALV 760
 RESULT 2
 ID 06LDZ3 PRELIMINARY; PRT; 962 AA.
 AC 06LDZ3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Leukocyte common antigen.
 GN Name=L-CA;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;
 RX MEDLINE=85201691; PubMed=3158393; DOI=10.1016/0092-8674(85)90063-7;
 RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.,
 RT "Evidence from cDNA clones that rat leukocyte-common antigen (T200)
 RT spans the lipid bilayer and contains a cytoplasmic domain of 80,000 M-
 RT r.";
 RL Cell 41:83-93(1985).
 DR EMBL: M10072; AAA41513.1; -.
 DR HSSP: P18031; 1A5Y.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0004470; F:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003957; PTPc motif.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRYHPHTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPc; 2.
 DR SMART: SM00404; PTPc_motif; 2.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolyase.
 SQ SEQUENCE 962 AA; 109934 MW; D2E6B7F23D29C92 CRC64;
 Query Match 100.0%; Score 44; DB 2; Length 962;
 Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YLIIHQALV 9
 Db 560 YLIIHQALV 568
 RESULT 3
 ID CD45 MOUSE
 AC P06800;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 01-JAN-1988 (rel. 06, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (Lymphocyte
 DE common antigen Ly-5) (CD45) (T200).
 DE Name=PpPrc; Synonyms=Ly-5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86313686; PubMed=2944116;
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RT "Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
 RN [2]
 RP REVISIONS.
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
 RN [3]
 RP SEQUENCE OF 10-124 FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=86042665; PubMed=3864163;
 RA Shen F.-W., Saga Y., Litman G., Freeman G., Tung J.-S., Cantor H.,
 RA Boyse E.A.;
 RT "Cloning of Ly-5 cDNA";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
 RN [4]
 RP SEQUENCE OF 822-1152 FROM N.A.

RX MEDLINE=87092355; PubMed=2948186;
RA Raschke W.C.;
RT "Cloned murine T200 (ty-5) cDNA reveals multiple transcripts within B-
and T-lymphocyte lineages.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
RN [5]
RP INTERACTIONS WITH GANAB AND PRKCSH.
RX MEDLINE=97294720; PubMed=9148925; DOI=10.1074/jbc.272.20.13117,
RA Arent C.W., Oseberg H.L.;
RT "Identification of the CD45-associated 116-kDa and 80-kDa proteins as
the alpha- and beta-subunits of alpha-glucosidase II.";
RL J. Biol. Chem. 272:13117-13125(1997).
CC -1- FUNCTION: Required for T-cell activation through the antigen
receptor. The first PTPase domain has enzymatic activity, while
the second one seems to affect the substrate specificity of the
first one.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
tyrosine + phosphate.
CC -1- SUBUNIT: Binds GANAB and PRKCSH.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced;
Name=1;
CC -1- IsoId=P06800-1; Sequence=Displayed;
CC -1- DEVELOPMENTAL STAGE: Expression is restricted to the hematopoietic
compartment of development.
CC -1- PTM: Heavily N- and O-glycosylated.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Receptor class 1/6 subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.

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CC EMBL/ M14342; AAA39458.1; -
CC EMBL/ M11934; AAA39461.1; -
CC EMBL/ M15174; AAA40161.1; -
CC PIR/ A23329; A23329.
CC PIR/ A28334; A28334.
CC HSSP; P18052; 1YFO.
CC MOD; MGI:97810; PTPRC.
CC GO; GO:0009897; C:external side of plasma membrane; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR008957; FN_III-like.
CC InterPro: IPR000387; Tyr_phosphatase.
CC InterPro: IPR000242; Tyr_PP.
CC Pfam: PF00041; fn3; 3.
CC Pfam: PF00102; Y_phosphatase; 2.
CC PRINTS; PR00700; PRTYPHPTASE.
CC PROSITE; PS50853; FN3; 2.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
CC Alternative splicing; Antigen; Glycoprotein; Hydrolase;
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1152
FT DOMAIN 24 425
FT TRANSMEM 426 447
FT DOMAIN 448 1152
FT DOMAIN 232 328
FT DOMAIN 333 420
FT DOMAIN 520 769
FT DOMAIN 811 1084
Leukocyte common antigen.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Fibronectin type-III 1.
Fibronectin type-III 2.
Protein-tyrosine phosphatase 1.
Protein-tyrosine phosphatase 2.

FT ACT_SITE 701 701 Phosphocysteine intermediate (By
FT ACT_SITE 1016 1016 similarity).
FT CARBOHYD 68 68 Phosphocysteine intermediate (By
FT CARBOHYD 72 72 similarity).
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 119 119 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 208 208 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 277 277 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 288 288 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 318 318 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 350 350 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 379 379 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1152 AA; 130421 MW; BAD956B4E32EA812 CRC64;
Query Match 100.0%; Score 44; DB 1; Length 1152;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YIIHQALV 9
DB 750 YIIHQALV 758

RESULT 4
ID 091976 PRELIMINARY; PRT; 1237 AA.
AC 091976;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein tyrosine phosphatase lamda precursor (Protein tyrosine
phosphatase lambda precursor).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
OC [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RC TISSUE=Brain;
RC Fang K.S., Barker K., Sudol M., Hanafusa H.;
RT "A transmembrane protein-tyrosine-phosphatase contains spectrin-like
RT repeats in its extracellular domain.";
RL J. Biol. Chem. 269:14056-14063(1994).
RL EMBL/ L13285; AAA20561.1; -
DR PIR: A54080; A54080.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.


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FT CONFLICT 38 38 /Frid=VSP 005168.
SQ SEQUENCE 1255 AA; 141208 MW; C257CBD2A355CEA CRC64;
Query Match 100.0%; Score 44; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
| | | | |
| | | | |
Db 853 YIIHQALV 861

RESULT 6
Q6ED60 PRELIMINARY; PRT; 1290 AA.
ID Q6ED60
AC Q6ED60;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD45.
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human."
RL Tissue Antigens 64:165-172(2004).
DR GO; GO:0004725; P:Protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR00242; Tyr_PP.
DR SMART; SM00060; FNF3; 2.
DR SMART; SM00194; PTPc; 2.
DR SMART; SM00404; PTPc_motif; 2.
DR PROSITE; PS50853; FNF3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolyase.
SQ SEQUENCE 1290 AA; 145616 MW; 99E810C75D932824 CRC64;

Query Match 100.0%; Score 44; DB 2; Length 1290;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
| | | | |
| | | | |
Db 886 YIIHQALV 894

RESULT 7
Q6B12 PRELIMINARY; PRT; 1291 AA.
ID Q6B12
AC Q6B12;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lymphocyte common antigen precursor.
GN Name=PTPc; Synonyms=Ly5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=92361152; PubMed=1822988;
RA Zebadee S.L., Barritt D.S., Raschke W.C.;
RT "Comparison of mouse Ly5 A and Ly5 B leukocyte common antigen
alleles."
RL Dev. Immunol. 1:243-254(1991).
DR EMBL; M92933; AAA39459.1; -.
DR HSSP; P18052; 1YFO.
DR MGD; MGI:97810; PTPc.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0030183; P:B-cell differentiation; IMP.
DR GO; GO:0042100; P:B-cell proliferation; IMP.
DR GO; GO:0030217; P:T-cell differentiation; IMP.
DR GO; GO:0042098; P:T-cell proliferation; IMP.
DR GO; GO:0046652; P:thymocyte differentiation; IMP.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR00387; Tyr_PP.
DR InterPro; IPR00242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00700; PRTYPHTASE.
DR SMART; SM00060; FNF3; 2.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS50853; FNF3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolyase; Signal.
FT SIGNAL 1
SQ SEQUENCE 1291 AA; 144559 MW; 25C3CB1AF4350CE CRC64;

Query Match 100.0%; Score 44; DB 2; Length 1291;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
| | | | |
| | | | |
Db 889 YIIHQALV 897

RESULT 8
Q6ED61 PRELIMINARY; PRT; 1303 AA.
ID Q6ED61
AC Q6ED61;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD45.
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human."
RL Tissue Antigens 64:165-172(2004).
DR EMBL; AY445817; AAS06902.1; -.
DR GO; GO:0004725; P:Protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR00387; Tyr_PP.
DR InterPro; IPR00242; Tyr_PP.
```


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CC -----
DR EMBL; Y00638; CA68669.1; -
DR EMBL; Y00662; CA68269.1; -
DR EMBL; M23492; AAD15273.2; -
DR EMBL; M23496; AAD15273.2; JOINED.
DR EMBL; M23466; AAD15273.2; JOINED.
DR EMBL; M23467; AAD15273.2; JOINED.
DR EMBL; M23468; AAD15273.2; JOINED.
DR EMBL; M23469; AAD15273.2; JOINED.
DR EMBL; M23470; AAD15273.2; JOINED.
DR EMBL; M23471; AAD15273.2; JOINED.
DR EMBL; M23472; AAD15273.2; JOINED.
DR EMBL; M23473; AAD15273.2; JOINED.
DR EMBL; M23474; AAD15273.2; JOINED.
DR EMBL; M23475; AAD15273.2; JOINED.
DR EMBL; M23476; AAD15273.2; JOINED.
DR EMBL; M23477; AAD15273.2; JOINED.
DR EMBL; M23478; AAD15273.2; JOINED.
DR EMBL; M23479; AAD15273.2; JOINED.
DR EMBL; M23480; AAD15273.2; JOINED.
DR EMBL; M23481; AAD15273.2; JOINED.
DR EMBL; M23482; AAD15273.2; JOINED.
DR EMBL; M23483; AAD15273.2; JOINED.
DR EMBL; M23484; AAD15273.2; JOINED.
DR EMBL; M23485; AAD15273.2; JOINED.
DR EMBL; M23486; AAD15273.2; JOINED.
DR EMBL; M23487; AAD15273.2; JOINED.
DR EMBL; M23488; AAD15273.2; JOINED.
DR EMBL; M23489; AAD15273.2; JOINED.
DR EMBL; M23490; AAD15273.2; JOINED.
DR EMBL; M23491; AAD15273.2; JOINED.
DR PIR; A46546; A46546.
DR HSP; P18031; 1C88.
DR Inact; P08575; -
DR GlycoSiteDB; P08575; -
DR Genew; HGNC:9666; PTPRC.
DR MIM; 151460; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PTPPHPTASE.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PP; 2.
DR Alternative splicing; Antigen; Glycoprotein; Hydrolase;
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KW Transmembrane.
FT SIGNL 1 23
FT CHAIN 24 1304
FT DOMAIN 24 575
FT TRANSMEM 576 597
FT DOMAIN 598 1304
FT DOMAIN 390 478
FT DOMAIN 482 570
FT DOMAIN 670 919
FT DOMAIN 961 1235
FT ACT SITE 851
FT ACT_SITE 1167 1167

FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 197 197 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 260 260 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 276 276 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 335 335 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 378 378 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 419 419 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 468 468 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 529 529 N-linked (GlcNAc...) (Potential)
FT VARSPLIC 32 192 Missing (in isoform 2).
FT MUTAGEN 851 851 C->S: Loss of activity.
FT CONFLICT 650 650 L -> P (in Ref. 1).
FT CONFLICT 1207 1207 P -> L (in Ref. 1).
SQ SEQUENCE 1304 AA; 147253 MW; A08FC2D069BAF7 CRC64;

Query Match 100.0%; Score 44; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLIIHQALV 9
Db 900 YLIIHQALV 908

RESULT 11
Q64730 PRELIMINARY; PRT; 1343 AA.
AC Q64730;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leucocyte common antigen (L-Ca) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260986; PubMed=2955416;
RA Thomas M.L., Reynolds P.J., Chain A., Ben-Neriah Y., Trowbridge I.S.;
RT "B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA
RT splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5360-5363 (1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89197920; PubMed=2522930;
RA Johnson N.A., Meyer C.M., Pingel J.T., Thomas M.L.;
RT "Sequence conservation in potential regulatory regions of the mouse
RT and human leukocyte-common antigen gene.";
RJ J. Biol. Chem. 264:6220-6229 (1989).
LR EMBL; M23148; AAA39418.1; JOINED.
DR EMBL; M23149; AAA39418.1; JOINED.
DR EMBL; M23150; AAA39418.1; JOINED.
DR EMBL; M23151; AAA39418.1; JOINED.
DR EMBL; M23152; AAA39418.1; JOINED.
DR EMBL; M23153; AAA39418.1; JOINED.
DR EMBL; M23154; AAA39418.1; JOINED.
DR EMBL; M23155; AAA39418.1; JOINED.
DR EMBL; M23156; AAA39418.1; JOINED.
DR EMBL; M23157; AAA39418.1; JOINED.
DR EMBL; M23158; AAA39418.1; JOINED.
DR EMBL; M23159; AAA39418.1; JOINED.
DR EMBL; M23160; AAA39418.1; JOINED.
DR EMBL; M23161; AAA39418.1; JOINED.
DR EMBL; M23162; AAA39418.1; JOINED.
DR EMBL; M23163; AAA39418.1; JOINED.
DR EMBL; M23164; AAA39418.1; JOINED.
DR EMBL; M23165; AAA39418.1; JOINED.
DR EMBL; M23166; AAA39418.1; JOINED.
DR EMBL; M23167; AAA39418.1; JOINED.
DR EMBL; M23168; AAA39418.1; JOINED.
DR EMBL; M23169; AAA39418.1; JOINED.
DR EMBL; M23170; AAA39418.1; JOINED.
DR EMBL; M23171; AAA39418.1; JOINED.
DR EMBL; M23172; AAA39418.1; JOINED.
DR EMBL; M23173; AAA39418.1; JOINED.
DR EMBL; M23174; AAA39418.1; JOINED.
DR EMBL; M23175; AAA39418.1; JOINED.
DR EMBL; M23176; AAA39418.1; JOINED.
DR EMBL; M23177; AAA39418.1; JOINED.
DR EMBL; M23178; AAA39418.1; JOINED.
DR EMBL; M23179; AAA39418.1; JOINED.
DR EMBL; M23180; AAA39418.1; JOINED.
DR EMBL; M23181; AAA39418.1; JOINED.
DR EMBL; M23182; AAA39418.1; JOINED.
DR EMBL; M23183; AAA39418.1; JOINED.
DR EMBL; M23184; AAA39418.1; JOINED.
DR EMBL; M23185; AAA39418.1; JOINED.
DR EMBL; M23186; AAA39418.1; JOINED.
DR EMBL; M23187; AAA39418.1; JOINED.
DR EMBL; M23188; AAA39418.1; JOINED.
DR EMBL; M23189; AAA39418.1; JOINED.
DR EMBL; M23190; AAA39418.1; JOINED.
DR EMBL; M23191; AAA39418.1; JOINED.
DR EMBL; M23192; AAA39418.1; JOINED.
DR EMBL; M23193; AAA39418.1; JOINED.
DR EMBL; M23194; AAA39418.1; JOINED.
DR EMBL; M23195; AAA39418.1; JOINED.
DR EMBL; M23196; AAA39418.1; JOINED.
DR EMBL; M23197; AAA39418.1; JOINED.
DR EMBL; M23198; AAA39418.1; JOINED.
DR EMBL; M23199; AAA39418.1; JOINED.
DR EMBL; M23200; AAA39418.1; JOINED.
DR EMBL; M23201; AAA39418.1; JOINED.
DR EMBL; M23202; AAA39418.1; JOINED.
DR EMBL; M23203; AAA39418.1; JOINED.
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DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003361; FN_III.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00102; Y_phosphatase; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
FT NON_TER 1
SQ SEQUENCE 1343 AA; 150679 MW; 0DBB8C97FC4C6A9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 1343;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLHIOALV 9
DB 915 YLHIOALV 923

RESULT 12
Q91054 PRELIMINARY; PRT; 1200 AA.
AC Q91054;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CD45 homolog.
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_Taxid=7792;
RN [1]_Taxid=7792;
RP SEQUENCE FROM N.A.
RA Okumura M., Matthews R.J., Robb B., Bork P., Thomas M.L.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34750; AAB01087.1; -.
DR PIR; T43148; T43148.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1245 AA; 141324 MW; 6CB711BFF5797555 CRC64;

Query Match
Best Local Similarity 93.2%; Score 41; DB 2; Length 1245;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLHIOALV 9
DB 867 YLHIOALV 875

RESULT 14
Q918F1 PRELIMINARY; PRT; 1246 AA.
AC Q918F1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD45 precursor (EC 3.1.3.48).
GN Name=PTPRC;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

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DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1200 AA; 135372 MW; EFC6B2B4DC02BC2 CRC64;

Query Match
Best Local Similarity 93.2%; Score 41; DB 2; Length 1200;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLHIOALV 9
DB 800 YLHIOALV 808

RESULT 13
Q918F0 PRELIMINARY; PRT; 1245 AA.
AC Q918F0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD45 (EC 3.1.3.48).
GN Name=PTPRC;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_Taxid=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Diaz del Pozo E.M., Beverley P.C., Timon M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243430; CAB96212.1; -.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003361; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHTASE.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SQ SEQUENCE 1245 AA; 141324 MW; 6CB711BFF5797555 CRC64;

Query Match
Best Local Similarity 93.2%; Score 41; DB 2; Length 1245;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLHIOALV 9
DB 867 YLHIOALV 875

RESULT 14
Q918F1 PRELIMINARY; PRT; 1246 AA.
AC Q918F1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD45 precursor (EC 3.1.3.48).
GN Name=PTPRC;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Diaz del Pozo E.M., Beverley P.C., Timon M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243429; CAB96211.1; -
 DR HSSP; P18052; 1YFO.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0006470; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR00242; Tyr_PP.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS50853; FN3; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PP; 2.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 1246 CD45.
 SQ SEQUENCE 1246 AA; 141363 MW; 4643259F5CA48E8E CRC64;
 Query Match 93.2%; Score 41; DB 2; Length 1246;
 Best Local Similarity 88.9%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YLIIHQALV 9
 DB 868 YLIIHQALV 876
 RESULT 15
 ERLB_SCHPO STANDARD; PRT; 467 AA.
 ID ERLB_SCHPO
 AC 074401;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE ERO1-like protein B precursor (EC 1.8.4.-) (Endoplasmic oxidoreductin
 DE 1-like protein B)
 GN ORFNames=SPBC4F6.16c;
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NCBI_TaxID=4896;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA MEDLINE=11848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Brooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidayat J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Woltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Aner S.,
 RA Gabel K., Fuchs M., Filicz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucac M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussey D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Essential oxidoreductase that oxidizes proteins in the
 CC endoplasmic reticulum to produce disulfide bonds. Acts by
 CC oxidizing directly pdil isomerase through a direct disulfide
 CC exchange. Does not act as a direct oxidant of folding substrate,
 CC but relies on pdil to transfer oxidizing equivalent. Does not
 CC oxidize all pdil related proteins, suggesting that it can
 CC discriminate between pdil and related proteins. Its reoxidation
 CC probably involves electron transfer to molecular oxygen via FAD.
 CC Acts independently of glutathione. May be responsible for a
 CC significant proportion of reactive oxygen species (ROS) in the
 CC cell, thereby being a source of oxidative stress (By similarity).
 CC -1- COPACTOR: FAD (By similarity).
 CC -1- SUBUNIT: May function both as a monomer and a homodimer (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen; membrane-
 CC associated (By similarity).
 CC -1- SIMILARITY: Belongs to the EROs family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AL031534; CA20736.1; -
 DR PIR; T40513; T40513.
 DR GeneDB; SPombe; SPBC4F6.16c; -
 DR InterPro; IPR007266; ERO1.
 DR Pfam; PF04137; ERO1; 1.
 KW Electron transport; Endoplasmic reticulum; FAD; Flavoprotein;
 KM Membrane; Oxidoreductase; Redox-active center; Signal; Transport.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 467 ERO1-like protein B.
 FT NP_BIND 147 147 FAD (By similarity).
 FT NP_BIND 149 149 FAD (By similarity).
 FT NP_BIND 160 160 FAD (By similarity).
 FT NP_BIND 223 223 FAD (By similarity).
 FT NP_BIND 226 226 FAD (By similarity).
 FT NP_BIND 255 255 FAD (By similarity).
 FT NP_BIND 355 355 By similarity.
 FT DISULFID 78 83 Redox-active (By similarity).
 FT DISULFID 358 361 Redox-active (By similarity).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 129 129 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 286 286 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 421 421 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 467 AA; 54625 MW; 49DB8E3B4DB5035E CRC64;

Query Match 84.1%; Score 37; DB 1; Length 467;
 Best Local Similarity 77.8%; Pred. No. 45;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YLIIHQALV 9
 DB 270 YLIIHQALV 278

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Job time : 47.1351 secs

CC antigen-presenting cell contains an expression vector including the
 CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
 CC for killing, and in the manufacture of a medicament for, target cells
 CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
 CC recognizing cells expressing the CD45 peptides, is useful for killing
 CC target cells (cancer cells) in a patient which involves obtaining CTLs
 CC from the patient, introducing into the CTLs the polynucleotide encoding
 CC the TCR and then introducing the cells thus produced into the patient who
 CC has undergone an allogeneic stem cell transplantation. Tumour reactive
 CC CTLs have been shown to mediate tumour regression in animals models by
 CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
 CC colony formation. The cancer is leukaemia which expresses the CD45
 CC polypeptide. The method is useful as an immunotherapeutic for treating a
 CC patient with hematopoietic malignancy or to target and kill cells which
 CC express the CD45 polypeptide. The advantage this method provides is that
 CC the CTLs destroy the malignant haematopoietic cells but not the
 CC transplanted cells. The sequence presented is the peptide, huCD45/900,
 CC comprising an HLA-binding peptide of human CD45
 XX

SO Sequence 9 AA;

Query Match 100.0%; Score 44; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLIIHQALV 9
 |||||
 1 YLIIHQALV 9

RESULT 2

ID ADJ92680 standard; protein; 235 AA.

ADJ92680;

06-MAY-2004 (first entry)

Human leukocyte common antigen (LCA) phosphatase domain (PD) 1.

Receptor-type protein tyrosine phosphatase; RPTP;
 phosphotyrosine phosphatase; cancer; diabetes; human;
 leukocyte common antigen; LCA; phosphatase domain; PD.

Homo sapiens.

US6682905-B1.

27-JAN-2004.

29-MAR-1999; 99US-00280597.

11-JUL-1990; 90US-00551270.

26-FEB-1991; 91US-00654188.

10-FEB-1993; 93US-00015985.

23-MAY-1995; 95US-00448288.

(UYNV) UNIV NEW YORK STATE.

Schlessinger J, Sap JM;

WPI; 2004-118574/12.

Identifying a compound that modulates the phosphotyrosine phosphatase
 activity of a polypeptide by incubating the compound with the
 polypeptide, which is in pure form, in a membrane preparation or in a
 whole cell.

Example; SEQ ID NO 5; 52pp; English.

The invention relates to receptor-type protein tyrosine phosphatase
 (RPTP) and its corresponding nucleic acid. The invention also relates to
 a method for identifying a compound that modulates the phosphotyrosine

CC phosphatase activity. The method is useful for identifying a compound
 CC that modulates the phosphotyrosine phosphatase activity of a polypeptide
 CC and for identifying susceptibility to cancer, diabetes or other diseases
 CC associated with alterations in cellular phosphotyrosine metabolism. The
 CC present sequence is human leukocyte common antigen (LCA) phosphatase
 CC domain (PD) 1. This sequence is used to illustrate the method of the
 CC invention.

SO Sequence 235 AA;

Query Match 100.0%; Score 44; DB 8; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLIIHQALV 9
 |||||
 226 YLIIHQALV 234

RESULT 3

ID ADD22988 standard; protein; 248 AA.

ADD22988;

15-JAN-2004 (first entry)

Human protein tyrosine phosphatase, CD45-D1.

Human; enzyme; protein tyrosine phosphatase; PRPH1; cytosolic;
 gene therapy; retroviral vector; phosphotyrosine; pp60(v-src);

breast cancer; leukaemia; CD45-D1.

Homo sapiens.

US2003113294-A1.

19-JUN-2003.

12-NOV-2002; 2002US-00293231.

14-MAR-1990; 90US-00494036.

01-MAR-1991; 91US-00663579.

16-AUG-1993; 93US-00107420.

04-DEC-1996; 96US-00759536.

22-MAY-1999; 99US-00235251.

03-MAY-2001; 2001US-00848294.

(COLD-) COLD SPRING HARBOR LAB.

Tonke NK;

WPI; 2003-810871/76.

New isolated RNA encoding protein tyrosine phosphatase designated as
 PRPH1 useful for treating malignancies such as breast cancer, leukemia.

Disclosure; Fig 4B, 12pp; English.

The invention relates to an isolated RNA encoding a protein tyrosine
 phosphatase designated as PRPH1 appearing as ADD22982. Also included is a
 retroviral vector comprising the RNA. The RNA is useful for treating or
 preventing a condition in which abnormally high levels of phosphotyrosine
 occur in a mammalian cell (which involves introducing into the mammalian
 cell and agent which comprises DNA or RNA encoding all or a portion of a
 PRPH1, under conditions sufficient to express PRPH1 where the polypeptide
 can catalyse dephosphorylation of tyrosyl residues that are

phosphorylated through action of a protein tyrosine kinase. The RNA is
 also useful for reversing a malignant phenotype of a mammalian cell which
 is associated with tyrosyl phosphorylation catalysed by a protein

tyrosine kinase. The DNA or RNA is delivered via a recombinant retrovirus
 or a recombinant vaccinia virus. At least one tyrosyl residue that is

dephosphorylated by the protein tyrosine phosphatase polypeptide can be

dephosphorylated by the protein tyrosine phosphatase polypeptide can be

CC aberrantly phosphorylated by pp60(V-src). The RNA is useful for treating
CC or preventing malignancies such as breast cancer and leukaemia. The
CC present sequence is a PTP similar to PTPH1.

XX Sequence 248 AA;

Query Match 100.0%; Score 44; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
Db 226 YIIHQALV 234

RESULT 4
AAB59374
ID AAB59374 standard; protein; 253 AA.

XX AAB59374;

AC 21-MAR-2001 (first entry)

XX Murine protein tyrosine phosphatase #1.

KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KM substrate trapping.

OS Mus sp.

XX WO200075339-A1.

XX 14-DEC-2000.

PF 24-MAY-2000; 2000WO-US014211.

XX 03-JUN-1999; 99US-0137319P.

PR 16-JUN-1999; 99US-00334575.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Tonks NK, Zhang S;

XX WPI; 2001-080598/09.

PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in
PT which the wild type PTP catalytic domain invariant aspartate is replaced
PT with an unphosphorylated amino acid, useful in gene therapy.

XX Disclosure; Fig 1; 109pp; English.

CC The present invention provides substrate trapping mutant protein tyrosine
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine
CC phosphorylated proteins and to screen for modulators capable of altering
CC the binding of protein tyrosine phosphatases to their substrate. These
CC may be used in disease diagnosis and treatment

XX Sequence 253 AA;

Query Match 100.0%; Score 44; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
Db 235 YIIHQALV 243

RESULT 5
AAG78272
ID AAG78272 standard; protein; 309 AA.

XX AAG78272;

XX 19-DEC-2001 (first entry)

XX Mouse CD45-D1.

KM PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
KM dephosphorylation; phosphotyrosine; human, PTP1B, mouse; fruit fly;
KM yeast.

OS Mus sp.

XX WO200161031-A2.

XX 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US005180.

PR 14-FEB-2000; 2000US-0181769P.

XX (CEPT-) CEPTYR INC.

XX Flint AJ, Cool DE;

XX WPI; 2001-570570/64.

PT Screening assays to identify agents that alter protein tyrosine
PT phosphatase (PTP) binding to, and PTP-mediated catalytic
PT dephosphorylation of phosphotyrosine peptide substrates.

XX Disclosure; Fig 1; 79pp; English.

CC The invention relates to identifying agents which alter the interaction
CC between a protein tyrosine phosphatase (PTP) and a tyrosine
CC phosphorylated polypeptide using fluorescence energy signals. The methods
CC are useful for performing screening assay to identify agents that alter
CC PTP binding to and PTP-mediated catalytic dephosphorylation of
CC phosphotyrosine peptide substrates. The present sequence is that of a
CC catalytic domain of a PTP for comparison with human PTP1B (AAG78262)

XX Sequence 309 AA;

Query Match 100.0%; Score 44; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
Db 235 YIIHQALV 243

RESULT 6

ABO84454
ID ABO84454 standard; protein; 764 AA.

XX ABO84454;

XX 18-NOV-2004 (first entry)

XX Human cancer-associated protein HPI3-011.1.

KM Human; cancer-associated protein; cytosolic; cancer; leukaemia;
KM lymphoma; CMP.

XX Homo sapiens.

XX WO2004074320-A2.

XX 02-SEP-2004.

XX 17-FEB-2004; 2004WO-US004730.

XX 14-FEB-2003; 2003US-00367094.

XX 14-MAR-2003; 2003US-00388838.

DT 06-MAY-2004 (first entry)
XX
DE Rat protein tyrosine phosphatase #7.
XX
KW cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
OS Rattus norvegicus.
XX
PN W02003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
XX
PR 12-FEB-2003; 2003US-0036547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PA (CEPT-) CEPTYR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-PSDB; ADL16235.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 85; 238pp; English.
XX
XX The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP, (ii) isolating PTP
CC anaerobically, in presence of a sulphydryl-reactive agent (ii) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
SQ Sequence 962 AA;
XX
Query Match 100.0%; Score 44; DB 7; Length 962;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 YLTHQALV 9
DB 560 YLTHQALV 568
XX
RESULT 9
ABU05246
ID ABU05246 standard; protein; 1114 AA.
XX
AC ABU05246;
XX
DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1912.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN W0200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
XX
PR 21-MAY-2001; 2001US-0292544P.
XX
PR 08-AUG-2001; 2001US-0310801P.
XX
PR 01-OCT-2001; 2001US-0326370P.
XX
PR 04-DEC-2001; 2001US-0336780P.
XX
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1912; 134pp; English.
XX
PS The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIFO at
CC ftp.wifo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;
XX
Query Match 100.0%; Score 44; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 YLTHQALV 9
DB 710 YLTHQALV 718
XX
RESULT 10
ABU05239
ID ABU05239 standard; protein; 1114 AA.
XX
AC ABU05239;
XX
DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1905.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1905; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1114 AA;
XX
XX Query Match 100.0%; Score 44; DB 6; Length 1114;
XX Best Local Similarity 100.0%; Pred. No. 7.4;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YILIHQALV 9
XX |||||
XX 710 YILIHQALV 718
XX
XX RESULT 11
XX ABU05240
XX ID ABU05240 standard; protein; 1143 AA.
XX
XX AC ABU05240;
XX
XX 29-JAN-2003 (first entry)
XX
XX

DE Human expressed protein tag (EPT) #1906.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1906; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1143 AA;
XX
XX Query Match 100.0%; Score 44; DB 6; Length 1143;
XX Best Local Similarity 100.0%; Pred. No. 7.6;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YILIHQALV 9
XX |||||
XX 739 YILIHQALV 747
XX
XX RESULT 12
XX ABU05245
XX ID ABU05245 standard; protein; 1143 AA.
XX
XX AC ABU05245;
XX
XX 29-JAN-2003 (first entry)
XX
XX

DE Human expressed protein tag (EPT) #1911.
 XX
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WC0200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PE 28-MAR-2002; 2002MO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 XX (ZYCO-) ZYCOs INC.
 XX
 PA Chicx RM, Tomlinson AJ, Urban RG;
 PI
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1911, 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 1143 AA;
 Query Match 100.0%; Score 44; DB 6; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 7.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YLIIHQALV 9
 | | | | | | | | | |
 Db 739 YLIIHQALV 747
 RESULT 13
 ID ADL16232 standard; protein; 1143 AA.
 XX
 AC ADL16232;
 XX
 DT 06-MAY-2004 (first entry)
 XX

DE Human protein tyrosine phosphatase #27.
 XX
 XX
 KW cytostatic; immunosuppressive; anti-allergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signalling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WC02003068984-A2.
 XX
 PD 21-AUG-2003.
 XX
 PE 13-FEB-2003; 2003MO-EP001446.
 XX
 PR 13-FEB-2002; 2002US-0356810P.
 PR 12-FEB-2003; 2003US-00366547.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (CEPT-) CEPTyr INC.
 XX
 PI Tonks NK, Tzu-Ching M, Cool DE;
 PI
 DR WPI; 2003-712572/67.
 DR N-PSDB; ADL16231.
 XX
 PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 81; 238pp; English.
 XX
 CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 XX
 SO Sequence 1143 AA;
 Query Match 100.0%; Score 44; DB 7; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 7.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YLIIHQALV 9
 | | | | | | | | | |
 Db 739 YLIIHQALV 747
 RESULT 14
 ID ADQ18845 standard; protein; 1143 AA.
 XX
 AC ADQ18845;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
 XX

KM soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 XX Homo sapiens.
 OS
 XX WO2004048938-A2.
 PN
 XX 10-JUN-2004.
 PD
 XX 26-NOV-2003; 2003WO-US038193.
 PF
 XX 26-NOV-2002; 2002US-0429739P.
 PR
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA
 XX Aziz N, Gineburg WM, Zlotnick A;
 PI WPI; 2004-441208/41.
 DR
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 PS
 XX Example 2; SEQ ID NO 1664; 210pp; English.
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 SQ Sequence 1143 AA;
 XX
 Query Match 100.0%; Score 44; DB 8; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 7.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 YIIHQALV 9
 DB 739 YIIHQALV 747
 RESULT 15
 ID AAM41048 standard; protein; 1149 AA.
 AC AAM41048;
 XX
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 5979.
 XX
 KM Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KM leukaemia.
 XX
 OS Homo sapiens.
 XX WO20015312-A1.
 PN
 XX 26-JUL-2001.
 PD

PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Dymnac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AA160204.
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 PS
 XX Example 2; SEQ ID NO 5979; 10078pp; English.
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 SQ Sequence 1149 AA;
 XX
 Query Match 100.0%; Score 44; DB 4; Length 1149;
 Best Local Similarity 100.0%; Pred. No. 7.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 YIIHQALV 9
 DB 745 YIIHQALV 753
 RESULT 16
 ID ABU05242 standard; protein; 1149 AA.
 AC ABU05242;
 XX
 DT 29-JAN-2003 (first entry)
 DE Human expressed protein tag (EPT) #1908.
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX WO200278524-A2.
 PN
 XX

PD 10-OCT-2002.
XX
XX 28-MAR-2002; 2002MO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
PI
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1908; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPR) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1149 AA;
SQ
Query Match 100.0%; Score 44; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YIIHQALV 9
Db 745 YIIHQALV 753
RESULT 17
ABO84453
ID ABO84453 standard; protein; 1157 AA.
XX
XX ABO84453;
AC
XX 18-NOV-2004 (first entry)
DT
XX
XX Mouse cancer-associated protein MP13-011.1.
DE
XX
XX Mouse; cancer-associated protein; cytoskeletal; cancer; leukemia;
KW lymphoma; CAP.
XX
XX Mus musculus.
OS
XX
XX WO2004074320-A2.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 17-FEB-2004; 2004MO-US004730.
PF

XX
XX 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00413735.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Morris DW, Malandro MS;
PI
XX WPI; 2004-652914/63.
XX
XX N-PSDB; ABD2623.
DR
XX
XX New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
XX disclosure; seqid 142; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1157 AA;
SQ
Query Match 100.0%; Score 44; DB 8; Length 1157;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YIIHQALV 9
Db 755 YIIHQALV 763
RESULT 18
ADR39747
ID ADR39747 standard; protein; 1192 AA.
XX
XX ADR39747;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX

DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
XX human; kinase and phosphatase protein; KPP; enzyme; cytosolic;
XX antiarteriosclerotic; anticonvulsant; neuroprotective;
XX cerbroprotective; anti-HIV; antiallergic; antiinflammatory;
XX chymotrypsin; gene therapy; cell proliferative disorder; cancer;
XX atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
XX stroke; immune disorder; inflammatory disorder; AIDS; allergy; infection;
XX developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX KPP-20.
XX Homo sapiens.
XX OS
XX PN WO2004074453-A2.
XX PD 02-SEP-2004.
XX PF 20-FEB-2004; 2004WO-US005092.
XX PR 20-FEB-2003; 2003US-0449059P.
XX PR 19-MAR-2003; 2003US-0456932P.
XX PR 28-MAR-2003; 2003US-0458844P.
XX PR 09-APR-2003; 2003US-0461678P.
XX PR 17-APR-2003; 2003US-0463937P.
XX PA (INCYTE) INCYTE CORP.
XX PI Ramkumar J, Marguis JP, Swarnakar A, Chawla NK, Tran UK,
XX PI Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X,
XX PI Jackson AA, Yang J, Gorvad AE;
XX DR MPI: 2004-635568/61.
XX DR N-PSDB; AD839793.
XX PT New human kinases and phosphatases (KPP) for diagnosing, treating and
XX PT preventing diseases or conditions associated with aberrant KPP expression
XX PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX PS Claim 1, SEQ ID NO 20; 299pp; English.
XX CC The present sequence represents the human kinase and phosphatase protein
XX CC (KPP), designated KPP-20. The human KPP sequences from the present
XX CC invention have cytosolic, antiarteriosclerotic, anticonvulsant,
XX CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
XX CC antiinflammatory and thymomimetic activities, and can be used in gene
XX CC therapy. The human KPP proteins and polynucleotides can be used in
XX CC diagnosing, treating and preventing diseases or conditions associated
XX CC with the decreased expression or overexpression of KPP, such as cell
XX CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
XX CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
XX CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
XX CC disorders, or infections. They can also be used in assessing the effects
XX CC of exogenous compounds on the expression of nucleic acid and amino acid
XX CC sequences of KPP. The KPP or its fragments are useful in screening
XX CC compounds for effectiveness as agonist or antagonist of the polypeptides,
XX CC or in altering the expression of the target polynucleotide and compounds
XX CC that specifically bind to or modulate the activity of the polypeptide.
XX SQ Sequence 1192 AA;
QY Query Match 100.0%; Score 44; DB 8; Length 1192;
Db Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YILIHQALV 9
788 YILIHQALV 796
RESULT 19
ADO39378
XX ADO39378 standard; protein; 1219 AA.

AC ADO39378;
XX DT 18-NOV-2004 (first entry)
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiant; gene therapy; human.
XX OS
XX PN WO2004058052-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US040978.
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0451135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX PA (APPL-) APPLERA CORP.
XX PI Cargill M, Devlin J, Iakoubova O;
XX PI MPI: 2004-533949/51.
XX DR N-PSDB; ADO38550.
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX PS Claim 10; SEQ ID NO 1041; 145pp; English.
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiant activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC sequence represents the protein of a human myocardial infarction-
XX CC associated gene containing one or more SNPs of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.
XX SQ Sequence 1219 AA;
QY Query Match 100.0%; Score 44; DB 8; Length 1219;
Db Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YILIHQALV 9
815 YILIHQALV 823


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RESULT 20
AAW44729
ID AAW44729 standard; protein; 1237 AA.
XX
XX AAW44729;
AC
XX 17-OCT-2003 (revised)
DT 12-MAY-1998 (first entry)
XX
DE Chicken protein tyrosine phosphatase-lambda protein.
XX
XX Chicken; protein tyrosine phosphatase-lambda; brain; probe; primer; PCR;
XX hybridisation; human CD45; amplification; alternative splicing product;
XX diagnosis; cancer; immune system disorder; ligand.
XX
XX Gallus gallus.
OS
XX US5693488-A.
XX
XX 02-DEC-1997.
PD
XX 12-MAY-1994; 94US-00241853.
PF
XX 12-MAY-1994; 94US-00241853.
PR
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Hanafusa H, Fang KS;
PI
XX WPI; 1998-031746/03.
DR
XX N-PSDB; AAV05762.
XX
XX Nucleic acid molecule encoding chicken protein tyrosine phosphatase -
PT specifically transmembrane protein tyrosine phosphatase-lambda, useful to
XX develop probes and primers.
XX
XX Claim 1; Col 31-40; 51pp; English.
XX
XX This is the amino acid sequence of a novel chicken protein tyrosine
XX phosphatase (PTP)-lambda. The gene sequence was isolated from a chicken
XX brain cDNA library, using, as a probe, a fragment encoding the
XX intracellular domain of the human CD45 sequence. The gene has a
XX transcript of around 5.6 kb and is abundant in spleen and intestine. The
XX protein contains a Ser/Thr/Pro-rich region, a fibronectin type III domain
XX and several spectrin-like repeats. The sequence has been shown to contain
XX 5 alternative splicing products which vary near the N-terminus of the
XX protein. Nucleic acid molecules, especially encoding residues 22-1237, 22
XX -509, 510-531 or 532-1237 of the 1237 residue PTP-lambda protein, can be
XX used as probes and primers to detect levels of phosphatase expression.
XX This is useful for the diagnosis and treatment of diseases such as cancer
XX or immune system functional disorders. The protein can also be used to
XX isolate ligands of the PTP. (Updated on 17-OCT-2003 to standardise OS
XX field)
XX
XX Sequence 1237 AA;
SQ
XX
XX Query Match 100.0%; Score 44; DB 2; Length 1237;
XX Best Local Similarity 100.0%; Pred. No. 8.3;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YIIHQALV 9
XX |||||
XX 835 YIIHQALV 843
XX
XX RESULT 21
XX AAW89347
XX ID AAW89347 standard; protein; 1237 AA.
XX
XX AAW89347;
AC
XX 17-OCT-2003 (revised)
DT

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DT 04-MAR-1999 (first entry)
XX
XX Chicken transmembrane protein tyrosine phosphatase lambda.
XX
XX Chicken; transmembrane protein tyrosine phosphatase lambda; CHPTP-lambda.
XX
XX Gallus gallus.
OS
XX US5854045-A.
XX
XX 29-DEC-1998.
PD
XX 02-MAY-1997; 97US-00850917.
PF
XX 12-MAY-1994; 94US-00241853.
PR
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Hanafusa H, Fang KS;
PI
XX WPI; 1999-094913/08.
DR
XX N-PSDB; AAV81897.
XX
XX Chicken protein tyrosine phosphatase lambda polypeptides - useful for
XX antibody production or in ligand screening assays.
XX
XX Claim 1; Fig 2; 50pp; English.
XX
XX The present sequence represents chicken transmembrane protein tyrosine
XX phosphatase lambda (CHPTP-lambda). (Updated on 17-OCT-2003 to standardise
XX OS field)
XX
XX Sequence 1237 AA;
SQ
XX
XX Query Match 100.0%; Score 44; DB 2; Length 1237;
XX Best Local Similarity 100.0%; Pred. No. 8.3;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YIIHQALV 9
XX |||||
XX 835 YIIHQALV 843
XX
XX RESULT 22
XX ADM67187
XX ID ADM67187 standard; protein; 1256 AA.
XX
XX ADM67187;
AC
XX 03-JUN-2004 (first entry)
DT
XX Human adipocyte specific PTPase receptor type C protein Segid 541.
DE
XX human; adipocyte specific; adipose tissue; anti-obesity;
XX high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
XX adipogenesis; hypertension; cardiovascular disease; anorectic;
XX antidiabetic; hypotensive; PTPase receptor type C.
XX
XX Homo sapiens.
OS
XX WO2004011618-A2.
XX
XX 05-FEB-2004.
PD
XX 29-JUL-2003; 2003WO-US023684.
PF
XX 29-JUL-2002; 2002US-0398785P.
PR
XX 12-JUN-2003; 2003US-0478206P.
XX
XX (HMGF-) HMGF INC.
XX
XX Chada K, Chouinard R, Ashar H, Sayed AMD;
XX

```

DR WPI; 2004-143846/14.
DR N-PSDB; ADM66908.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 541; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti-
CC obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMG1-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
CC
SQ Sequence 1256 AA;
XX
Query Match 100.0%; Score 44; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLIIHQALV 9
DB 852 YLIIHQALV 860
XX
RESULT 23
ADP12966
ID ADP12966 standard; protein; 1256 AA.
XX
AC ADP12966;
XX
DT 12-ANG-2004 (first entry)
XX
DE Protein encoding reference mRNA sequence #51.
XX
XX transplamt rejection; immune system; rheumatoid arthritis; lupus;
KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
PT diagnosing or monitoring transplamt rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplamt

PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2975; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplamt
CC rejection, e.g. cardiac or kidney transplamt rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplamt rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplamt rejection,
CC xenotransplamt rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein encoded by an mRNA sequence of the invention which show altered
CC expression in renal transplantation and expression.
XX
SQ Sequence 1256 AA;
XX
Query Match 100.0%; Score 44; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLIIHQALV 9
DB 852 YLIIHQALV 860
XX
RESULT 24
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.
XX
AC ADQ39376;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
XX cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-046412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Iakubova O;
XX
DR WPI; 2004-533949/51.
DR N-PSDB; ADQ38548.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1039; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's
CC nucleic acid, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1258 AA;

Query Match 100.0%; Score 44; DB 8; Length 1258;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
Db 854 YIIHQALV 862

RESULT 25
ADQ39379
ID ADQ39379 standard; protein; 1267 AA.

XX AC ADQ39379;

XX DT 18-NOV-2004 (first entry)

XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.

XX KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;

XX KW cardiant; gene therapy; human.

XX OS Homo sapiens.

XX PN WO2004058052-A2.

XX PD 15-JUL-2004.

XX PF 22-DEC-2003; 2003WO-US040978.

XX PR 20-DEC-2002; 2002US-0434778P.

XX PR 10-MAR-2003; 2003US-0453135P.

XX PR 30-APR-2003; 2003US-0466412P.

XX PR 23-SEP-2003; 2003US-0504955P.

XX PA (APPL-) APPLERA CORP.

XX PI Cargill M, Devlin JT, Iakubova O;

XX DR WPI; 2004-533949/51.

XX DR N-PSDB; ADQ38551.

PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX

PS Claim 10; SEQ ID NO 1042; 145pp; English.

XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1267 AA;

Query Match 100.0%; Score 44; DB 8; Length 1267;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIIHQALV 9
Db 863 YIIHQALV 871

RESULT 26
ADL16234
ID ADL16234 standard; protein; 1291 AA.

XX AC ADL16234;

XX DT 06-MAY-2004 (first entry)

XX DE Mouse protein tyrosine phosphatase #7.

XX KW cytosolic; immunosuppressive; antiallergic;

XX KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;

XX KW inducible signalling pathway; cell proliferation; cancer;

XX KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;

XX KW cell-cycle abnormality; enzyme.

XX OS Mus musculus.

XX PN WO2003068984-A2.

XX PD 21-AUG-2003.

XX PF 13-FEB-2003; 2003WO-EP001446.

XX PR 13-FEB-2002; 2002US-0356810P.

XX PR 12-FEB-2003; 2003US-00366547.

XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PA (CEPT-) CEPTYR INC.
XX PI Tonks NK, Tzu-Ching M, Cool DE;
XX


```
XX DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 44; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YIIHQALV 9
Db 900 YIIHQALV 908
XX
RESULT 29
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1910.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
```

```
XX DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1910; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 44; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YIIHQALV 9
Db 900 YIIHQALV 908
XX
RESULT 30
ADL16230
ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #26.
XX
KM cytosolic; immunosuppressive; antiallergic;
KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KM inducible signalling pathway; cell proliferation; cancer;
KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KM cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-00366547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI (CEPT-) CEPTYR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-PSDB; ADL16229.
```

XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 79; 238bp; English.
XX
XX The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. . No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
XX Sequence 1304 AA:
SQ
Query Match 100.0%; Score 44; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLIIHQALV 9
Db 900 YLIIHQALV 908
RESULT 31
ADP65158
ID ADP65158 standard; protein; 1304 AA.
XX
XX ADP65158;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
XX
XX autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
XX Homo sapiens.
OS
XX
XX WO2003072827-A1.
PN
XX
XX 04-SEP-2003.
PD
XX
XX 31-OCT-2002; 2002WO-US035433.
PF
XX
XX 31-OCT-2001; 2001US-0336220P.
PR
XX
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
PA
XX
XX Hirsch R, Thornton SL;
PI
XX
XX WPI; 2003-712740/67.
DR
XX
XX GENBANK; NP_002829.
PT
XX
XX Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating

PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
XX Disclosure; Page; 56pp; English.
XX
XX The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analysis of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
XX Sequence 1304 AA:
SQ
Query Match 100.0%; Score 44; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YLIIHQALV 9
Db 900 YLIIHQALV 908
RESULT 32
ADM67209
ID ADM67209 standard; protein; 1304 AA.
XX
XX ADM67209;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
DE Human adipocyte specific leukocyte common antigen protein Segid 563.
XX
XX human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; lepin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; leukocyte common antigen.
XX
XX Homo sapiens.
OS
XX
XX WO2004011618-A2.
PN
XX
XX 05-FEB-2004.
PD
XX
XX 29-JUL-2003; 2003WO-US023684.
PF
XX
XX 29-JUL-2002; 2002US-0398785P.
PR
XX
XX 12-JUN-2003; 2003US-0478206P.
PA
XX
XX (HMG-) HMGNE INC.
PI
XX
XX Chada K, Chouinard R, Ashar H, Sayed AMD;
XX

DR WPI; 2004-143846/14.
 XX N-PSDB; ADM66930.
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 PS Disclosure; SEQ ID NO 563; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMG1-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 XX
 SQ Sequence 1304 AA;
 XX
 Query Match 100.0%; Score 44; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 8.8; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YIIHQALV 9
 Db 900 YIIHQALV 908
 XX
 RESULT 33
 ABO84455
 ID ABO84455 standard; protein; 1304 AA.
 XX
 AC ABO84455;
 DT 18-NOV-2004 (first entry)
 XX
 DE Human cancer-associated protein HPL3-011.2.
 XX
 KM Human; cancer-associated protein; cytostatic; cancer; leukaemia;
 KM lymphoma; CAP.
 OS Homo sapiens.
 OS
 XX
 PN WO2004074320-A2.
 PD
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.

DR N-PSDB; ABD32626.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS claim 18; seqid 147; 310pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 1304 AA;
 XX
 Query Match 100.0%; Score 44; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 8.8; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YIIHQALV 9
 Db 900 YIIHQALV 908
 XX
 RESULT 34
 ADQ39380
 ID ADQ39380 standard; protein; 1304 AA.
 XX
 AC ADQ39380;
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
 XX
 KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KM cardiac; gene therapy; human.
 OS Homo sapiens.
 OS
 XX
 PN WO2004058052-A2.
 PD
 XX
 PD 15-UTL-2004.
 XX
 PR 22-DEC-2003; 2003WO-US040978.

KM high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KM adipogenesis; hypertension; cardiovascular disease; anorectic;
 KM antidiabetic; hypotensive; leukocyte common antigen.

OS Mus musculus.

PN MO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003MO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMGF-) HMGF INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

XX WPI; 2004-143846/14.

DR N-PSDB; ADM66929.

PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.

PS Disclosure; SEQ ID NO 562; 91pp; English.

CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C^{-/-}, ob/ob, or HMGI-C^{-/-} ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a murine adipocyte
 CC specific protein sequence of the invention.

XX SQ Sequence 1343 AA;

Query Match 100.0%; Score 44; DB 8; Length 1343;

Best Local Similarity 100.0%; Pred. No. 9.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YLILHQLV 9

DB 915 YLILHQLV 923

Search completed: May 3, 2005, 07:38:27
 Job time : 66 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 6.68919 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-14

Perfect score: 52

Sequence: 1 FOLHDCTQV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	1304	1 A46546	leukocyte common a
2	38	73.1	1291	1 A28334	protein-tyrosine-p
3	37	71.2	444	2 B48129	STD1 protein - yea
4	35	67.3	455	2 B71335	probable purine-bi
5	34	65.4	238	2 F91235	hypothetical prote
6	34	65.4	238	2 F86082	hypothetical prote
7	34	65.4	220	2 F83914	transcription regu
8	34	65.4	329	2 D84612	probable peroxidase
9	34	65.4	494	2 S48769	hypothetical prote
10	34	65.4	1183	2 A89135	protein F2566.2 [1
11	33	63.5	94	2 AH1377	thioredoxin homolo
12	33	63.5	273	2 S28132	gas vesicle protei
13	33	63.5	274	2 UC2474	glutamate-cysteine
14	33	63.5	447	2 AE2418	hypothetical prote
15	33	63.5	453	2 T02503	hypothetical prote
16	33	63.5	557	2 S73434	aspartate-CRNA 11g
17	33	63.5	578	2 T48795	origin recognition
18	33	63.5	667	2 H98141	hypothetical prote
19	32	61.5	139	2 S76391	hypothetical prote
20	32	61.5	197	2 S23240	hypothetical prote
21	32	61.5	222	2 T37108	probable oxidoredu
22	32	61.5	238	2 S75830	hypothetical prote
23	32	61.5	370	2 B95420	probable spheroph
24	32	61.5	381	2 AD0897	conserved hydropho
25	32	61.5	387	2 B85974	hypothetical prote
26	32	61.5	392	2 D84130	hypothetical prote
27	32	61.5	408	2 D81129	hypothetical prote
28	32	61.5	408	2 JQ0614	yhad protein - Esc
29	32	61.5	426	2 C84202	hypothetical prote

30	32	61.5	436	2 A53227	galactosyltransfer
31	32	61.5	457	2 AB2657	glutamate-cysteine
32	32	61.5	457	2 G97438	glutamate-cysteine
33	32	61.5	457	2 AG3575	glutamate-cysteine
34	32	61.5	483	2 S44550	hypothetical prote
35	32	61.5	487	1 A26660	steroid 21-monooxy
36	32	61.5	487	2 S54785	cytochrome P450 -
37	32	61.5	492	1 A32525	steroid 21-monooxy
38	32	61.5	492	2 F84352	hypothetical prote
39	32	61.5	564	1 VHXBJV	major structural n
40	32	61.5	564	2 S12480	nucleocapsid prote
41	32	61.5	564	2 S06896	nucleocapsid prote
42	32	61.5	579	4 D40201	artifact-warning s
43	32	61.5	642	2 AB0297	chreonine-CRNA 11g
44	32	61.5	807	2 T42924	glycoprotein B - a
45	32	61.5	808	1 VGBESM	glycoprotein B pre

ALIGNMENTS

RESULT 1
A46546
leukocyte common antigen long splice form precursor - human
N/Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N/Contents: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #ext, change 09-Jul-2004
C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Salto, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A/Reference number: A46546; MUID:88061067; PMID:2824653
A/Accession: A46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.6/2
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-32,99-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.111 and clone LCA.260
A/Accession: C46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-31,193-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.1
R/Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A/Reference number: A91066; MUID:87275816; PMID:2556900
A/Accession: A29449
A/Molecule type: mRNA
A/Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RA>
A/Cross-references: GB:Y0062; NID:934275; PIDN:CAA6269.1; PID:934276
A/Experimental source: clones pHLC-1 and lambdaHLCL1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Tsai, A.Y.; Streuli, M.; Salto, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative
A/Reference number: I57658; MUID:90066468; PMID:2531281
A/Accession: I57658
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:g187020; PIDN:AAA59497.1; PID:g553521
C:Genetics:
A:Gene: GDB:PTPRC; CD45
A:Cross-references: GDB:119768; OMIM:151460
A:Map position: 1q31-1q32
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 52; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTQV 9
DB 304 FOLHDTQV 312

RESULT 2
A28334
protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
N:Contains: protein-tyrosine-phosphatase (T-cell variant)
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C:Accession: A28334; A29381; A61180; A60933; A35522; A39075; I54450; A28335; A23329; I57
R:Thomas, M.D.; Reynolds, P.J.; Chait, A.; Ben-Neriah, Y.; Trowbridge, I.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
A:Reference number: A28334; MUID:87260986; PMID:2955416

A:Accession: A28334
A:Molecule type: mRNA
A:Residues: 1-1291 <THO>
A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
A:Title: Sequences of ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
A:Reference number: A29381; MUID:86313686; PMID:2944116

A:Accession: A29381
A:Molecule type: mRNA
A:Residues: 1-30,170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, '
A:Cross-references: GB:M14342; NID:g198914; PIDN:AAA9458.1; PID:g198915
R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
A:Reference number: A61180; MUID:92032882; PMID:1932742

A:Accession: A61180
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 730-838 <YTA>
R:Gomez, L.U.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
Immunogenetics 25, 263-266, 1987
A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
A:Reference number: A60933; MUID:87192931; PMID:3570377

A:Accession: A60933
A:Molecule type: protein
A:Residues: 'R', 289-298; '329', 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375; 595-608; 638-649; 669-
R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
J. Biol. Chem. 264, 6220-6229, 1989
A:Title: Sequence conservation in potential regulatory regions of the mouse and human le
A:Reference number: A35522; MUID:89197920; PMID:2522930

A:Accession: A35522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <JCH>
A:Cross-references: GB:M22456; NID:g198755; PIDN:AAA6374.1; PID:g554185; GB:J04640; GB:
R:Raschke, W.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
A:Reference number: A29075; MUID:87092355; PMID:2948186

A:Accession: A29075
A:Molecule type: mRNA
A:Residues: 961-1291 <RAS>
A:Cross-references: GB:M15174; NID:g201105; PIDN:AAA40161.1; PID:g201106
R:Tung, J.
Immunogenetics 28, 271-277, 1988
A:Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
A:Reference number: I54450; MUID:88330145; PMID:3417340

A:Accession: I54450
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 32-73 <RES>
A:Cross-references: GB:M23241; NID:g340850; PIDN:AAA39460.1; PID:g548174
R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
A:Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguish
A:Reference number: A28335; MUID:87260987; PMID:3037546

A:Accession: A28335
A:Molecule type: mRNA
A:Residues: 1-30,74-226 <SA2>
A:Cross-references: GB:M14342
R:Shen, F.W.; Saga, Y.; Litman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyse, E.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
A:Reference number: A23329; MUID:86042665; PMID:3864163

A:Accession: A23329
A:Molecule type: mRNA
A:Residues: 10-30,170-263 <SHE>
A:Cross-references: GB:M11934; NID:g198919; PIDN:AAA39461.1; PID:g198920
R:Saga, Y.; Tung, J.
Mol. Cell. Biol. 9, 4889-4895, 1988
A:Title: Organization of the Ly-5 Gene.
A:Reference number: I57644; MUID:89096862; PMID:3211131

A:Accession: I57644
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'MT', 1-22 <RE2>
A:Cross-references: GB:M23354; NID:g340890; PIDN:AAA39462.1; PID:g554192

C:Genetics:
A:Gene: Ly-5
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MNT>
F:24-664/Domain: extracellular #status predicted <EXT>
F:24-30,170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predi
F:565-586/Domain: transmembrane #status predicted <TM>
F:583-1223/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:587-1291/Domain: intracellular #status predicted <INT>
F:664-888/Domain: protein-tyrosine-phosphatase homology <PTP>
F:64,150,161,207,211,218,253,258,290,311,322,347,416,427,457,489,520,556/Binding site: c
F:840/Active site: Cys (phosphocysteine intermediate) #status predicted
F:846/Binding site: substrate phosphate (Arg) #status predicted

Query Match 73.1%; Score 38; DB 1; Length 1291;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDT 7
DB 278 FOLHDT 284

RESULT 3
B48129
STDI protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: MSN3 protein; protein O2777; protein YOR047c
C:Species: Saccharomyces cerevisiae
C:Date: 21-Jan-1994 #sequence revision 18-Nov-1994 #text change 09-Jul-2004
C:Accession: B48129; S47543; S66921; S66930; S30809
R:Canter, R.W.; Shen, W.; Schmidt, M.C.
Mol. Cell. Biol. 13, 3650-3659, 1993
A:Title: Isolation of STDI, a high-copy-number suppressor of a dominant negative mutation
A:Reference number: A48129; MUID:93368314; PMID:8497275

A/Accession: B48129
A/Molecule type: DNA
A/Residues: 1-444 <GAN>
A/Cross-references: UNIPROT:Q02794; EMBL:L06011; NID:G172737; PIDN:AAA16951.1; PID:G1727
A/Note: sequence extracted from NCBI backbone (NCBIN:132804, NCBI:P.132806)
R./Jiang, R.; Carlson, M.
submitted to the EMBL Data Library, November 1993
A/Reference number: S47550
A/Accession: S47550
A/Molecule type: DNA
A/Residues: 1-138, 'D', 140-444 <JIA>
A/Cross-references: EMBL:L21932; NID:G416157; PID:G416158
R./Hubbard, E.J.A.; Jiang, R.; Carlson, M.
Mol. Cell. Biol. 14, 1972-1978, 1994
A/Title: Dosage-dependent modulation of glucose repression by MSN3 (STD1) in *Saccharomyces*
A/Reference number: S46668; MUID:94158870; PMID:8114728
A/Accession: S47543
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-138, 'D', 140-436, 'Y', 438-444 <HUB>
A/Cross-references: EMBL:L21932
R./Land, O.; Hiesel, R.; Unseld, M.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S66907
A/Accession: S66921
A/Molecule type: DNA
A/Residues: 1-444 <LAN>
A/Cross-references: EMBL:Z74955; NID:G1420176; PID:G1420177; MIPS:YOR047C
A/Experimental source: strain S288C
R./Bohm, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S66929
A/Accession: S66930
A/Molecule type: DNA
A/Residues: 1-444 <BOH>
A/Cross-references: EMBL:Z74955; NID:G1420176; PID:G1420177; MIPS:YOR047C
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:STD1, MSN3
A/Cross-references: SGD:S0005573, MIPS:YOR047C
A/Map position: 15R
C/Keywords: transcription regulation

Query Match 71.2%; Score 37; DB 2; Length 444;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDC 7
DB 368 FKIHDC 374

RESULT 4
B7135
probable purine-binding chemotaxis protein (CheW-1) - *Syphilis spirochete*
C/Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: B7135
R./Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weisman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of *Treponema pallidum*, the *syphilis spirochete*.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: B7135
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-455 <COL>
A/Cross-references: UNIPROT:P61124; GB:AE001215; GB:AE000520; NID:G3322631; PIDN:AA66534
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0364

Query Match 67.3%; Score 35; DB 2; Length 455;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDC 7
DB 379 FEYHDC 385

RESULT 5
F91235
hypothetical protein EC84854 [imported] - *Escherichia coli* (strain O157:H7, substrain R
C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: F91235
R./Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F91235
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-238 <HAY>
A/Cross-references: UNIPROT:O8X793; GB:BA000007; PIDN:BA838277.1; PID:G13364330; GSPDB:
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: EC84854

Query Match 65.4%; Score 34; DB 2; Length 238;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDC 6
DB 168 FQFHDC 173

RESULT 6
F86082
hypothetical protein Z5474 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: F86082
R./Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; DiMantana, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: F86082
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-238 <STO>
A/Cross-references: UNIPROT:O8X793; GB:AE005174; NID:G12518830; PIDN:AAG59122.1; GSPDB:
A/Experimental source: strain O157:H7, substrain EDL33
C/Genetics:
A/Gene: Z5474

Query Match 65.4%; Score 34; DB 2; Length 238;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDC 6
DB 168 FQFHDC 173

RESULT 7
E83914
transcription regulator (lysr family) BH2117 [imported] - *Bacillus halodurans* (strain C
C/Species: *Bacillus halodurans*
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: E83914

R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeaki, R.; Masui, N.; Fujii, F.; Hara
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: E83914
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-290 <STO>
A/Cross-references: UNIPROT:Q9KB18; GB:AP001514; GB:BA000004; NID:910174613; PIDN:BA056
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH2117

Query Match 65.4%; Score 34; DB 2; Length 290;
Best Local Similarity 44.4%; Pred. No. 52;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FOLHDCQV 9
|:|:|:|:|:
|:|:|:|:|:
Db 218 FEVHDCATI 226

RESULT 8
D84612
Probable peroxidase [imported] - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: D84612
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: D84612
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-329 <STO>
A/Cross-references: UNIPROT:Q9SUJ2; GB:AE002093; NID:94544449; PIDN:AA022357.1; GSPDB:GN
C/Genetics:
A/Gene: Atg22420
A/Map position: 2
C/Superfamily: peroxidase

Query Match 65.4%; Score 34; DB 2; Length 329;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDC 6
|:|:|:|:|:
|:|:|:|:|:
Db 60 FOFHDC 65

RESULT 9
S48769
Hypothetical protein YDR082w - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: hypothetical protein D4456; hypothetical protein Y08554.15
C/Species: *Saccharomyces cerevisiae*
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S48769; S49837; S55829; S67899
R/Coster, F.; Jomiaux, J.L.; Goffeau, A.
submitted to the EMBL Data Library, October 1994
A/Reference number: S48758
A/Accession: S48769
A/Molecule type: DNA
A/Residues: 1-494 <COS>
A/Cross-references: UNIPROT:P38960; EMBL:X82086; NID:9558241; PIDN:CAAS7609.1; PID:95582
R/Richard, C.; Harris, D.E.
submitted to the EMBL Data Library, November 1994
A/Reference number: S49823
A/Accession: S49837
A/Molecule type: DNA
A/Residues: 1-494 <RIC>

A/Cross-references: EMBL:Z46796; NID:9577794; PIDN:CA86804.1; PID:9577809
R/Coster, F.; Jomiaux, J.L.; Goffeau, A.
Yeast 11, 673-679, 1995
A>Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading fr
A/Reference number: S55819; MUID:96093910; PMID:7483840
A/Accession: S55829
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-494 <COM>
A/Cross-references: EMBL:X82086; NID:9558241; PIDN:CAAS7609.1; PID:9558253
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
R/Poury, F.; Jomiaux, J.L.; Purrelle, B.; Coester, F.; Goffeau, A.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S67889
A/Accession: S67899
A/Molecule type: DNA
A/Residues: 1-494 <FOU>
A/Cross-references: EMBL:Z74378; NID:91431552; PIDN:CAAS9802.1; PID:91431553; MIPS:YDR08
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:STN1
A/Cross-references: SGD:S0002489; MIPS:YDR082w
A/Map position: 4R
C/Superfamily: *Saccharomyces cerevisiae* hypothetical protein YDR082w

Query Match 65.4%; Score 34; DB 2; Length 494;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDC 7
|:|:|:|:|:
|:|:|:|:|:
Db 95 FOLHDC 101

RESULT 10
A89135
protein P25G6.2 [imported] - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: A89135
R/anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: A89135
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1183 <STO>
A/Cross-references: UNIPROT:O16929; GB:chr_V; PIDN:AA025795.1; PID:92384832; GSPDB:GN000
A/Map position: 5

Query Match 65.4%; Score 34; DB 2; Length 1183;
Best Local Similarity 71.4%; Pred. No. 21e-02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QULHDC 8
|:|:|:|:|:
|:|:|:|:|:
Db 764 QULHDC 770

RESULT 11
AH1377
thiorodxin homolog lmo2424 [imported] - *Listeria monocytogenes* (strain EGD-e)
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C/Accession: AH1377
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karsch, U.

Science 294, 849-852, 2001
A:Authors: Krefetz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak
ok, C.; Schluter, T.; Simes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1377
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-94 <GUA>
A:Cross-references: UNIPROT:Q814L3; GB:NC_003210; PIDN:CAD00502.1; PID:g16411912; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2424
C:Superfamily: Thioredoxin

Query Match 63.5%; Score 33; DB 2; Length 94;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FOLHDCQV 9
:|||||
Db 79 YOLHDATAI 87

RESULT 12
S28132
gas vesicle protein gvpL [imported] - *Halobacterium salinarum*
C:Species: Halobacterium salinarum
C>Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 21-Jul-2000
C:Accession: S28132; T46771
R:Engelart, C.; Krueger, K.; Offner, S.; Pfeifer, F.
J. Mol. Biol. 227, 586-592, 1992
A:Title: Three different but related gene clusters encoding gas vesicles in halophilic
A:Reference number: S28113; MUID:93021102; PMID:1404376
A:Accession: S28132
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-273 <ENG>
A:Cross-references: EMBL:X64730; NID:g43657; PID:g809701; PIDN:CAA55965.1
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
A>Note: the source is designated as *Halobacterium salinarum*
R:Krueger, K.; Pfeifer, F.
J. Bacteriol. 178, 4012-4019, 1996
A:Title: Transcript analysis of the c-vac region and differential synthesis of the two
A:Reference number: Z24092; MUID:96312339; PMID:8763925
A:Accession: T46771
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <KRU>
A:Cross-references: EMBL:X94688; NID:g1154776; PIDN:CAA64351.1; PID:g1154789
A:Experimental source: strain PHH1, sub strain NRC817
C:Genetics:
A:Gene: gvpL

Query Match 63.5%; Score 33; DB 2; Length 273;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LHDCTQV 9
:|||||
Db 55 VHDCTSV 61

RESULT 13
JC2474
glutamate-cysteine ligase (EC 6.3.2.2) regulatory light chain - human
N:Alternate names: gamma-glutamylcysteine synthetase light chain
C:Species: Homo sapiens (man)
C>Date: 21-Feb-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: JC2474
R:Giip, J.; Bailey, H.H.; Mulcahy, R.T.
Biochem. Biophys. Res. Commun. 206, 584-589, 1995
A:Title: Cloning and sequencing of the cDNA for the light subunit of human liver gamma-g

A:Reference number: JC2474; MUID:95126958; PMID:7826375
A:Accession: JC2474
A:Molecule type: mRNA
A:Residues: 1-274 <GIP>
A:Cross-references: UNIPROT:P48507; GB:L35546; NID:g530136; PIDN:AAA65028.1; PID:g53013
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:GLCLR
A:Cross-references: GDB:448904
A:Map position: 1p21-1p21
C:Superfamily: human glutamate-cysteine ligase regulatory light chain
C:Keywords: ligase

Query Match 63.5%; Score 33; DB 2; Length 274;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLHDCQ 8
:|||||
Db 42 ELHDCQ 48

RESULT 14
AE2418
hypothetical protein al14901 [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2418
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous nitrogen-fixing *Cyanobacterium* An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <KUR>
A:Cross-references: UNIPROT:Q8YMN2; GB:BA000019; PIDN:BA076600.1; PID:g17134039; GSPDB:
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: al14901

Query Match 63.5%; Score 33; DB 2; Length 447;
Best Local Similarity 62.5%; Pred. No. 12e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FOLHDCQ 8
:|||||
Db 21 FELHPCVQ 28

RESULT 15
T02503
hypothetical protein AT2938420 [imported] - *Arabidopsis thaliana*
N:Alternate names: hypothetical protein T19C21.9
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02503; G84804
R:Roundley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau]
submitted to the EMBL Data Library, August 1998
A:Description: *Arabidopsis thaliana* chromosome II BAC T19C21 genomic sequence.
A:Reference number: Z14676
A:Accession: T02503
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-453 <ROU>
A:Cross-references: UNIPROT:Q80909; EMBL:AC004683; NID:g3395421; PID:g3395430
A:Experimental source: cultivar Columbia
R:Lin, X.; Kau], S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
eaus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MID:20083487; PMID:10617197
A:Accession: G84804
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-453 <STO>
A:Cross-references: GB:AE002093; NID:G3395430; PIDN:AAC28762.1; GSPDB:GN00139
C:Genetics:
A:Gene: T19C21.9; AT2G38420
A:Map position: 2

Query Match 63.5%; Score 33; DB 2; Length 453;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQJHDC 6
|||:
|||:
|||:
DB 63 FQJHNC 68

Search completed: May 3, 2005, 06:17:18
Job time : 22.6892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-14

Perfect score: 52

Sequence: 1 FGLHDTQV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	756	1	Q6PJ7	Q6PJ7 homo sapien
2	52	100.0	1304	1	CD45 HUMAN	P08575 homo sapien
3	40	76.9	195	2	Q8PE8	Q8PE8 xanthomonas
4	38	73.1	878	2	Q8C6Q7	Q8C6Q7 mus musculi
5	38	73.1	959	2	Q94GZ0	Q94GZ0 oryza sativ
6	38	73.1	1152	1	CD45 MOUSE	P06800 mus musculi
7	38	73.1	1291	2	Q61812	Q61812 mus musculi
8	38	73.1	1343	2	Q64730	Q64730 mus musculi
9	37	71.2	253	2	Q97A32	Q97A32 thermoplasma
10	37	71.2	389	2	Q9VE68	Q9VE68 dirosophila
11	37	71.2	444	1	STD1 YEAST	Q02794 saccaromyc
12	37	71.2	5412	2	Q7R3N4	Q7R3N4 giardia lam
13	36	69.2	202	2	Q7VWR7	Q7VWR7 bordetella
14	36	69.2	202	2	Q7WAM7	Q7WAM7 bordetella
15	36	69.2	202	2	Q7WUT0	Q7WUT0 bordetella
16	36	69.2	494	2	Q7UP29	Q7UP29 rhodospirillum rubrum
17	36	69.2	733	2	Q9FNV2	Q9FNV2 rhodospirillum rubrum
18	36	69.2	840	2	Q7N1K1	Q7N1K1 gloeobacter
19	36	69.2	963	2	Q91U70	Q91U70 bovine vira
20	36	69.2	1130	2	Q71955	Q71955 bovine vira
21	36	69.2	1133	2	Q71954	Q71954 bovine vira
22	36	69.2	1180	2	Q76B27	Q76B27 bovine vira
23	36	69.2	1560	2	Q76B27	Q76B27 bovine vira
24	36	69.2	1565	2	Q95285	Q95285 leishmania
25	36	69.2	3907	1	P0LG BVDVC	Q96662 b genome po
26	36	69.2	3914	2	Q70DK0	Q70DK0 bovine vira
27	36	69.2	3975	2	Q65815	Q65815 bovine vira
28	36	69.2	4197	2	Q80729	Q80729 bovine vira
29	35	67.3	222	2	Q6SNN1	Q6SNN1 papio papio
30	35	67.3	284	2	Q8KCY9	Q8KCY9 chlorobium
31	35	67.3	308	2	Q91G68	Q91G68 epiphyas po

32	35	67.3	444	2	Q85748	Q85748 treponema d
33	35	67.3	444	2	Q9RBN4	Q9RBN4 treponema p
34	35	67.3	444	2	Q73ML6	Q73ML6 treponema d
35	35	67.3	454	2	Q873Z2	Q873Z2 leptospira
36	35	67.3	455	2	P96124	P96124 treponema p
37	35	67.3	519	2	Q9KIF2	Q9KIF2 streptomyces
38	35	67.3	544	2	Q7RUC4	Q7RUC4 plasmodium
39	35	67.3	684	2	Q7XVZ2	Q7XVZ2 oryza sativ
40	35	67.3	761	2	Q9UHI2	Q9UHI2 homo sapien
41	35	67.3	871	2	Q76976	Q76976 strongyloce
42	35	67.3	932	2	Q7Q0M7	Q7Q0M7 anopheles g
43	35	67.3	1051	2	Q7YU29	Q7YU29 dirosophila
44	35	67.3	1080	2	Q8OP47	Q8OP47 bovine vira
45	35	67.3	1434	2	Q7X5J4	Q7X5J4 oryza sativ

ALIGNMENTS

RESULT 1

Q6PJ7 ID Q6PJ7 PRELIMINARY; PRT; 756 AA.

AC Q6PJ7; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE PTPRC protein (Fragment).

GN Name=PTPRC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Magnet L., Shennan C.M., Schler G.D.,

RA Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Slaughter M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tashiro S., Carninci P., Prange C.,

RA Baha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

RA Krzywinski M.I., Skalski U., Smalls D.E., Scherch A., Schein J.E.,

RT Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC014239; AB014239.1; -.

DR HSSP; P18031; IAA.

DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR008957; FN_III-like.

DR InterPro; IPR000242; Tyr_PP.

DR Pfam; PF00041; fn3; 2.

DR Pfam; PF00102; Y_phosphatase; 1.

DR PRINTS; PR00700; PRTYPTPRTASB.

DR SMART; SM00060; FN3; 2.

DR SMART; SM00194; PTPC; 1.

DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
FT NON_TER 756 756
SQ SEQUENCE 756 AA; 85430 MW; 8A9A863827BD65E6 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 756;
Best local similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FOLHCTOV 9
DB 256 FOLHCTOV 264
RESULT 2
CD45 HUMAN
ID CD45 HUMAN STANDARD; PRT; 1304 AA.
AC P08575; Q16614; Q9H0Y6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)
DE (T200).
GN Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RA MEDLINE=88061067; PubMed=2824653;
RT Strull M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different
mRNAs encoding human leukocyte common antigens";
RT J. Exp. Med. 166:1548-1566 (1987).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RA MEDLINE=87275816; PubMed=2956090;
RT Ralph S.J., Thomas M.L., Morton C.C., Trombridge I.S.;
RT "Structural variants of human T200 glycoprotein (Leukocyte-common
antigen)";
RT EMBO J. 6:1251-1257 (1987).
RN (3)
RP SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE=89009812; PubMed=2971730;
RT Hall L.R., Strull M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
antigen (CD45) gene";
RT J. Immunol. 141:2781-2787 (1988).
RN (4)
RP FUNCTION.
RA MEDLINE=89017162; PubMed=2845400;
RT Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
protein tyrosine phosphatase";
RT Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186 (1988).
RN (5)
RP MUTAGENESIS.
RA MEDLINE=90316093; PubMed=1695146;
RT Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
domains of the receptor-linked protein tyrosine phosphatases LCA and
LAR";
RT EMBO J. 9:2239-2407 (1990).
RN (6)
RP FUNCTION. Required for T-cell activation through the antigen
receptor. The first PTPase domain has enzymatic activity, while
the second one seems to affect the substrate specificity of the
first one.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -1- SUBUNIT: Binds GANAB and PRKCSH (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=At least 8 isoforms are produced;
CC Name=1;
CC IsoId=P08575-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P08575-2; Sequence=VSP_007780;
CC -1- PTM: Heavily N- and O-glycosylated.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class I/6 subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD45 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00638; CAA68669.1; -;
CC EMBL; Y00062; CAA68269.1; -;
CC EMBL; M23482; AAD15273.2; -;
CC EMBL; M23496; AAD15273.2; JOINED.
CC EMBL; M23467; AAD15273.2; JOINED.
CC EMBL; M23467; AAD15273.2; JOINED.
CC EMBL; M23468; AAD15273.2; JOINED.
CC EMBL; M23469; AAD15273.2; JOINED.
CC EMBL; M23470; AAD15273.2; JOINED.
CC EMBL; M23471; AAD15273.2; JOINED.
CC EMBL; M23472; AAD15273.2; JOINED.
CC EMBL; M23473; AAD15273.2; JOINED.
CC EMBL; M23474; AAD15273.2; JOINED.
CC EMBL; M23475; AAD15273.2; JOINED.
CC EMBL; M23476; AAD15273.2; JOINED.
CC EMBL; M23477; AAD15273.2; JOINED.
CC EMBL; M23478; AAD15273.2; JOINED.
CC EMBL; M23479; AAD15273.2; JOINED.
CC EMBL; M23480; AAD15273.2; JOINED.
CC EMBL; M23481; AAD15273.2; JOINED.
CC EMBL; M23482; AAD15273.2; JOINED.
CC EMBL; M23483; AAD15273.2; JOINED.
CC EMBL; M23484; AAD15273.2; JOINED.
CC EMBL; M23485; AAD15273.2; JOINED.
CC EMBL; M23486; AAD15273.2; JOINED.
CC EMBL; M23487; AAD15273.2; JOINED.
CC EMBL; M23488; AAD15273.2; JOINED.
CC EMBL; M23489; AAD15273.2; JOINED.
CC EMBL; M23490; AAD15273.2; JOINED.
CC EMBL; M23491; AAD15273.2; JOINED.
CC PIR; A46546; A46546.
CC HSSP; P18031; 1C88.
CC Inactive; P08575; -;
CC GlycoSiteDB; P08575; -;
CC Genew; HGNC; 9666; PTPRC.
CC MIM; 151460; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
CC GO; GO:0001061; P:cell surface receptor linked signal transdu. . .; TAS.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00102; Y_phosphatase; 2.
CC PRINTS; PR00700; PRTYHPHTASE.
CC DR PROSITE; PS50853; FN3; 2.
CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
CC DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PSS0055; TYR. PHOSPHATASE PRP; 2.
KM Alternative splicing; Antigen; Glycoprotein; Hydrolase;
KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KW Transmembrane.
FT CHAIN 1 23
FT DOMAIN 24 1304
FT TRANSMEM 576 575
FT DOMAIN 598 597
FT DOMAIN 598 1304
FT DOMAIN 390 478
FT DOMAIN 482 570
FT DOMAIN 670 919
FT DOMAIN 961 1235
FT ACT_SITE 851 851
FT ACT_SITE 1167 1167
FT CARBOHYD 78 78
FT CARBOHYD 90 90
FT CARBOHYD 95 95
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 197 197
FT CARBOHYD 232 232
FT CARBOHYD 260 260
FT CARBOHYD 270 270
FT CARBOHYD 276 276
FT CARBOHYD 335 335
FT CARBOHYD 378 378
FT CARBOHYD 419 419
FT CARBOHYD 468 468
FT CARBOHYD 488 488
FT CARBOHYD 529 529
FT VARSPPLIC 32 192
FT MUTAGEN 851 851
FT CONFLICT 650 650
FT CONFLICT 1207 1207
SQ SEQUENCE 1304 AA; 147253 MW; A08FC2D6069BAF7 CRC64;
Query Match Best Local Similarity 100.0%; Score 52; DB 1; Length 1304;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FOLHDTQV 9
Db 304 FOLHDTQV 312
RESULT 3
O8BP8 PRELIMINARY; PRT; 195 AA.
AC O8BP8; 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein XAC0647.
GN OrderedlocusNames=XAC0647;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RC MEDLINE=2022145; PubMed=12074217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.S., Camargo L.B.A.,
RA Ciccarotte G., Camarvan F., Cardoso J., Chambergio F., Chaplita L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.T.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Melians J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL; AE011693; AM35536.1; -;
DR GO; GO:0003824; F.catalytic activity; IEA.
DR GO; GO:0008967; F.phosphoglycolate phosphatase activity; IEA.
DR GO; GO:0008152; P.metabolism; IEA.
DR InterPro; IPR005834; Dehal-like hydro.
DR InterPro; IPR006402; HAD_SF-IA-v3.
DR InterPro; IPR006439; HAD_SF_A_v1.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMs; TIGR01549; HAD-SF-IA-v1; 1.
DR TIGRFAMs; TIGR01509; HAD-SF-IA-v3; 1.
KW Complete proteome.
SQ SEQUENCE 195 AA; 21286 MW; 2A9FA9E4C6C3D91 CRC64;
Query Match Best Local Similarity 76.9%; Score 40; DB 2; Length 195;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 FOLHDTQV 9
Db 181 WRHDTQL 189
RESULT 4
O8C6Q7 PRELIMINARY; PRT; 878 AA.
AC O8C6Q7; 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-
DE length enriched library, clone:E230015G23 product:Protein tyrosine
DE phosphatase, receptor type, C, full insert sequence. (Fragment).
GN Name=Ptyrc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RT Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RA The PANTOM Consortium;
RT The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:11617-1630(2000).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RA Adachi U., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurahara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC054056; BAC35638.1; -.
 DR HSSP: P18052; 1YFO.
 DR MGD: MG1:97810; PEPIC.
 DR GO: GO:0009897; C:external side of plasma membrane; IDA.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0005515; P:protein binding; IPI.
 DR GO: GO:0030183; P:B-cell differentiation; IMP.
 DR GO: GO:0042100; P:B-cell proliferation; IMP.
 DR GO: GO:0030217; P:T-cell differentiation; IMP.
 DR GO: GO:0042098; P:T-cell proliferation; IMP.
 DR GO: GO:0046652; P:thymocyte differentiation; IMP.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 3.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASR.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS00853; FN3; 2.
 DR PROSITE: PS00383; Tyr_PHOSPHATASE_1; 1.
 DR PROSITE: PS0056; Tyr_PHOSPHATASE_2; 1.
 DR PROSITE: PS0055; Tyr_PHOSPHATASE_PTP; 2.
 KM Hydroxylase; Receptor.
 FT NON_TER 878 878
 SQ SEQUENCE 878 AA; 99891 MW; 1985FCD7909D4CA6 CRC64;
 QY 1 FOLDCT 7
 Db 141 FSLHCT 147
 RESULT 5
 Q94GZ0

ID Q94GZ0 PRELIMINARY; PRT; 959 AA.
 AC Q94GZ0;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Putative disease resistance protein.
 GN Name=OSJNB0018H01.20;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocaulaceae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Buell C.R., Yuan O., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsirlin T.,
 RA Riggs F., Hsiao U., Zismann V., Blunt S., Pai G., VanKen S.B.,
 RA Utterback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC087181; AAK38505.1; -.
 DR Gramene; Q94GZ0; -.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0006915; P:apoptosis; IEA.
 DR GO: GO:0042829; P:defense response to pathogen; IEA.
 DR InterPro: IPR000767; Disease_resist.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR002182; NB-ARC.
 DR Pfam: PF00560; LRR_1; 2.
 DR Pfam: PR00931; NB-ARC; 2.
 DR PRINTS: PR00364; DISKERSIST.
 DR SEQUENCE 959 AA; 108559 MW; DDBCC17F0C4E5EB3 CRC64;
 QY 1 FOLDCT 8
 Db 910 FSLHCTE 917
 RESULT 6
 CD45_MOUSE STANDARD; PRT; 1152 AA.
 ID CD45_MOUSE
 AC P06800;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (BC 3.1.3.48) (L-CA) (Lymphocyte
 DE common antigen Ly-5) (CD45) (T200).
 GN Name=Pfprc; Synonyms=Ly-5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86313686; PubMed=2944116;
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RT "Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
 RN [2]
 RP REVISIONS.
 RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
 RN [3]
 RP SEQUENCE OF 10-124 FROM N.A.
 RC TISSUE=T-cell;

RX MEDLINE=86042665; PubMed=3864163;
 RA Shen F.-W., Saga Y., Litman G., Freeman G., Tung J.-S., Cantor H.,
 RA Boyse E.A.;
 RT "Cloning of Ly-5 cDNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
 RN [4]
 RP SEQUENCE OF 822-1152 FROM N.A.
 RX MEDLINE=87092355; PubMed=2948186;
 RA Raschke W.C.;
 RT "Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B-
 and T-lymphocyte lineages.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
 RN [5]
 RP INTERACTIONS WITH GANAB AND PRKCSH.
 RX MEDLINE=97294720; PubMed=9148925; DOI=10.1074/jbc.272.20.13117;
 RA Arendt C.W., Ostergaard H.L.;
 RT "Identification of the CD45-associated 116-kDa and 80-kDa proteins as
 the alpha- and beta-subunits of alpha-glucosidase II.";
 RL J. Biol. Chem. 272:13117-13125(1997).
 CC -1- FUNCTION: Required for T-cell activation through the antigen
 receptor. The first PRPase domain has enzymatic activity, while
 the second one seems to affect the substrate specificity of the
 first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 tyrosine + phosphate.
 CC -1- SUBUNIT: Binds GANAB and PRKCSH..
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=1;
 Comment=A number of isoforms are produced;
 Name=1;
 CC -1- IsoId=P06800-1; Sequence=Displayed;
 CC -1- DEVELOPMENTAL STAGE: Expression is restricted to the hematopoietic
 compartment of development.
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
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 or send an email to license@ebi.ac.uk).

FT	DOMAIN	24	425	Extracellular (Potential).
FT	TRANSMEM	426	447	Potential.
FT	DOMAIN	448	1152	Cytoplasmic (Potential).
FT	DOMAIN	332	328	Fibronectin type-III 1.
FT	DOMAIN	333	420	Fibronectin type-III 2.
FT	DOMAIN	520	769	Protein-tyrosine phosphatase 1.
FT	DOMAIN	811	1084	Protein-tyrosine phosphatase 2.
FT	ACT_SITE	701	701	Phosphotyrosine intermediate (By similarity).
FT	ACT_SITE	1016	1016	Phosphotyrosine intermediate (By similarity).
FT	CARBOHYD	68	68	N-linked (GlcNAc...)
FT	CARBOHYD	72	72	N-linked (GlcNAc...)
FT	CARBOHYD	79	79	N-linked (GlcNAc...)
FT	CARBOHYD	114	114	N-linked (GlcNAc...)
FT	CARBOHYD	119	119	N-linked (GlcNAc...)
FT	CARBOHYD	151	151	N-linked (GlcNAc...)
FT	CARBOHYD	172	172	N-linked (GlcNAc...)
FT	CARBOHYD	183	183	N-linked (GlcNAc...)
FT	CARBOHYD	208	208	N-linked (GlcNAc...)
FT	CARBOHYD	277	277	N-linked (GlcNAc...)
FT	CARBOHYD	288	288	N-linked (GlcNAc...)
FT	CARBOHYD	318	318	N-linked (GlcNAc...)
FT	CARBOHYD	350	350	N-linked (GlcNAc...)
FT	CARBOHYD	379	379	N-linked (GlcNAc...)
SO	SEQUENCE	1152 AA;	130421 MW;	BAD956BA432EA012 CRC64;

Query Match 73.1%; Score 38; DB 1; Length 1152;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 139 FSLHDC1 145

Qy 1 FOLHDC1 7

Db 139 FSLHDC1 145

RESULT 7

061812 PRELIMINARY; PRT; 1291 AA.

AC 061812;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lymphocyte common antigen precursor.
 GN Name=Ptpcr; Synonyms=Ly5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=92361152; PubMed=1822988;
 RA Zebende S.L., Barritt D.S., Raschke W.C.;
 RT "Comparison of mouse Lys A and Lys B leukocyte common antigen
 alleles.";
 RL Dev. Immunol. 1:243-254(1991).
 DR EMBL; M92933; AAA39459.1; -.
 DR HSSP; P18052; 1YFO.
 DR MGD; MGI:97810; Ptpcr.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:000515; F:protein binding; IPI.
 DR GO; GO:0030183; F:B-cell differentiation; IMP.
 DR GO; GO:0042107; P:B-cell proliferation; IMP.
 DR GO; GO:0030217; P:T-cell differentiation; IMP.
 DR GO; GO:0042098; P:T-cell proliferation; IMP.
 DR GO; GO:0046552; P:lymphocyte differentiation; IMP.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00102; Y_phosphatase; 2.

DR	EMBL; M23147; AAA39418.1; JOINED.
DR	EMBL; M23146; AAA39418.1; JOINED.
DR	EMBL; M23145; AAA39418.1; JOINED.
DR	EMBL; M23158; AAA39418.1; -.
DR	EMBL; M23152; AAA39418.1; JOINED.
DR	HSSP; P18052; IYFO.
DR	GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR000387; Tyr_phosphatase.
DR	InterPro; IPR00242; Tyr_pp.
DR	Pfam; PF00041; fn3; 3.
DR	Pfam; PF0102; Y_phosphatase; 2.
DR	PRINTS; PR00700; PRTYPHPTASE.
DR	SMART; SMO0060; FN3; 2.
DR	SMART; SMO0194; PTpc; 2.
DR	PROSITE; PSS0853; FN3; 2.
DR	PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
DR	PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
FT	NON_TER 1 1
SQ	SEQUENCE 1343 AA; 150679 MW; 0DBBDEC97FC4C6A9 CRC64;
Oy	Query Match Best Local Similarity 73.1%; Score 38; DB 2; Length 1343; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Db	1 FOLHDCCT 7 278 FSLHDCCT 284
RESULT 9	
ID Q97A32	PRELIMINARY; PRT; 253 AA.
AC O97A32	
DT 01-OCT-2001 (TrEMBLrel. 18, Created)	
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE Translation initiation factor eIF2 beta subunit.	
GN Name=TVG099664; OrderedLocustNames=TV0978;	
OS Thermoplasma volcanum.	
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;	
OC Thermoplasmataceae; Thermoplasma.	
OX NCBI_TaxID=50339;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;	
RX MEDLINE=30570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;	
RA Kawasaki T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawamoto T.,	
RA Numoshima T., Yamamoto Y., Watanabe K., Yamazaki M., Kanehori K.,	
RA Numoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,	
RT "Archaeal adaptation to higher temperatures revealed by genomic	
RT sequence of Thermoplasma volcanum";	
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).	
RU EMBL; AP000994; BAB60120.1; -.	
DR GO; GO:0005851; C:eukaryotic translation initiation factor 2B. . ; IEA.	
DR GO; GO:0005525; F:GTP binding; IEA.	
DR GO; GO:0003743; F:translation initiation factor activity; IEA.	
DR GO; GO:0006413; P:translational initiation; IEA.	
DR InterPro; IPR000649; IF-2B.	
DR Pfam; PF01008; IF-2B; 1.	
KW Complete proteome; Initiation factor.	
SQ SEQUENCE 253 AA; 27966 MW; FE8EEF6DF865E7F3 CRC64;	
Oy	Query Match Best Local Similarity 71.2%; Score 37; DB 2; Length 253; Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0
Db	1 FOLHDCCT 9 209 FOLHSCNEI 217

RESULT 10
 O9VE68 PRELIMINARY; PRT; 369 AA.
 AC O9VE68;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE CG10864-PA.
 GN ORFNames=CG10864;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer V., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheier F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett M., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frisoe E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frisoe E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Prochuk S.E.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bergman B.P.,
 RA Beilencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 DR EMBL; AE003722; AAF5561.1; -
 DR FLYBASE; FBgn0038621; CG10864.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; P:ion channel activity; IEA.
 DR GO; GO:0005267; P:potassium channel activity; IEA.
 DR GO; GO:0006813; P:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K+Channel_2pore.
 DR InterPro; IPR001622; K+Channel_pore.
 DR PRINTS; PR01333; 2PORECHANNEL.
 KM Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 389 AA; 43883 MW; B6023BA7FDEB85C7 CRC64;
 Query Match 71.2%; Score 37; DB 2; Length 389;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LHDCTQ 8
 DB 206 LHDCTQ 211
 RESULT 11
 ID STD1_YEAST
 AC 002794; STANDARD; PRT; 444 AA.
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE STD1 protein (Glucose repression modulator MSN1).
 GN Name=STD1; Synonyms=MSN3, SFS3; OrderedLocustNames=YOR047C;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BUI1991;
 RA MEDLINE=93268314; PubMed=8497275;
 RA Ganster R.W., Shen W., Schmidt M.C.;
 RT "Isolation of STD1, a high-copy-number suppressor of a dominant
 RT negative mutation in the yeast TATA-binding protein.";
 RL Mol. Cell. Biol. 13:3650-3659(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288C;
 RX MEDLINE=94158670; PubMed=8114728;

RA Hubbard E.J.A., Jiang R., Carlson M.;
 RT "Doseage-dependent modulation of glucose repression by MSN3 (STD1) in
 RT Saccharomyces cerevisiae.";
 RL Mol. Cell. Biol. 14:1972-1978 (1994).
 RN (3)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97313270; PubMed=9169874;
 RA Dujon B., Albermann K., Aldea M., Alexandrakl D., Ansgorge W.,
 RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,
 RA Boyer J., Camases A., Casas C., Chet G.,
 RA Czipluch C., Daignan-Fornier B., Dang D.V., de Haan M., Delius H.,
 RA Durand P., Faithhead C.A., Feldmann H., Gallion L., Gallsen F.,
 RA Gamo F.J., Gancedo C., Goffeau A., Goulding S.E., Griwall L.A.,
 RA Habbig B., Hand N.J., Hani J., Hattemore U., Hebling U.,
 RA Hernandez Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,
 RA Hollenberg C.P., Hughes B., Jauniaux J.-C., Kalogeropoulos A.,
 RA Katsoulou C., Kordes E., Latuente M.J., Landt O., Louis E.J.,
 RA Maare A.C., Madania A., Manhaupt G., Marck C., Martin R.P.,
 RA Mewes H.-W., Michaux G., Paces V., Parle-McDermott A.G., Pearson B.M.,
 RA Perrin A., Petersson B., Poch O., Pohl T.M., Polrey R.,
 RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rechmann S.,
 RA Schaefer C., Schweizer M., Sor F., Sterky F., Tarasov I.A.,
 RA Teodoru C., Tettein H., Thierry A., Tobiasch E., Tzerila M.,
 RA Uhlen M., Unselid M., Valens M., Vandenbol M., Vetter I., Vleck C.,
 RA Voet M., Volckaert G., Voss H., Wamburt R., Wedler H., Wiemann S.,
 RA Wansor B., Wolfe K.H., Zollner A., Zumbstein E., Kleine K.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";
 RL Nature 387:98-102(1997).
 CC -1- FUNCTION: Potential transcriptional activator. Suppressor of TARA-
 CC binding protein (TBP) with a deletion of the nonconserved N-
 CC terminus which disrupts normal transcriptional regulation in the
 CC cell. Physically interacts with the SNF1 kinase.
 CC -1- SIMILARITY: Strong, to MTH1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L06011; AAA16951.1; -
 CC EMBL; L21932; AAA18535.1; -
 CC EMBL; Z74955; CAA9238.1; -
 CC PIR; B48129; B48129.
 CC Inact; Q02794; -
 CC Germonline; 143635; -
 CC TRANSFAC; T01260; -
 CC SGD; S00005573; STD1.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:0005886; C:plasma membrane; IDA.
 CC GO; GO:0030295; F:protein kinase activator activity; IGI.
 CC GO; GO:0006006; P:glucose metabolism; IMP.
 CC GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IMP.
 CC GO; GO:0009651; P:signal transduction; IMP.
 CC GO; GO:0007165; P:signal transduction; IMP.
 CC Activator; Transcription regulation.
 CC ACTIVITY: 139 139 E -> D (in Ref. 2).
 CC CONFLICT 139 139
 CC FT SEQUENCE 444 AA; 50260 MW; 8882D78A72A6507 CRC64;
 CC SQ

Query Match 71.2%; Score 37; DB 1; Length 444;
 Best Local Similarity 71.4%; Pred. No. 70;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDC7 7
 Db 368 FKIHDC7 374

RESULT 12
 Q7R3N4 PRELIMINARY; PRT; 5412 AA.

AC Q7R3N4;
 DT 01-MAR-2004 [TREMBLrel. 26, Created]
 DT 01-MAR-2004 [TREMBLrel. 26, Last annotation update]
 DT 01-MAR-2004 [TREMBLrel. 26, Last annotation update]
 DE GIIP_39_56745_40507.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
 NCBI_TaxID=184922;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Ale S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AACB01000014; EAA41922.1; -
 CC DR InterPro; IPR008990; Capsid_hemag.
 CC SQ SEQUENCE 5412 AA; 601108 MW; 82BB3AFA5951E69C CRC64;
 CC SQ

Query Match 71.2%; Score 37; DB 2; Length 5412;
 Best Local Similarity 75.0%; Pred. No. 9.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHHDCTGV 9
 Db 4727 ELHDCTTV 4734

RESULT 13
 Q7WR7 PRELIMINARY; PRT; 202 AA.
 ID Q7WR7;
 AC Q7WR7;
 DT 01-OCT-2003 [TREMBLrel. 25, Created]
 DT 01-OCT-2003 [TREMBLrel. 25, Last sequence update]
 DT 01-MAR-2004 [TREMBLrel. 26, Last annotation update]
 DE Hypothetical protein.
 GN OrderedLocNames=BP2131;
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 NCBI_TaxID=520;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebatia M., Preston A., Murphy L.D., Thomson N.R.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cordero-Farraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltham J., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 RL EMBL; BX640417; CAB42410.1; -
 DR GO; GO:0004176; P:ATP-dependent peptidase activity; IEA.
 DR GO; GO:0006510; P:ATP-dependent proteolysis; IEA.
 DR InterPro; IPR003111; Pept_S16_N.
 DR Pfam; PF02190; ION; 1.
 CC Complete proteome; Hypothetical protein.
 CC SQ SEQUENCE 202 AA; 22230 MW; 9A28926A666322C CRC64;
 CC SQ

Query Match 69.2%; Score 36; DB 2; Length 202;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDCQTQ 8
|:|||||
Db 92 FRHACTQ 99

RESULT 14

Q7WAM7 PRELIMINARY; PRT; 202 AA.
AC Q7WAM7;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Hypoetical protein.
GN OrderedLocuNames=BBP1347;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Ruter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin I., Whitehead S., Skelton J., Skelton B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640427; CAB32907.1; -;
DR GO; GO:0004176; F:ATP-dependent peptidase activity; IEA.
DR GO; GO:0006510; P:ATP-dependent proteolysis; IEA.
DR InterPro; IPR003111; Pept_S16_N.
DR Pfam; PF02190; LON; 1.
KW Complete proteome; Hypoetical protein.
SQ SEQUENCE 202 AA; 22230 MW; 9A28926A6F66322C CRC64;

Query Match 69.2%; Score 36; DB 2; Length 202;
Best Local Similarity 75.0%; Pred. NO. 49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDCQTQ 8
|:|||||
Db 92 FRHACTQ 99

RESULT 15

Q7WJTO PRELIMINARY; PRT; 202 AA.
AC Q7WJTO;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Hypoetical protein.
GN OrderedLocuNames=BB2413;
OS Bordetella bronchiseptica
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Ruter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin I., Whitehead S., Skelton J., Skelton B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640444; CAB32907.1; -;
DR GO; GO:0004176; F:ATP-dependent peptidase activity; IEA.
DR GO; GO:0006510; P:ATP-dependent proteolysis; IEA.
DR InterPro; IPR003111; Pept_S16_N.
DR Pfam; PF02190; LON; 1.
KW Complete proteome; Hypoetical protein.
SQ SEQUENCE 202 AA; 22230 MW; 9A28926A6F66322C CRC64;

Query Match 69.2%; Score 36; DB 2; Length 202;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FOLHDCQTQ 8
|:|||||
Db 92 FRHACTQ 99

Search completed: May 3, 2005, 06:01:58
Job time : 55.1351 secs

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GenCore version 5.1.6
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Run on: May 3, 2005, 06:50:33 ; Search time 41.6842 Seconds

83.505 Million cell updates/sec

Title: US-10-003-983C-14

Sequence:.

Scoring table: BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

2: geneseqp190s: *
3: geneseqp200s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	9	5	ABG31984	Abg31984 Human CD4
2	52	100.0	553	5	AAW35856	AAw35856 Human CD4
3	52	100.0	553	6	ABU07335	Abu07335 Human exp
4	52	100.0	641	6	AAm23689	Aam23689 Human B5T
5	52	100.0	641	6	ABU07333	Abu07333 Human exp
6	52	100.0	664	6	AAm39262	Aam39262 Human pol
7	52	100.0	664	6	ABU07334	Abu07334 Human exp
8	52	100.0	1114	6	ABU05223	Abu05223 Human exp
9	52	100.0	1114	6	ABU05224	Abu05224 Human exp
10	52	100.0	1143	6	ABU05240	Abu05240 Human exp
11	52	100.0	1143	6	ABU05245	Abu05245 Human exp
12	52	100.0	1143	7	ADL16232	Adl16232 Human prc
13	52	100.0	1143	8	ADQ18845	Adq18845 Human gob
14	52	100.0	1192	8	ADR39747	Adr39747 Human kit
15	52	100.0	1219	8	ADQ39378	Adq39378 Human myo
16	52	100.0	1256	8	ADP67187	Adp67187 Human adi
17	52	100.0	1256	8	ADP12966	Adp12966 Protein e
18	52	100.0	1258	8	ADQ39376	Adq39376 Human myo
19	52	100.0	1267	8	ADQ39379	Adq39379 Human myo
20	52	100.0	1304	6	ABU05243	Abu05243 Human exp
21	52	100.0	1304	6	ABU05241	Abu05241 Human exp
22	52	100.0	1304	6	ABU05244	Abu05244 Human exp
23	52	100.0	1304	7	ADL16230	Adl16230 Human prc
24	52	100.0	1304	7	ADP65158	Adp65158 Human prc
25	52	100.0	1304	8	ADP67209	Adp67209 Human adi

ALIGNMENTS

27	52	100.0	1304	8	ABO84455	Human can
26	52	100.0	1304	8	AD039380	Human myo
28	52	100.0	1306	8	AA039375	Adg39375
29	40	76.9	78	4	AG77210	Human col
30	38	73.1	1157	8	ABO84453	ABO84453
31	38	73.1	1291	7	AD16238	Mouse can
32	38	73.1	1291	7	AD16238	Adm16238
33	37	71.2	267	5	ABG77370	Mouse pro
34	37	71.2	296	5	ABG77297	Selected
35	37	71.2	296	5	ABG77341	Selected
36	37	71.2	296	5	ABG77341	Selected
37	37	71.2	296	5	ABG77341	Selected
38	37	71.2	296	5	ABG77385	Selected
39	37	71.2	296	5	ABG77426	Selected
40	37	71.2	389	4	ABB72062	ABb72062
41	36	69.2	228	3	AY82117	AY82117
42	36	69.2	234	4	ABG24686	Novel hum
43	36	69.2	271	4	AAW93197	Peabvitr
44	36	69.2	453	3	AAK29511	AAr29511
45	36	69.2	823	2	AAK29510	BDV struc

RESULT 1

ID	ABG31984 standard; peptide; 9 AA.
XX	
AC	ABG31984;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Human CD45 HLA-binding peptide, huCD45/304.
XX	
KM	Human; CD45; human leukocyte antigen, HLA; cytotoxic T lymphocyte; CTL; antigen-presenting cell; APC; major histocompatibility complex; MHC;
KM	antigen; allogenic; T cell receptor; TCR; cancer; tumour;
KM	allogenic stem cell transplantation; CFU-GM; leukaemia;
KM	colony forming unit-granulocyte macrophage; immunotherapeutic;
KM	haematopoietic; malignant.
XX	
OS	Homo sapiens.
XX	
PN	MO200244207-A1.
XX	
PD	06-JUN-2002.
XX	
PF	30-NOV-2000; 2000MO-GB004566.
XX	
PR	30-NOV-2000; 2000MO-GB004566.
XX	
PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX	
PI	Staubs HJ, Amrolia PJ;
XX	
DR	WPI; 2002-599413/54.
XX	
PT	Novel peptide comprising leukocyte antigen binding peptide of human CD45 polypeptide, useful for producing activated cytotoxic T lymphocytes, for killing cancerous cells e.g. leukemia.
XX	
PS	Claim 2; Page 38; 56pp; English.
XX	
CC	The invention discloses a peptide comprising the human leukocyte antigen (HLA)-binding peptide of human CD45 polypeptide, its portion or variant, provided that the peptide is not the intact human CD45 polypeptide. The peptides are useful for producing activated cytotoxic T lymphocyte (CTL) in vitro which involves contacting the CTL with an antigen-presenting cell, where its major histocompatibility complex (MHC) class I molecules are loaded with the peptide, to activate, in an antigen specific manner, where the CTL and the antigen presenting cell are allogenic with respect to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animals models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/304,
CC comprising an HLA-binding peptide of human CD45
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 52; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQIHDCTQV 9
DB 1 FQIHDCTQV 9
RESULT 2
AAW35856
ID AAW35856 standard; protein; 553 AA.
AC AAW35856;
XX
DT 27-APR-1998 (first entry)
XX
DE Human CD45 for use in T lymphocyte veto molecule.
XX
KW Human; CD45; T lymphocyte veto molecule; chimeric molecule;
KW targeting polypeptide; suppression; immune response; treatment;
KW autoimmune disease; allergy; immunological disorder;
KW transplant rejection.
XX
OS Homo sapiens.
XX
PN WO9737687-A1.
XX
PD 16-OCT-1997.
XX
PF 10-APR-1997; 97WO-US005943.
XX
PR 10-APR-1996; 96US-00630172.
XX
PA (NAJL-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Straetz UD;
XX
DR WPI; 1997-512419/47.
XX
PT T lymphocyte veto molecule comprising response cell activating protein -
PT linked to molecule that targets stimulator cell marker, used for
PT selective suppression of immune response, e.g. prevention of graft
PT rejection or treatment of auto-immune disease.
XX
PS Claim 37; Page 70-72; 309pp; English.
XX
XX A novel T lymphocyte veto molecule is a chimeric molecule comprising a
CC protein, e.g. the present sequence, linked to a targeting polypeptide
CC that binds a molecule, which differentiates a host cell from a tissue
CC graft cell, or selectively targets a stimulator cell involved in the
CC autoimmune response. A veto molecule, in which the protein binds a

CC molecule that targets stimulator cells, can be used to suppress an immune
CC response and therefore treat autoimmune diseases, e.g. systemic lupus
CC erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
CC diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
CC thyroiditis, Addison's or Grave's diseases and rheumatoid carditis,
CC allergies and other immunological disorders. Where the protein binds a
CC molecule that differentiates graft and host cells, the veto molecule can
CC be used to reduce transplant rejection. The veto molecule provides
CC specific regulation of particular stimulator cells that can kill graft
CC cells or respond to autoantigens, but leave other stimulator cells
CC unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
CC affecting the other. The veto molecule can be administered locally to
CC minimise generalised immunosuppression
XX
SQ Sequence 553 AA;
Query Match 100.0%; Score 52; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQIHDCTQV 9
DB 281 FQIHDCTQV 289
RESULT 3
ABU07335
ID ABU07335 standard; protein; 553 AA.
AC ABU07335;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2036.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW proteinase; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2036; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 553 AA;

Query Match 100.0%; Score 52; DB 6; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTCTOV 9
Db 281 FOLHDTCTOV 289

RESULT 4

AA023689 standard; protein; 641 AA.

XX AAM23689;

DT 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1214.

KM Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KM diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

KM gene therapy; nutrition.

XX Homo sapiens.

PN WO200154477-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US002687.

PR 25-JAN-2000; 2000US-00491404.

PR 17-JUL-2000; 2000US-00617746.

PR 03-AUG-2000; 2000US-00631451.

PR 15-SEP-2000; 2000US-00663870.

PA (HYSR-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

DR WPI; 2001-476164/51.

DR N-PSDB; AAH98348.

PT Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use.

XX Claim 20; Page 875-876; 1275pp; English.

CC The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensic, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 52; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTCTOV 9
Db 145 FOLHDTCTOV 153

RESULT 5

ABU07333 standard; protein; 641 AA.

XX ABU07333;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #2034.

KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;

KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;

KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCOS INC.

PI Chiciz RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.

PS Example 2; SEQ ID NO 2034; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,

CC transporter, cytoskeletal protein, receptor or transcription factor. The

CC polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified

CC polypeptide. The purified polypeptide, or the antibody that binds to this

CC polypeptide, is useful for treating cancer. The polypeptide is also

CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing

CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for

CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 52; DB 6; Length 641;
 Best Local Similarity 100.0%; Pred. No. 0.59;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FQIHDTQYV 9
 Db 145 FQIHDTQYV 153
 RESULT 6
 AAM39262
 ID AAM39262 standard; protein; 664 AA.
 AC AAM39262;
 XX
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 2407.
 XX
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KM Leukaemia.
 XX
 XX Homo sapiens.
 OS
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PDB; AAI58418.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 4; SEQ ID NO 2407; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AAM38642-AA42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 664 AA;
 Query Match 100.0%; Score 52; DB 4; Length 664;
 Best Local Similarity 100.0%; Pred. No. 0.61;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FQIHDTQYV 9
 Db 145 FQIHDTQYV 153
 RESULT 7
 ABU07334
 ID ABU07334 standard; protein; 664 AA.
 XX
 AC ABU07334;
 XX
 DT 29-JAN-2003 (first entry)
 DE Human expressed protein tag (EPT) #2035.
 XX
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002MO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 PI WPI; 2003-040607/03.
 XX
 DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 2035; 134bp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 664 AA;

Query Match 100.0%; Score 52; DB 6; Length 664;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQIHDCTQV 9
| | | | | | | | | |
Db 145 FQIHDCTQV 153

RESULT 8
ABU05246
ID ABU05246 standard; protein; 1114 AA.

XX ABU05246;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1912.

DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX MPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

XX Example 2; SEQ ID NO 1912; 134p; English.

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for creating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1114 AA;

Query Match 100.0%; Score 52; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQIHDCTQV 9
| | | | | | | | | |
Db 114 FQIHDCTQV 122

RESULT 9
ABU05239
ID ABU05239 standard; protein; 1114 AA.

XX ABU05239;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1905.

DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX MPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

XX Example 2; SEQ ID NO 1905; 134p; English.

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for creating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;

Query Match 100.0%; Score 52; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTQV 9
| | | | | | | | | |
DB 114 FOLHDTQV 122

RESULT 10
ABU05240
ID ABU05240 standard; protein; 1143 AA.
XX
AC ABU05240;

DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1906.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

PI Chicx RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;

Query Match 100.0%; Score 52; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTQV 9
| | | | | | | | | |
DB 143 FOLHDTQV 151

RESULT 11
ABU05245
ID ABU05245 standard; protein; 1143 AA.
XX
AC ABU05245;

DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1911.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

PI Chicx RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

PS Example 2; SEQ ID NO 1911; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPR) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 1143 AA;

Query Match 100.0%; Score 52; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDCCTOV 9
| | | | |
Db 143 FOLHDCCTOV 151

RESULT 12

ADL16232
ID ADL16232 standard; protein; 1143 AA.

XX ADL16232;

XX 06-MAY-2004 (first entry)

XX Human protein tyrosine phosphatase #27.

XX cytostatic; immunosuppressive; antiallergic;
XX protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
XX inducible signalling pathway; cell proliferation; cancer;
XX guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX cell-cycle abnormality; enzyme.

OS Homo sapiens.

PN WO2003068984-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-EP001446.

XX 13-FEB-2002; 2002US-0356810P.

PR 12-FEB-2003; 2003US-00366547.

XX (COLD-) COLD SPRING HARBOR LAB.

PA (CEPT-) CEPTIR INC.

XX Tonks NK, Tzu-Ching M, Cool DE;

XX WPI; 2003-712572/67.

DR N-PSDB; ADL16231.

PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX screening for specific modulators, potential agents for treating e.g.
XX cancer or autoimmune disease.

PS Disclosure; SEQ ID NO 81; 238bp; English.

XX The invention relates to a method for identifying a protein tyrosine
XX phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX subjecting a sample, including a cell that contains at least one PTP, to
XX conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX anaerobically, in presence of a sulphydryl-reactive agent (II) that
XX irreversibly modifies the thiol group of an invariant Cys in the active
XX site of PTP; and (iii) determining, under reducing conditions, the level
XX of dephosphorylation, caused by PTP, of a labelled substrate (III), where
XX dephosphorylation indicates that an active PTP is present. . No details
XX of tests for these activities are given. The method is used to identify
XX reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX are involved. These agents are potentially useful, in human or veterinary
XX medicine, for treating abnormal cell proliferation or growth (cancer);
XX guest vs. host disease; autoimmune diseases; allergy or other
XX immunosuppressed states; metabolic disorders and cell-cycle

CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.

XX Sequence 1143 AA;

Query Match 100.0%; Score 52; DB 7; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDCCTOV 9
| | | | |
Db 143 FOLHDCCTOV 151

RESULT 13

ADQ18845
ID ADQ18845 standard; protein; 1143 AA.

XX ADQ18845;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnick A;

XX WPI; 2004-441208/41.

PT Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.

PS Example 2; SEQ ID NO 1664; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.

XX Sequence 1143 AA;

Query Match 100.0%; Score 52; DB 8; Length 1143;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDCCTOV 9
| | | | |
Db 143 FOLHDCCTOV 151

RESULT 14
ID ADR39747 standard; protein; 1192 AA.
AC ADR39747;
XX
XX 18-NOV-2004 (first entry)
DT
XX
DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
XX
XX human; kinase and phosphatase protein; KPP; enzyme; cytosolic;
XX antiarteriosclerotic; anti-HIV; antiallergic; antiinflammatory;
XX ceribroprotective; gene therapy; cell proliferative disorder; cancer;
XX thymomimetic; neurologic disorder; epilepsy; Huntington's disease;
XX stroke; immune disorder; inflammatory disorder; AIDS; allergy;
XX developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX KPP-20.
XX
XX Homo sapiens.
OS
XX
XX WO2004074453-A2.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 20-FEB-2004; 2004WO-US005092.
PF
XX
XX 20-FEB-2003; 2003US-0449059P.
PR
XX 19-MAR-2003; 2003US-0456932P.
PR 28-MAR-2003; 2003US-0458844P.
PR 09-APR-2003; 2003US-0461678P.
PR 17-APR-2003; 2003US-0463937P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Rankumar J, Margulis JP, Swarnakar A, Chawla NK, Tran UK;
PI Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
PI Jackson AA, Yang J, Gotrvad AB;
XX
XX WPI; 2004-635568/61.
DR N-PSDB; ADR39793.
XX
XX New human kinases and phosphatases (KPP) for diagnosing, treating and
PT preventing diseases or conditions associated with aberrant KPP expression
PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX
XX Claim 1; SEQ ID NO 20; 299pp; English.
PS
XX
XX The present sequence represents the human kinase and phosphatase protein
CC (KPP), designated KPP-20. The human KPP sequences from the present
CC invention have cytosolic, antiarteriosclerotic, anticonvulsant,
CC neurotrophic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thymomimetic activities, and can be used in gene
CC therapy. The human KPP proteins and polynucleotides can be used in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KPP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They can also be used in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
XX
XX Sequence 1192 AA;
SQ
Query Match 100.0%; Score 52; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FOLHDOCTOV 9
Db 192 FOLHDOCTOV 200
RESULT 15
ID ADQ39378 standard; protein; 1219 AA.
ADQ39378
AC ADQ39378;
XX
XX 18-NOV-2004 (first entry)
DT
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiant; gene therapy; human.
XX
XX Homo sapiens.
OS
XX
XX WO2004058052-A2.
PN
XX
XX 15-JUL-2004.
PD
XX
XX 22-DEC-2003; 2003WO-US040978.
PF
XX
XX 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
PA
XX
XX Cargill M, Devlin JI, Yakubova O;
PI WPI; 2004-533949/51.
DR N-PSDB; ADQ38550.
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1041; 145pp; English.
PS
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
XX Sequence 1219 AA;
SQ

Query Match 100.0%; Score 52; DB 8; Length 1219;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FOLHDTQV 9
| | | | |
Db 219 FOLHDTQV 227

RESULT 16
ID ADM67187
ADM67187 standard; protein; 1256 AA.

XX AC ADM67187;
XX DT 03-JUN-2004 (first entry)
XX DE Human adipocyte specific PTPase receptor type C protein SegID 541.

XX KW human; adipocyte specific; adipose tissue; anti-obesity;
XX KW high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
XX KW adipogenesis; hypertension; cardiovascular disease; anorectic;
XX KW anti-diabetic; hypotensive; PTPase receptor type C.

XX OS Homo sapiens.

XX PN WO2004011618-A2.

XX PD 05-FEB-2004.

XX PF 29-JUL-2003; 2003WO-US023684.

XX PR 29-JUL-2002; 2002US-0398785P.

XX PR 12-JUN-2003; 2003US-0478206P.

XX PA (HMG1-C) HMG1 INC.

XX PI Chada K, Chouinard R, Ashar H, Sayed AMD;

XX DR WPI; 2004-143846/14.

XX DR N-PSDB; ADM66908.

XX PT Identifying adipocyte specific genes, useful for treating obesity or
XX PT diabetes, and for identifying drug targets, by differential gene
XX PT expression analysis between adipose tissue or stromal vascular tissue of
XX PT mice of different genotypes.

XX PS Disclosure; SEQ ID NO 541; 91pp; English.

XX CC This invention relates to a novel method for identifying genes that are
XX CC over-expressed in adipose tissue and as such it provides targets for anti
XX CC -obesity pharmaceutical compositions. Specifically, it refers to a high
XX CC mobility group I-C protein (HMG1-C) that is associated with obesity and
XX CC is epistatic to leptin, furthermore, it refers to the ob gene where an
XX CC autosomal recessive trait is linked to obesity and diabetes. The present
XX CC invention describes performing differential gene expression analysis
XX CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
XX CC of any two different mice selected from a group consisting of wild-type,
XX CC HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
XX CC this method novel nucleotides and the encoded proteins thereof were
XX CC identified that are adipocyte specific, and as such can be used for
XX CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
XX CC hypertension and cardiovascular disease, as well as screening for
XX CC compounds that can modulate or prevent adipogenesis and treat diabetes or
XX CC obesity. These compositions exhibit anorectic, anti-diabetic and
XX CC hypotensive activities. This polypeptide sequence is a human homologue of
XX CC a murine adipocyte specific protein sequence of the invention.

XX SQ Sequence 1256 AA;

Query Match 100.0%; Score 52; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FOLHDTQV 9
| | | | |
Db 256 FOLHDTQV 264

RESULT 17
ID ADP12966
ADP12966 standard; protein; 1256 AA.

XX AC ADP12966;

XX DT 12-AUG-2004 (first entry)

XX DE Protein encoding reference mRNA sequence #51.

XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

XX OS Homo sapiens.

XX PN WO2004042346-A2.

XX PD 21-MAY-2004.

XX PF 24-APR-2003; 2003WO-US012946.

XX PR 24-APR-2002; 2002US-00131831.

XX PR 20-DEC-2002; 2002US-00325899.

XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

XX PI Rosenberg S;

XX DR WPI; 2004-400724/37.

XX PT diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX PT rejection, in an individual, comprises detecting the expression level of
XX PT the genes.

XX PS Claim 65; SEQ ID NO 2975; 1762pp; English.

XX CC The present invention relates to diagnosing or monitoring transplant
XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX CC comprises detecting the expression level of one or more genes. The
XX CC methods, system and kits are useful in diagnosing or monitoring
XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX CC islet, lung, bone marrow or stem cell transplant rejection, in an
XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
XX CC individual. The method is also useful in assessing the immune status of
XX CC an individual. The methods are also useful in diagnosing and monitoring
XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX CC viral, bacterial or fungal infection. The present sequence represents a
XX CC protein encoded by an mRNA sequence of the invention which show altered
XX CC expression in renal transplantation and expression.

XX SQ Sequence 1256 AA;

Query Match 100.0%; Score 52; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FOLHDTQV 9
| | | | |
Db 256 FOLHDTQV 264

RESULT 18
ADQ39376

ID ADQ39376 standard; protein; 1258 AA.
XX ADQ39376;
AC
XX
DT 18-NOV-2004 (first entry)
XX
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
XX
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX
XX
OS Homo sapiens.
XX
PN MO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
XX
PR 30-APR-2003; 2003US-0466412P.
XX
PR 23-SEP-2003; 2003US-0504955P.
XX
XX
PA (APPL-) APPLERA CORP.
XX
XX
PI Cargill M, Devlin JT, Iakubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PSDB; ADQ38548.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX
PS Claim 10; SEQ ID NO 1039; 145pp; English.
XX
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC composition represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
XX
SQ Sequence 1258 AA;
XX
XX
Query Match 100.0%; Score 52; DB 8; Length 1258;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FOLHDTQV 9
|||||||

Db 258 FOLHDTQV 266
RESULT 19
ADQ39379
ID ADQ39379 standard; protein; 1267 AA.
XX
XX
XX ADQ39379;
AC
XX
XX
DT 18-NOV-2004 (first entry)
XX
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
XX
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX
XX
OS Homo sapiens.
XX
PN MO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
XX
PR 30-APR-2003; 2003US-0466412P.
XX
PR 23-SEP-2003; 2003US-0504955P.
XX
XX
PA (APPL-) APPLERA CORP.
XX
XX
PI Cargill M, Devlin JT, Iakubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PSDB; ADQ38551.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX
PS Claim 10; SEQ ID NO 1042; 145pp; English.
XX
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC composition represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
XX
SQ Sequence 1267 AA;
XX
XX
Query Match 100.0%; Score 52; DB 8; Length 1267;
QY

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FOLHDTQV 9
Db 267 FOLHDTQV 275

RESULT 20

ABU05243
ID ABU05243 standard; protein; 1304 AA.

XX AC ABU05243;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1909.

XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chiciz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
cytoskeletal proteins, receptors or transcription factors), useful for
treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
leukemia.

XX PS Example 2; SEQ ID NO 1909; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a
mammal an immunogenic response directed against any of the purified
polypeptide. The purified polypeptide, or the antibody that binds to this
polypeptide, is useful for treating cancer. The polypeptide is also
useful for identifying compounds that binds to a naturally processed
class I or class II MHC-binding polypeptide. The polypeptides and
polynucleotides are particularly useful for treating or preventing
myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
lymphoma or leukemia. These are also useful for screening agents for
treating the above mentioned diseases. This sequence represents an
expressed protein tag (EPT) isolated from human tissue for translational
profiling. Note: This sequence does not appear in the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 6; Length 1304;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FOLHDTQV 9
Db 304 FOLHDTQV 312

RESULT 21

ABU05241
ID ABU05241 standard; protein; 1304 AA.

XX AC ABU05241;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1907.

XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chiciz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
cytoskeletal proteins, receptors or transcription factors), useful for
treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
leukemia.

XX PS Example 2; SEQ ID NO 1907; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a
mammal an immunogenic response directed against any of the purified
polypeptide. The purified polypeptide, or the antibody that binds to this
polypeptide, is useful for treating cancer. The polypeptide is also
useful for identifying compounds that binds to a naturally processed
class I or class II MHC-binding polypeptide. The polypeptides and
polynucleotides are particularly useful for treating or preventing
myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
lymphoma or leukemia. These are also useful for screening agents for
treating the above mentioned diseases. This sequence represents an
expressed protein tag (EPT) isolated from human tissue for translational
profiling. Note: This sequence does not appear in the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 6; Length 1304;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTQV 9
|||||
Db 304 FOLHDTQV 312

RESULT 22

ABU05244
ID ABU05244 standard; protein; 1304 AA.

AC ABU05244;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1910.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

PI Chicz RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Example 2; SEQ ID NO 1910; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 6; Length 1304;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTQV 9
|||||
Db 304 FOLHDTQV 312

RESULT 23

ADL16230
ID ADL16230 standard; protein; 1304 AA.

AC ADL16230;

DT 06-MAY-2004 (first entry)

DE Human protein tyrosine phosphatase #26.

XX cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.

OS Homo sapiens.

PN WO2003068984-A2.

PD 21-AUG-2003.

PF 13-FEB-2003; 2003WO-EP001446.

PR 13-FEB-2002; 2002US-0356810P.

PR 12-FEB-2003; 2003US-00366547.

PA (COLD-) COLD SPRING HARBOR LAB.

PA (CEPT-) CEPTYR INC.

PI Toms NK, Tzu-Ching M, Cool DE;

DR WPI; 2003-712572/67.

DR N-PSDB; ADL16229.

XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.

XX Disclosure; SEQ ID NO 79; 238pp; English.

CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulphydryl-reactive agent (ii) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.

XX Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDCOV 9
 |||||
 Db 304 FOLHDCOV 312

RESULT 24

ADP65158
 ID ADP65158 standard; protein; 1304 AA.

AC ADP65158;

DT 12-AUG-2004 (first entry)

DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.

XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigen; antinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.

XX Homo sapiens.

PN WO2003072827-A1.

PD 04-SEP-2003.

PF 31-OCT-2002; 2002WO-US035433.

PR 31-OCT-2001; 2001US-0336220P.

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

PI Hirsch R, Thornton SL;

DR WPI: 2003-712740/67.

GENBANK: NP_002829.

PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

PS Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antipain, antinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDCOV 9
 |||||
 Db 304 FOLHDCOV 312

RESULT 25

ADM67209
 ID ADM67209 standard; protein; 1304 AA.

AC ADM67209;

DT 03-JUN-2004 (first entry)

DE Human adipocyte specific leukocyte common antigen protein SeqID 563.

XX human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antiobesity; hypotensive; leukocyte common antigen.

XX Homo sapiens.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

(HMG-) HMGNE INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI: 2004-143846/14.

N-PSDB; ADM66930.

PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.

PS Disclosure; SEQ ID NO 563; 91pp; English.

XX This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C^{-/-}, ob/ob, or HMGI-C^{-/-} ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred.No.1.2; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTQV 9
 |||||
 DB 304 FOLHDTQV 312

RESULT 26
 ABO84455
 ID ABO84455 standard; protein; 1304 AA.
 XX
 AC ABO84455;
 XX
 DT 18-NOV-2004 (first entry)
 DE Human cancer-associated protein HPI3-011.2.
 XX
 KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
 KM lymphoma; CAP.
 OS Homo sapiens.
 XX
 PN WO2004074320-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 XX
 PR 15-APR-2003; 2003US-00388838.
 XX
 PR 13-JUN-2003; 2003US-00417375.
 XX
 PR 15-SEP-2003; 2003US-00461862.
 XX
 PR 15-DEC-2003; 2003US-00663431.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 PI Morris DW, Morris DW, Malandro MS;
 DR N-PSDB; ABD32626.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 PS
 XX claim 18; seqid 147; 310pp; English.

The invention relates to an isolated nucleic acid comprising at least 10
 contiguous nucleotides of any of the 233 polynucleotide sequences given
 in the specification, or its complement. The nucleic acids encode cancer-
 associated proteins. Also included are an expression vector comprising
 the isolated nucleic acid cited above, a host cell comprising the above
 recombinant nucleic acid or expression vector, a microarray for detecting
 a cancer-associated (CA) nucleic acid comprising at least one probe
 comprising at least 10 contiguous nucleotides of any of the above-
 mentioned nucleotide sequences, an isolated polypeptide (encoded within
 an open reading frame of a CA sequence selected from any of the 95
 polynucleotide sequences as mentioned in the specification, or its
 complement), an isolated antibody, (or its antigen binding fragment) that
 binds to the above polypeptide, a hybridoma that produces the above
 monoclonal antibody, a pharmaceutical composition comprising the above
 antibody and a pharmaceutical excipient, a kit for detecting cancer
 cells (comprising the antibody cited above, methods for diagnosing cancer
 or for detecting the presence or absence of cancer cells in an
 individual, a method for inhibiting growth of cancer cells in an
 individual, a method for delivering a therapeutic agent to cancer cells
 in an individual, an electronic library comprising the above
 polynucleotide or polypeptide (or their fragments), methods of screening
 for anticancer activity or for a bioactive agent capable of modulating
 the activity of a CA protein (CAP), methods for detecting cancer

CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred.No.1.2; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTQV 9
 |||||
 DB 304 FOLHDTQV 312

RESULT 27
 ADQ39380
 ID ADQ39380 standard; protein; 1304 AA.
 XX
 AC ADQ39380;
 XX
 DT 18-NOV-2004 (first entry)
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KM cardiac; gene therapy; human.
 OS Homo sapiens.
 XX
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 XX
 PR 10-MAR-2003; 2003US-0453135P.
 XX
 PR 30-APR-2003; 2003US-0466412P.
 XX
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin UT, Iakoubova O;
 DR N-PSDB; ADQ38552.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 PS
 XX Claim 10; SEQ ID NO 1043; 145pp; English.

The invention relates to a novel method for identifying an individual who
 has an altered risk for developing myocardial infarction. The method
 comprises detecting a single nucleotide polymorphism (SNP) in any one of
 the nucleotide sequences given in the specification in the individual's
 nucleic acids, where the presence of the SNP is correlated with an
 altered risk for myocardial infarction in the individual. The invention
 further comprises: an isolated nucleic acid molecule comprising at least
 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 the specification or its complement and encoding any one of the amino
 acid sequences given in the specification; an isolated polypeptide
 comprising an amino acid sequence given in the specification; an antibody
 that specifically binds to the polypeptide or its antigen-binding
 fragment; an amplified polynucleotide containing an SNP given in the

CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

XX
 SQ Sequence 1304 AA;

Query Match 100.0%; Score 52; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTCTOV 9
 |||||
 DB 304 FOLHDTCTOV 312

RESULT 28
 ADQ39375 ID ADQ39375 standard; protein; 1306 AA.
 XX
 AC ADQ39375;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
 XX
 KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 XX
 KM cardiant; gene therapy; human.
 OS Homo sapiens.
 XX
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JJ, Iakubova O;
 XX
 DR WPI; 2004-533949/51.
 DR N-PSDB; ADQ38547.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1038; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in

CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

XX
 SQ Sequence 1306 AA;

Query Match 100.0%; Score 52; DB 8; Length 1306;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FOLHDTCTOV 9
 |||||
 DB 306 FOLHDTCTOV 314

Search completed: May 3, 2005, 07:31:00
 Job time : 66.6842 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:35:45 ; Search time 53.1579 Seconds

(without alignments)
96.332 Million cell updates/sec

Title: US-10-003-983C-15
Perfect score: 49
Sequence: 1 KLLAFGFAPL 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	34	2 O9H3X6	O9h3x6 homo sapien
2	49	100.0	126	2 O8M1N3	O8m1n3 equus caball
3	49	100.0	240	2 O6Q1P2	O6q1p2 homo sapien
4	49	100.0	453	2 O9GMB6	O9gmb6 bos indicus
5	49	100.0	454	2 O6SZ80	O6sz80 sus scrofa
6	49	100.0	461	2 O9GMB4	O9gmb4 bos taurus
7	49	100.0	463	2 O9GMB5	O9gmb5 bos indicus
8	49	100.0	465	2 O9GMB1	O9gmb1 syncerus ca
9	49	100.0	466	2 O6SZ81	O6sz81 sus scrofa
10	49	100.0	501	2 O6SZ82	O6sz82 sus scrofa
11	49	100.0	517	2 O6SZ83	O6sz83 sus scrofa
12	49	100.0	567	2 O6SZ84	O6sz84 sus scrofa
13	49	100.0	583	2 O6SZ85	O6sz85 sus scrofa
14	49	100.0	756	2 O6PJK7	O6pjk7 homo sapien
15	49	100.0	1290	2 O6EDC0	O6edc0 actus vocifer
16	49	100.0	1303	2 O6ED61	O6ed61 actus nancy
17	49	100.0	1303	2 O6ED62	O6ed62 actus nigrit
18	49	100.0	1304	1 CD45 HUMAN	CD45 homo sapien
19	43	87.8	22	2 O78BF1	O78bf1 mus musculus
20	43	87.8	24	2 O61815	O61815 mus musculus
21	43	87.8	183	2 O61814	O61814 mus musculus
22	43	87.8	878	2 O8C6Q7	O8c6q7 mus musculus
23	43	87.8	1152	1 CD45 MOUSE	CD45 mus musculus
24	43	87.8	1291	2 O61812	O61812 mus musculus
25	43	87.8	1343	2 O64730	O64730 mus musculus
26	42	85.7	1237	2 O91976	O91976 gallus gall
27	40	81.6	568	2 O6ZMK4	O6zmk4 burkholderi
28	40	81.6	568	2 O63X68	O63x68 burkholderi
29	39	79.6	213	2 O49930	O49930 mycobacteri
30	39	79.6	336	2 O69510	O69510 mycobacteri
31	39	79.6	459	2 O83123	O83123 enterococci

32	38	77.6	78	2 O8TH48	O8th48 methanopyru
33	38	77.6	272	2 O8DRX2	O8drx2 streptococc
34	38	77.6	289	2 O9CJL3	O9cj13 pasteurella
35	38	77.6	347	2 O97VD0	O97vd0 sulfolobus
36	37	75.5	198	2 O9FMX8	O9fmx8 arabidopsis
37	37	75.5	230	2 O6F753	O6f753 acinetobact
38	37	75.5	253	2 O01866	O01866 caenorhabdi
39	37	75.5	399	2 O6EZH2	O6ezh2 caenorhabdi
40	37	75.5	458	2 O96XT8	O96xt8 sulfolobus
41	36	73.5	138	2 O8XK73	O8xk73 clostridium
42	36	73.5	153	2 O63SB8	O63sb8 burkholderi
43	36	73.5	166	2 O7RX25	O7rx25 neuropeptid
44	36	73.5	200	2 O7VIM9	O7vim9 helicobacte
45	36	73.5	254	2 O62LQ7	O62lq7 burkholderi

ALIGNMENTS

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RESULT 1
O9H3X6 PRELIMINARY; PRT; 34 AA.
ID O9H3X6;
AC O9H3X6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE T200 leukocyte common antigen (Fragment).
GN Name=PTPRC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89009812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
antigen (CD45) gene.";
RL J. Immunol. 141:2781-2787(1988).
DR EMBL; M23463; AAG26082.1; JOINED.
DR EMBL; M23461; AAG26082.1; JOINED.
DR EMBL; M23462; AAG26082.1; JOINED.
FT CHAIN 32 >34 T200 leukocyte common antigen.
FT NON_TER 34
SQ SEQUENCE 34 AA; 3749 MW; 0C261F8943734758 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 34;
Best Match Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAPL 10
Db 6 KLLAFGFAPL 15

RESULT 2
O8M1N3 PRELIMINARY; PRT; 126 AA.
ID O8M1N3;
AC O8M1N3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE Leukocyte common antigen (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV114350; AAM76678.1; -

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FT  NON TER      126      126
SQ  SEQUENCE     126 AA; 12927 MW; B3D35062F709F14C CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 2; Length 126;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KLLAFGFAFL 10
    |||||
Db  6 KLLAFGFAFL 15

RESULT 3
O6Q1P2  PRELIMINARY; PRT; 240 AA.
AC  O6Q1P2;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  CD45 transcript variant (Fragment).
GN  Name=PTPRC;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Li D., Brackenridge S., Sreaton G.R.; /
RL  Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY567999; AA575254.1; -.
FT  NON TER      240
SQ  SEQUENCE     240 AA; 25329 MW; 65067EDA0312D87 CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 2; Length 240;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KLLAFGFAFL 10
    |||||
Db  6 KLLAFGFAFL 15

RESULT 4
O9GMB6  PRELIMINARY; PRT; 453 AA.
AC  O9GMB6;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Membrane tyrosine phosphatase (Fragment).
GN  Name=cd45;
OS  Bos indicus (Zebu).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovinae; Bos.
OX  NCBI_TaxID=9915;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  STRAIN=Bozan; TISSUE=Peripheral blood;
RL  MEDLINE=21115144; PubMed=11220630; DOI=10.1007/s002510000276;
DR  Ballingall K.T., Walbochi L., Holmes E.C., Woelk C.H., MacHugh N.D.,
RA  Lutje V., McKeever D.J.;
RT  "the CD45 locus in cattle: allelic polymorphism and evidence for
exceptional positive natural selection.";
RL  Immunogenetics 52:276-283(2001).
DR  EMBL; AJ400865; CAC05415.1; -.
DR  InterPro; IPR003961; FN III.
DR  Pfam; PF00041; fn3; 2.
DR  SMART; SM00060; FN3; 3.
DR  PROSITE; PSS0853; FN3; 2.
FT  NON TER      453
SQ  SEQUENCE     453 AA; 51211 MW; 2E01CCE6F6C5268 CRC64;

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Query Match
Best Local Similarity 100.0%; Score 49; DB 2; Length 453;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KLLAFGFAFL 10
    |||||
Db  6 KLLAFGFAFL 15

RESULT 5
O6S280  PRELIMINARY; PRT; 454 AA.
AC  O6S280;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  CD45 antigen isoform 6 (EC 3.1.3.48) (Fragment).
GN  Name=CD45;
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Schmitzlein W.M., Zuckermann F.A.;
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY444871; AR16435.1; -.
DR  GO; GO:0016787; F:hydrolase activity; IEA.
DR  GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR  InterPro; IPR003961; FN III.
DR  InterPro; IPR008957; FN_III-like.
DR  Pfam; PF00041; fn3; 2.
DR  SMART; SM00060; FN3; 2.
DR  PROSITE; PSS0853; FN3; 2.
KW  Hydrolase.
FT  NON TER      454
SQ  SEQUENCE     454 AA; 50996 MW; 9FD5CCAEB96DF48B CRC64;

Query Match
Best Local Similarity 100.0%; Score 49; DB 2; Length 454;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KLLAFGFAFL 10
    |||||
Db  6 KLLAFGFAFL 15

RESULT 6
O9GMB4  PRELIMINARY; PRT; 461 AA.
AC  O9GMB4;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Membrane tyrosine phosphatase (Fragment).
GN  Name=cd45;
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  TISSUE=Peripheral blood;
RL  MEDLINE=21115144; PubMed=11220630; DOI=10.1007/s002510000276;
DR  Ballingall K.T., Walbochi L., Holmes E.C., Woelk C.H., MacHugh N.D.,
RA  Lutje V., McKeever D.J.;
RT  "the CD45 locus in cattle: allelic polymorphism and evidence for
exceptional positive natural selection.";
RL  Immunogenetics 52:276-283(2001).
DR  EMBL; AJ400864; CAC05417.1; -.
DR  InterPro; IPR003961; FN_III.

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DR InterPro; IPR008957; FN_III-like.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PSS0853; FN3; 2.
 FT NON_TER 461 461
 SQ SEQUENCE 461 AA; 51941 MW; 8736F59346454240 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 461;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAPL 10
 |||||
 Db 6 KLLAFGFAPL 15

RESULT 7
 Q9GMB5 PRELIMINARY; PRT; 463 AA.

AC Q9GMB5;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DE Membrane tyrosine phosphatase (Fragment).
 GN Name=cd45;

OS Bos indicus (Zebu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9915;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bozan; TISSUE=Peripheral blood;
 RX MEDLINE=2115144; PubMed=11220630; DOI=10.1007/s002510000276;
 RA Ballingall K.T., Waldoch L., Holmes E.C., Weik C.H., MacHugh N.D.,
 RA Lurie V., McKeever D.J.;
 RT "The CD45 locus in cattle: allelic polymorphism and evidence for
 RT exceptional positive natural selection."
 RL Immunogenetics 52:276-283(2001).

DR EMBL; AJ400866; CAC05416.1; -.
 DR InterPro; IPR003961; FN_III.
 DR SMART; PF00041; fn3; 2.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PSS0853; FN3; 2.
 FT NON_TER 463 463
 SQ SEQUENCE 463 AA; 52236 MW; FABF7F83F387596F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAPL 10
 |||||
 Db 6 KLLAFGFAPL 15

RESULT 8
 Q9GMB1 PRELIMINARY; PRT; 465 AA.

AC Q9GMB1;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Membrane tyrosine phosphatase (Fragment).
 GN Name=cd45;

OS Syncerus caffer (Cape buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Syncerus.
 NCBI_TaxID=9970;
 GN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood;
 RX MEDLINE=2115144; PubMed=11220630; DOI=10.1007/s002510000276;
 RA Ballingall K.T., Waldoch L., Holmes E.C., Weik C.H., MacHugh N.D.,
 RA Lurie V., McKeever D.J.;
 RT "The CD45 locus in cattle: allelic polymorphism and evidence for
 RT exceptional positive natural selection."
 RL Immunogenetics 52:276-283(2001).

DR EMBL; AJ400867; CAC05420.1; -.
 DR InterPro; IPR003961; FN_III.
 DR SMART; PF00041; fn3; 1.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PSS0853; FN3; 2.
 FT NON_TER 465 465
 SQ SEQUENCE 465 AA; 52289 MW; 9415673F219A368A CRC64;

Query Match 100.0%; Score 49; DB 2; Length 465;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAPL 10
 |||||
 Db 6 KLLAFGFAPL 15

RESULT 9
 Q6S281 PRELIMINARY; PRT; 466 AA.

AC Q6S281;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DE CD45 antigen isoform 5 (EC 3.1.3.48) (Fragment).
 GN Name=CD45;

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Schmitzlein W.M., Zuckermann F.A.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY444870; BAB1634.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR InterPro; IPR003961; FN_III.
 DR SMART; PF00041; fn3; 2.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PSS0853; FN3; 2.
 KW Hydrolase.
 FT NON_TER 466 466
 SQ SEQUENCE 466 AA; 52183 MW; 377CF34BAE18A28 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAPL 10
 |||||
 Db 6 KLLAFGFAPL 15

RESULT 10
 Q6S282 PRELIMINARY; PRT; 501 AA.

AC Q6S282;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DE CD45 antigen isoform 4 (EC 3.1.3.48) (Fragment).
 GN Name=CD45;
 OS Sus scrofa (Pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY444869; AAR16433.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PSS0853; FN3; 2.
KM Hydrolase.
FT NON_TER
SQ SEQUENCE 501 AA; 55600 MW; B9E514C9183E3689 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILAFGFAFL 10
DB 6 KILAFGFAFL 15

RESULT 11
Q6S283 PRELIMINARY; PRT; 517 AA.
ID Q6S283;
AC Q6S283;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CD45 antigen isoform 3 (EC 3.1.3.48) (Fragment).
GN Name=CD45;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY444868; AAR16432.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PSS0853; FN3; 2.
KM Hydrolase.
FT NON_TER
SQ SEQUENCE 517 AA; 57184 MW; D4BD2C74E186339 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILAFGFAFL 10
DB 6 KILAFGFAFL 15

RESULT 12
Q6S284 PRELIMINARY; PRT; 567 AA.
ID Q6S284;
AC Q6S284;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE CD45 antigen isoform 2 (EC 3.1.3.48) (Fragment).
GN Name=CD45;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY444867; AAR16431.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PSS0853; FN3; 2.
KM Hydrolase.
FT NON_TER
SQ SEQUENCE 567 AA; 62298 MW; 5CDBB886254187FD CRC64;

Query Match 100.0%; Score 49; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILAFGFAFL 10
DB 6 KILAFGFAFL 15

RESULT 13
Q6S285 PRELIMINARY; PRT; 583 AA.
ID Q6S285;
AC Q6S285;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD45 antigen isoform 1 (EC 3.1.3.48) (Fragment).
GN Name=CD45;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Schmitzlein W.M., Zuckermann F.A.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY444866; AAR16430.1; -.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PSS0853; FN3; 2.
KM Hydrolase.
FT NON_TER
SQ SEQUENCE 583 AA; 63951 MW; 52FPA170EF0283E CRC64;

Query Match 100.0%; Score 49; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KILAFGFAFL 10
DB 6 KILAFGFAFL 15

RESULT 14
Q6PUK7 PRELIMINARY; PRT; 756 AA.
ID Q6PUK7;
AC Q6PUK7;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE PPRC protein (Fragment).
 GN Name=PPRC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RX [1]
 SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Vallaloon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzyzanski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC014239; AAI14239.1; -.
 DR HSP; P18031; IMAK.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR002424; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PSS0853; FN3; 2.
 DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 1.
 DR NON TER 756 756
 FT SEQUENCE 756 AA; 85430 MW; 8A9A863827BD69E6 CRC64;
 SQ
 Query Match 100.0%; Score 49; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAPL 10
 Db 6 KLLAFGFAPL 15

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 NX NCBI_TaxID=57176;
 RX [1]
 SEQUENCE FROM N.A.
 RC PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human";
 RT Tissue Antigens 64:165-172(2004).
 DR EMBL; AY445818; AAS06903.1; -.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003595; PTPC motif.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC motif; 2.
 DR PROSITE; PSS0853; FN3; 2.
 DR PROSITE; PSS0383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrolase.
 SQ SEQUENCE 1290 AA; 145616 MW; 99E810C75D932824 CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 1290;
 Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLLAFGFAPL 10
 Db 8 KLLAFGFAPL 17

RESULT 16
 Q6ED61 PRELIMINARY; PRT; 1303 AA.
 AC Q6ED61;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CD45.
 OS Aotus nancymae (Mae's night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 NX NCBI_TaxID=57293;
 RX [1]
 SEQUENCE FROM N.A.
 RC PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 vs. human";
 RT Tissue Antigens 64:165-172(2004).
 DR EMBL; AY445817; AAS06902.1; -.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003595; PTPC motif.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR002424; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR SMART; SM00404; PTPC motif; 2.

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DR PROSITE: PS50853; FN3; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolaase.
SQ SEQUENCE 1303 AA; 146929 MW; DOBBOC640D1D17B8 CRC64;
RN
Query Match 100.0%; Score 49; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLLAFGFAPFL 10
DB 8 KLLAFGFAPFL 17

RESULT 17
Q6ED62 PRELIMINARY; PRT; 1303 AA.
AC Q6ED62;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE CD45.
OS Aotus nigricolor (Black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57115;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.B., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
RT vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL; A445816; AAS06901.1; -
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003595; PTPc motif.
DR InterPro: IPR00387; TYR_phosphatase.
DR InterPro: IPR00242; Tyr_PP.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; RTYPHPTTAS.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPc; 2.
DR SMART; SM00404; PTPc motif; 2.
DR PROSITE: PS50853; FN3; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolaase.
SQ SEQUENCE 1303 AA; 146586 MW; 9BB023EBF4BC165 CRC64;
RN
Query Match 100.0%; Score 49; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLLAFGFAPFL 10
DB 8 KLLAFGFAPFL 17

RESULT 18
CD45_HUMAN STANDARD; PRT; 1304 AA.
AC P08575; O16614; Q9H0Y6;
DT 01-APR-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)

```

```

DE (T200).
GN Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (human); Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RX MEDLINE=88061067; PubMed=2824653;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different
RT mRNAs encoding human leukocyte common antigens.";
RL J. Exp. Med. 166:1548-1566(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RX MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common
RT antigen).";
RL EMBO J. 6:1251-1257(1987).
RN [3]
RP SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89009812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
RT antigen (CD45) gene.";
RL J. Immunol. 141:2781-2787(1988).
RN [4]
RP FUNCTION.
RX MEDLINE=89017162; PubMed=2845400;
RA Chabouneau H., Tonke N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
RT protein tyrosine phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
RN [5]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
RT domains of the receptor-linked protein tyrosine phosphatases LCA and
RT LAR.";
RL EMBO J. 9:2399-2407(1990).
RN [6]
RP FUNCTION. Required for T-cell activation through the antigen
RP receptor. The first PTPase domain has enzymatic activity, while
RP the second one seems to affect the substrate specificity of the
RP first one.
RN [7]
RP CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
RP tyrosine + phosphate.
RN [8]
RP SUBUNIT: Binds GANAB and PRKSH (By similarity).
RN [9]
RP SUBCELLULAR LOCATION: Type I membrane protein.
RN [10]
RP ALTERNATIVE PRODUCTS:
RN Event=Alternative splicing; Named isoforms=2;
RN Comment=At least 8 isoforms are produced;
RN Name=1;
RN IsoId=P08575-1; Sequence=Displayed;
RN Name=2;
RN IsoId=P08575-2; Sequence=VSP_007780;
RN [11]
RP PTM: Heavily N- and O-glycosylated.
RN [12]
RP SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
RN [13]
RP Receptor class 1/6 subfamily.
RN [14]
RP SIMILARITY: Contains 2 fibronectin type III domains.
RN [15]
RP SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
RN [16]
RP DATABASE: NAME=PRO; NOTE=CD guide CD45 entry;
RN WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd45.htm".
RN [17]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
RP between the Swiss Institute of Bioinformatics and the EMBL outstation -
RP the European Bioinformatics Institute. There are no restrictions on its
RP use by non-profit institutions as long as its content is in no way
RP modified and this statement is not removed. Usage by and for commercial
RP entities requires a license agreement (See http://www.isb.ch/announce/

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or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; Y00638; CA68669.1; -
 DR EMBL; Y00662; CA68669.1; -
 DR EMBL; M23492; AAD15273.2; -
 DR EMBL; M23496; AAD15273.2; JOINED.
 DR EMBL; M23466; AAD15273.2; JOINED.
 DR EMBL; M23467; AAD15273.2; JOINED.
 DR EMBL; M23468; AAD15273.2; JOINED.
 DR EMBL; M23469; AAD15273.2; JOINED.
 DR EMBL; M23470; AAD15273.2; JOINED.
 DR EMBL; M23471; AAD15273.2; JOINED.
 DR EMBL; M23472; AAD15273.2; JOINED.
 DR EMBL; M23473; AAD15273.2; JOINED.
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 DR EMBL; M23475; AAD15273.2; JOINED.
 DR EMBL; M23476; AAD15273.2; JOINED.
 DR EMBL; M23477; AAD15273.2; JOINED.
 DR EMBL; M23478; AAD15273.2; JOINED.
 DR EMBL; M23479; AAD15273.2; JOINED.
 DR EMBL; M23480; AAD15273.2; JOINED.
 DR EMBL; M23481; AAD15273.2; JOINED.
 DR EMBL; M23482; AAD15273.2; JOINED.
 DR EMBL; M23483; AAD15273.2; JOINED.
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 DR EMBL; M23489; AAD15273.2; JOINED.
 DR EMBL; M23490; AAD15273.2; JOINED.
 DR EMBL; M23491; AAD15273.2; JOINED.
 DR PIR; A46546; A46546.
 DR HSSP; P18031; IC88.
 DR Intact; P08575; -
 DR GlycoSuiteDB; P08575; -
 DR Genew; HGNC:9666; PTPRC.
 DR MIM; 151460; -
 DR GO; GO:0005687; C:Integral to plasma membrane; TAS.
 DR GO; GO:0005001; F:Transmembrane receptor protein tyrosine pho. .; TAS.
 DR GO; GO:0007166; P:Cell surface receptor linked signal transdu. .; TAS.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PP; 2.
 DR Alternative splicing; Antigen; Glycoprotein; Hydrolase;
 KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 Transmembrane.
 FT STGNAL 1 23
 FT CHAIN 24 1304
 FT DOMAIN 24 575
 FT TRANSMEM 576 597
 FT DOMAIN 598 1304
 FT DOMAIN 390 478
 FT DOMAIN 482 570
 FT DOMAIN 670 919
 FT DOMAIN 961 1235
 FT ACT_SITE 851 851
 FT ACT_SITE 1167 1167
 FT CARBOHYD 78 78
 FT CARBOHYD 90 90
 FT CARBOHYD 95 95
 FT CARBOHYD 184 184
 FT CARBOHYD 190 190
 FT CARBOHYD 197 197

FT CARBOHYD 232 232 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 260 260 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 270 270 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 276 276 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 335 335 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 378 378 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 419 419 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 468 468 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 488 488 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 529 529 N-linked (GlcNAc. .) (Potential).
 FT VARSPLIC 32 192 Missing (in isoform 2).
 FT NOTAGEN 851 851 /Frid-VSP 007780.
 FT CONFLICT 650 650 C->S: Loss of activity.
 FT CONFLICT 1207 1207 L -> P (in Ref. 1).
 FT CONFLICT 1207 1207 P -> L (in Ref. 1).
 SQ SEQUENCE 1304 AA; 147253 MW; A08FC2D069BAF7 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. NO. 2.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLIAFGFAPL 10
 |||||
 Db 6 KLIAFGFAPL 15

Search completed: May 3, 2005, 07:40:56
 Job time : 64.1579 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 7.43243 Seconds
(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-16

Perfect score: 61

Sequence: 1 YQYQYTNMSV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	1304	1 A46546	leukocyte common a
2	48	78.7	1301	1 A41622	protein-tyrosine-p
3	43	70.5	450	2 B40183	outer membrane pro
4	43	70.5	455	2 A40183	outer membrane pro
5	43	70.5	459	2 P64065	outer membrane pro
6	43	70.5	459	2 A28787	outer membrane pro
7	43	70.5	646	2 H95155	polyl oligopeptid
8	43	70.5	646	2 C98022	oligopeptidase B
9	41	67.2	550	1 A40449	protein-tyrosine-p
10	41	67.2	1237	2 A54080	protein-tyrosine-p
11	40	65.6	129	2 H83712	hypothetical prote
12	40	65.6	607	2 S19585	serotonin transpor
13	40	65.6	630	2 S30604	neurotransmitter t
14	39	63.9	382	1 S48748	protein-tyrosine-p
15	39	63.9	411	1 SYBYCS	carbamoyl-phosphat
16	39	63.9	412	2 G82406	long-chain fatty a
17	39	63.9	750	2 S67100	protein-tyrosine-p
18	39	63.9	773	2 JH0609	protein-tyrosine-p
19	39	63.9	775	2 S53345	protein-tyrosine-p
20	39	63.9	780	1 UC1368	protein-tyrosine-p
21	39	63.9	2559	2 T30850	fat facets protein
22	38	62.3	123	2 T19123	hypothetical protei
23	38	62.3	311	1 LNHU2A	asialoglycoprotein
24	38	62.3	377	1 A48711	protein-tyrosine-p
25	38	62.3	802	1 B44390	protein-tyrosine-p
26	38	62.3	1273	1 TDR1UT	leukocyte common a
27	38	62.3	1291	1 A28334	protein-tyrosine-p
28	38	62.3	1409	2 T42522	protein-tyrosine-p
29	38	62.3	1422	2 T30111	hypothetical prote

30	37	60.7	48	2 T11313	ATP synthase chain
31	37	60.7	552	2 C83965	transposase (12) B
32	37	60.7	588	2 B56336	retinoid element PA
33	37	60.7	630	2 A47398	serotonin transpor
34	37	60.7	1502	2 S53602	carbamoyl-phosphat
35	36.5	59.8	578	2 B64012	hypothetical prote
36	36	59.0	115	2 S01281	hypothetical prote
37	36	59.0	139	2 T34244	hypothetical prote
38	36	59.0	252	2 T46661	beta 1,4 glucosylt
39	36	59.0	252	2 B81053	beta-1,4-glucosylt
40	36	59.0	254	2 D81824	reaction center pr
41	36	59.0	274	2 A25102	hypothetical prote
42	36	59.0	374	2 T29154	hypothetical prote
43	36	59.0	437	2 T15241	hypothetical prote
44	36	59.0	449	2 E91068	hypothetical prote
45	36	59.0	449	2 F85912	hypothetical prote

ALIGNMENTS

RESULT 1

A46546
leukocyte common antigen long splice form precursor - human
N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 09-Jul-2004
C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Salto, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs enco
A/Reference number: A46546; MUID:88061067; PMID:2824653
A/Accession: A46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1304 <STR>
A/Cross-references: UNIPROT:P08575; GB:Y00638
A/Experimental source: clone LCA.6/2
A/Accession: B46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-332,99-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clone LCA.111 and clone LCA.260
A/Accession: C46546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-31,193-264 <STR>
A/Cross-references: GB:Y00638
A/Experimental source: clones pHLc-1 and lambdaH1c1
A/Accession: A29449
A/Molecule type: mRNA
A/Residues: 1-31,193-649,'L',651-869,'G',871-872,'A',874-1206,'P',1208-1304 <RAI>
A/Cross-references: GB:Y00622; NID:G34275; PIDN:CAA68269.1; PID:G34276
A/Experimental source: clones pHLc-1 and lambdaH1c1
A/Accession: B29449
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 32-192 <RA2>
A/Experimental source: clone HLC-2
R/Tsai, A.Y.; Streuli, M.; Salto, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative ;
A/Reference number: I57658; MUID:90066468; PMID:2531281
A/Accession: I57658
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:g187020; PIDN:AAA59497.1; PID:g553521
C:Genetics:
A:Gene: GDB:PTPRC; CD45
A:Cross-references: GDB:119768; OMIM:151460
A:Map position: 1q31-1q32
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homolog
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 61; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
DB 1116 YQYQYTNMSV 1125

RESULT 2
A41622
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 99A precursor - fruit fly (Dro
N:Alternate names: phosphotyrosine phosphatase 99A
C:Species: Drosophila melanogaster
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A41622; A41214; B41214; B41215
R:Harsharan, I.K.; Chuang, P.T.; Rubin, G.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 11266-11270, 1991
A>Title: Cloning and characterization of a receptor-class phosphotyrosine phosphatase ge
A:Reference number: A41622; MUID:92107920; PMID:1662390
A:Accession: A41622
A:Molecule type: mRNA
A:Residues: 1-1301 <HAR>
A:Cross-references: UNIPROT:P35832; GB:M81795; NID:g157293; PIDN:AAA28483.1; PID:g157294
R:Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, W.
Cell 67, 661-673, 1991
A>Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sube
A:Reference number: A41214; MUID:92034988; PMID:1657401
A:Accession: A41214
A:Molecule type: mRNA
A:Residues: 1-585, 'R', 587-1049, 1120-1204, 'H', 1206-1301 <YAN>
A:Cross-references: GB:M80464; NID:g157299; PIDN:AAA28486.1; PID:g1572300
A:Accession: B41214
A:Molecule type: mRNA
A:Residues: 1-585, 'R', 587-1049, 1290-1301 <YAN>
A:Cross-references: GB:M80464
R:Tian, S.S.; Tsoulfas, P.; Zinn, K.
Cell 67, 675-685, 1991
A>Title: Three receptor-linked protein-tyrosine phosphatases are selectively expressed c
A:Reference number: A41215; MUID:92034989; PMID:1657402
A:Accession: B41215
A:Molecule type: mRNA
A:Residues: 1-585, 'R', 587-1049, 1120-1184, 'S', 1186-1301 <TIA>
A:Cross-references: GB:M80539
C:Genetics:
A:Gene: FlyBase:Ptg99A
A:Cross-references: FlyBase:Fgn0004369
C:Superfamily: protein-tyrosine-phosphatase, receptor type 99A; fibronectin type III reg
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; trans
F:1-29/Domain: signal sequence #status predicted <SIG>
F:130-1301/Product: protein-tyrosine-phosphatase, receptor type 99A #status predicted <MA
F:130-1049, 1120-1301/Product: protein-tyrosine-phosphatase, receptor type 99A, medium spl
F:130-1049, 1290-1301/Product: protein-tyrosine-phosphatase, receptor type 99A, short spl
F:593-416/Domain: transmembrane #status predicted <TM>
F:502-730/Domain: protein-tyrosine-phosphatase homology <PTP>
F:789-1008/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1059-1091/Region: glutamine-rich
F:682/Active site: Cys (phosphocysteine intermediate) #status predicted
F:688/Binding site: substrate phosphate (Arg) #status predicted

Query Match 78.7%; Score 48; DB 1; Length 1301;

Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQYQYTNW 8
DB 641 YQYQYTNW 648

RESULT 3
B40183
outer membrane protein P1 precursor, subtype 6U - Haemophilus influenzae (strain 8358, c
C:Species: Haemophilus influenzae
C>Date: 28-Oct-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C:Accession: B40183
R:Monson Jr., R.; Grass, S.; Einhorn, M.; Bailey, C.; Newell, C.
Infect. Immun. 57, 3300-3305, 1989
A>Title: Comparative analysis of the structures of the outer membrane protein P1 genes f
A:Reference number: A40183; MUID:90035394; PMID:2572549
A:Accession: B40183
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <MUN>
A:Cross-references: UNIPROT:Q00754; GB:M27683
C:Superfamily: long-chain fatty acid transport protein fadL
C:Keywords: membrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-450/Product: outer membrane protein P1 #status predicted <MAT>

Query Match 70.5%; Score 43; DB 2; Length 450;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQYQYTNMS 9
DB 311 YQYQYTNMS 319

RESULT 4
A40183
outer membrane protein P1 precursor, subtype 3L - Haemophilus influenzae (strain 1613, c
C:Species: Haemophilus influenzae
C>Date: 28-Oct-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C:Accession: A40183
R:Monson Jr., R.; Grass, S.; Einhorn, M.; Bailey, C.; Newell, C.
Infect. Immun. 57, 3300-3305, 1989
A>Title: Comparative analysis of the structures of the outer membrane protein P1 genes f
A:Reference number: A40183; MUID:90035394; PMID:2572549
A:Accession: A40183
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <MUN>
A:Cross-references: UNIPROT:Q00450; GB:M63151; GB:M27682; NID:g148954; PIDN:AAA24991.1;
C:Superfamily: long-chain fatty acid transport protein fadL
C:Keywords: membrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-455/Product: outer membrane protein P1 #status predicted <MAT>

Query Match 70.5%; Score 43; DB 2; Length 455;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQYQYTNMS 9
DB 313 YQYQYTNMS 321

RESULT 5
F64065
outer membrane protein P1 precursor - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: F64065
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.J.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: F64065
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-459 <TIGR>
A:Cross-references: UNIPROT:P43839; GB:U32723; GB:U42023; NID:g1573363; PIDN:AAC22060.1;
C:Superfamily: long-chain fatty acid transport protein fadL
C:Keywords: membrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-459/Product: outer membrane protein P1 #status predicted <MAT>

Query Match 70.5%; Score 43; DB 2; Length 459;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YOXQYTNWS 9
Db 317 YSYKTYHWS 325

RESULT 6
A28787
outer membrane protein P1 precursor - Haemophilus influenzae (type b)
C:Species: Haemophilus influenzae
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A30510; A28787
R:Munson Jr., R.; Grass, S.
Infect. Immun. 56, 2235-2242, 1988
A:Title: Purification, cloning, and sequence of outer membrane protein P1 of Haemophilus
A:Reference number: A30510; MUID:8314258; PMID:2842261
A:Accession: A30510
A:Molecule type: DNA
A:Residues: 1-459 <MUN>
A:Cross-references: UNIPROT:P10641; GB:U03381; NID:g148952; PIDN:AAA24990.1; PID:g148953
C:Superfamily: long-chain fatty acid transport protein fadL
C:Keywords: membrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-459/Product: outer membrane protein P1 #status predicted <MAT>

Query Match 70.5%; Score 43; DB 2; Length 459;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YOXQYTNWS 9
Db 317 YSYKTYHWS 325

RESULT 7
H95155
prolyl oligopeptidase family protein [imported] - Streptococcus pneumoniae (strain TIGR4
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95155
R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Lotfian, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95155
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-646 <KUR>
A:Cross-references: UNIPROT:Q97083; GB:AE005672; PIDN:AAK75441.1; PID:g14972826; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:

A:Gene: SP1343

Query Match 70.5%; Score 43; DB 2; Length 646;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOXQYTNWSV 10
Db 42 YWQFDNWSI 51

RESULT 8
C98022
oligopeptidase B (EC 3.4.21.83) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: C98022
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McHenry, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: C98022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-646 <KUR>
A:Cross-references: UNIPROT:Q8CWO8; GB:AE007317; PIDN:AAL00008.1; PID:g15458838; GSPDB:G
A:Genetics: p18B
C:Keywords: hydrolase; serine proteinase

Query Match 70.5%; Score 43; DB 2; Length 646;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOXQYTNWSV 10
Db 42 YWQFDNWSI 51

RESULT 9
A40449
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PYPL - fission yeast (Schl.
C:Species: Schizosaccharomyces pombe
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A40449; T38410
R:Ottillie, S.; Chernoff, J.; Hannig, G.; Hoffman, C.S.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 88, 3455-3459, 1991
A:Title: A fission-yeast gene encoding a protein with features of protein-tyrosine-phos
A:Reference number: A40449; MUID:91195370; PMID:1849659
A:Accession: A40449
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-550 <ONT>
A:Cross-references: UNIPROT:P27574; GB:M63257; NID:g173441; PIDN:AAA35328.1; PID:g17344
R:Brown, D.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z21792
A:Accession: T38410
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-550 <BRO>
A:Cross-references: EMBL:Z73100; PIDN:CAA97367.1; GSPDB:GN00066; SPDB:SPAC26F1.10C
A:Experimental source: strain 97zh-; cosmid c26F1
C:Genetics: SPAC26F1.10C
A:Map position: 1
C:Superfamily: Schizosaccharomyces protein-tyrosine-phosphatase, nonreceptor type pypl;
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata
F:295-528/Domain: protein-tyrosine-phosphatase homology <PTP>
F:470/Active site: Cys (phosphocysteine intermediate) #status predicted

F;476/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 67.2%; Score 41; DB 1; Length 550;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQYQYTNMS 9

Db 431 HHYQYPNMS 439

RESULT 10

A54080
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken

C/Species: Gallus gallus (chicken)
C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C/Accession: A54080; 150592
R./Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.

J. Biol. Chem. 269, 14056-14063, 1994

A./Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in
A./Reference number: A54080; MUID:94245724; PMID:8188686

A./Accession: A54080
A./Status: preliminary

A./Molecule type: mRNA
A./Residues: 1-1237 <FAN>

A./Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:G510510; PIDD:CAA79972.1; PID:G5105

C./Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C./Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

F;528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;510-834/Domain: protein-tyrosine-phosphatase homology <PTR>

F;786/Active site: Cys (phosphocysteine intermediate) #status predicted
F;792/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 67.2%; Score 41; DB 2; Length 1237;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQYQYTNMS 9

Db 1051 YQYQYTNMS 1059

RESULT 11

H83712
hypothetical protein BH0504 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: H83712
R./Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000
A./Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A./Reference number: A83650; MUID:20512582; PMID:11058132

A./Accession: H83712
A./Status: preliminary

A./Molecule type: DNA
A./Residues: 1-129 <STO>

A./Cross-references: UNIPROT:Q9KHS5; GB:AP001508; GB:BA000004; NID:G10172890; PIDD:BA042
A./Experimental source: strain C-125

C./Genetics:
A./Gene: BH0504

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 129;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYQYTNMS 9

Db 56 QYQYTNMS 63

Db 56 QYQYTNMS 63

RESULT 12

S19585
serotonin transport protein - rat

C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19585
R./Blahely, R.D.; Berson, H.E.; Fremieu Jr., R.T.; Caron, M.G.; Peek, M.M.; Prince, H.K.;

Nature 354, 66-70, 1991
A./Title: Cloning and expression of a functional serotonin transporter from rat brain.

A./Reference number: S19585; MUID:92049754; PMID:1944572

A./Accession: S19585
A./Status: preliminary

A./Molecule type: mRNA
A./Residues: 1-607 <BLA>

A./Cross-references: UNIPROT:P31652; EMBL:X63253
C./Superfamily: gamma-aminobutyric acid transporter

C./Keywords: transmembrane protein

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 607;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10

Db 543 PQYNYPHMSI 552

RESULT 13

S30604
neurotransmitter transport protein - rat

C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: S30604
R./Mayer, W.; Betz, H.; Schloess, P.

FEBS Lett. 295, 203-206, 1991
A./Title: Isolation of cDNAs encoding a novel member of the neurotransmitter transporter

A./Reference number: S30604; MUID:92111740; PMID:1765155

A./Accession: S30604
A./Status: preliminary

A./Molecule type: mRNA
A./Residues: 1-630 <MAY>

A./Cross-references: UNIPROT:P31652; EMBL:X63995; NID:G56779; PIDD:CAA45401.1; PID:G56780
C./Superfamily: gamma-aminobutyric acid transporter

C./Keywords: transmembrane protein

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 630;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10

Db 566 PQYNYPHMSI 575

RESULT 14

S48748
protein-tyrosine-phosphatase (EC 3.1.3.48), probable nonreceptor type 12 splice form - r

C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: S48748
R./Moriyama, T.; Kawanishi, S.; Inoue, T.; Imai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; N

FEBS Lett. 353, 305-308, 1994
A./Title: cDNA cloning of a cytosolic protein tyrosine phosphatase (RKPT) from rat kidney

A./Reference number: S48748; MUID:95046282; PMID:7957881

A./Accession: S48748
A./Molecule type: mRNA

A./Residues: 1-382 <MOR>
A./Cross-references: UNIPROT:Q63745; GB:D38072; NID:G567262; PIDD:BA07266.1; PID:G699627

C./Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosph
C./Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

F;58-282/Domain: protein-tyrosine-phosphatase homology <PTR>
F;231/Active site: Cys (phosphocysteine intermediate) #status predicted

F;237/Binding site: substrate phosphate (Arg) #status predicted

Query Match

Best Local Similarity 63.9%; Score 39; DB 1; Length 382;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQYQYTNW 8
||:||||

Db 190 YQPHYVNW 197

RESULT 15

SYBYCS

carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) small chain - yeast (S. cerevisiae)

N/Alternate names: carbamoyl-phosphate synthetase (glutamine-hydrolyzing) glutamine chain

C/Species: Saccharomyces cerevisiae

C/Date: 28-Dec-1987 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004

C/Accession: S67207; A21714; S05834; S05898

R/Ciepluch, C.; Janniaux, J.C.; Korde, E.; Poirey, R.; Pujol, A.; Tobiasch, E. submitted to the Protein Sequence Database, July 1996

A/Reference number: S67194

A/Accession: S67207

A/Molecule type: DNA

A/Residues: 1-411 <CZI>

A/Cross-references: UNIPROT:P07258; EMBL:Z75211; NID:G1420668; PIDN:CAA99621.1; PID:G142

R/Experimental source: strain S286C

R/Werner, M.; Feller, A.; Pierard, A.

Eur. J. Biochem. 146, 371-381, 1985

A/Title: Nucleotide sequence of yeast gene CPA1 encoding the small subunit of arginine-phosphatase.

A/Reference number: A21714; MUID:85101411; PMID:3881260

A/Accession: A21714

A/Molecule type: DNA

A/Residues: 1-88,"Y",90-411 <WER>

A/Cross-references: EMBL:X01764

A/Note: the authors translated the codon TAT for residue 89 as His and GGT for residue 2

R/Wynnyja, H.; Lusty, C.J.

J. Biol. Chem. 259, 9790-9798, 1984

A/Title: Sequence of the small subunit of yeast carbamyl phosphate synthetase and identification of the active site

A/Accession: S05834

A/Molecule type: DNA

A/Residues: 1-411 <NYU>

A/Cross-references: EMBL:X02133; NID:G171304; PIDN:AAA34525.1; PID:G171305

C/Genetics:

A/Gene: SGD:CPA1; MIPS:YOR303W

A/Cross-references: SGD:S0005829; MIPS:YOR303W

A/Map position: 15R

C/Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbamoyl-phosphate synthetase (glutamine-hydrolyzing) small chain

C/Keywords: arginine biosynthesis; heterodimer; ligase; pyrimidine nucleotide biosynthesis

F/10-367/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology F/186-367/Domain: trpG homology <TRG>

F/264/Active site: Cys #status predicted

QY 1 YQYQYTNW 9
|||:||||

Db 98 YQYQYSHW 106

Search completed: May 3, 2005, 06:17:31

Job time : 16.4324 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 34.5946 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-16

Perfect score: 61

Sequence: 1 YQYQYTNMSV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	365	2	Q8MJQ2 actus vocif
2	61	100.0	1290	2	Q8MJQ2 actus vocif
3	61	100.0	1303	2	Q8ED61 actus nancy
4	61	100.0	1304	1	CD45_HUMAN
5	57	93.4	1303	2	Q8ED62 actus nancy
6	49	80.3	115	1	PT21_STYPL
7	48	78.7	730	2	Q7OCM4 anopheles g
8	48	78.7	1226	2	Q9VAL3 drosophila
9	48	78.7	1241	2	Q7KRM3 drosophila
10	48	78.7	1297	2	Q8IMK9 drosophila
11	48	78.7	1301	1	PTP9_DROME
12	44	72.1	511	2	Q9GHF8 alectis gla
13	44	72.1	511	2	Q9GHF9 alectis gla
14	44	70.5	115	2	PT18_STYPL
15	43	70.5	115	1	PT19_STYPL
16	43	70.5	115	1	PT22_STYPL
17	43	70.5	115	1	PT23_STYPL
18	43	70.5	115	1	PT24_STYPL
19	43	70.5	116	1	PT20_STYPL
20	43	70.5	427	2	Q48051 haemophilus
21	43	70.5	449	2	Q00754 haemophilus
22	43	70.5	449	2	Q9K2Q4 haemophilus
23	43	70.5	449	2	Q9KHF5 haemophilus
24	43	70.5	449	2	Q9KHF5 haemophilus
25	43	70.5	450	2	Q9KHF3 haemophilus
26	43	70.5	450	2	Q9KHF4 haemophilus
27	43	70.5	451	2	Q9KHF6 haemophilus
28	43	70.5	451	2	Q9KHF7 haemophilus
29	43	70.5	451	2	Q9KHF8 haemophilus
30	43	70.5	451	2	Q9KHG0 haemophilus
31	43	70.5	451	2	Q9KHG2 haemophilus

32	43	70.5	454	2	Q9KHG1 haemophilus
33	43	70.5	455	2	Q00450 haemophilus
34	43	70.5	455	2	Q9KH1 haemophilus
35	43	70.5	455	2	Q9KH2 haemophilus
36	43	70.5	455	2	Q9KH3 haemophilus
37	43	70.5	455	2	Q9KH4 haemophilus
38	43	70.5	455	2	Q9KH5 haemophilus
39	43	70.5	455	2	Q9KH6 haemophilus
40	43	70.5	456	2	Q9KH4 haemophilus
41	43	70.5	456	2	Q9KH5 haemophilus
42	43	70.5	456	2	Q9KH7 haemophilus
43	43	70.5	456	2	Q9KH8 haemophilus
44	43	70.5	456	2	Q9KH9 haemophilus
45	43	70.5	456	2	Q9KH6 haemophilus

ALIGNMENTS

RESULT 1					
Q8MJQ2	PRELIMINARY;	PRT;	365 AA.		
AC Q8MJQ2;					
DT 01-OCT-2002 (TREMBLrel. 22, Created)					
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)					
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)					
DE CD45 phosphatase (Fragment)					
OS Actus vociferans (Spix's owl monkey)					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.					
OX NCBI_Taxid=57176;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;					
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AF364096; AAM48512.1; -					
DR HSSP; P18052; P15.					
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.					
DR GO; GO:0004700; P:protein amino acid dephosphorylation; IEA.					
DR InterPro; IPR000387; TYR_phosphatase.					
DR InterPro; IPR000242; TYR_PP.					
DR Pfam; PFO0102; Y_phosphatase; 1.					
DR PRINTS; PR00700; PRTYHPHTASE.					
DR SMART; SM00194; PRC; 1.					
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.					
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.					
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.					
FT NON TER 1					
FT NON TER 365					
SQ SEQUENCE 365 AA; 41720 MW; BA950C4E56E27902 CRC64;					
Query Match					
Best Local Similarity 100.0%; Score 61; DB 2; Length 365;					
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 YQYQYTNMSV 10					
DB 188 YQYQYTNMSV 197					
RESULT 2					
Q8ED60	PRELIMINARY;	PRT;	1290 AA.		
AC Q8ED60;					
DT 25-OCT-2004 (TREMBLrel. 28, Created)					
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)					
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)					
DE CD45					
OS Actus vociferans (Spix's owl monkey)					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.					
OX NCBI_Taxid=57176;					
RN [1]					

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RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
   vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL: AY445818; AAS06903.1; -.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003595; PTPC motif.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; FN3_2.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHTASE.
DR SMART: SM00060; FN3_2.
DR SMART: SM00194; PTPC motif; 2.
DR SMART: SM00404; PTPC motif; 2.
DR PROSITE: PS0853; FN3_2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolase.
SQ SEQUENCE 1290 AA, 145616 MW, 99EB10C75D932824 CRC64;

Query Match 100.0%; Score 61; DB 2; Length 1290;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVOYXTNMSV 10
   |||||
Db 1102 YVOYXTNMSV 1111

RESULT 3
ID Q6ED61 PRELIMINARY; PRT; 1303 AA.
AC Q6ED61;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD45.
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
   vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL: AY445817; AAS06902.1; -.
DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003595; PTPC motif.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; FN3_2.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHTASE.
DR SMART: SM00060; FN3_2.
DR SMART: SM00194; PTPC motif; 2.
DR SMART: SM00404; PTPC motif; 2.
DR PROSITE: PS0853; FN3_2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

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```

KM Hydrolase.
SQ SEQUENCE 1303 AA, 146929 MW, D0EB0C6400D17E8 CRC64;

Query Match 100.0%; Score 61; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVOYXTNMSV 10
   |||||
Db 1115 YVOYXTNMSV 1124

RESULT 4
ID CD45_HUMAN STANDARD; PRT; 1304 AA.
AC P08575; Q16614; Q9H0Y6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)
   (T200).
DB (T200).
GN Name=PTPRC; Synonyms=CD45;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
RC TISSUE=Lymphocytes;
RX MEDLINE=88061067; PubMed=2824653;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different
   mRNAs encoding human leukocyte common antigens.";
RL J. Exp. Med. 166:1548-1566(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
RX MEDLINE=87275816; PubMed=2956090;
RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
RT "Structural variants of human T200 glycoprotein (leukocyte-common
   antigen).";
RL EMBO J. 6:1251-1257(1987).
RN [3]
RP SEQUENCE OF 191-1304 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=8909812; PubMed=2971730;
RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
RT "Complete exon-intron organization of the human leukocyte common
   antigen (CD45) gene.";
RL J. Immunol. 141:2781-2787(1988).
RN [4]
RP FUNCTION.
RX MEDLINE=89017162; PubMed=2845400;
RA Chaboudneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
   protein tyrosine phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
RN [5]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
   domains of the receptor-linked protein tyrosine phosphatases LCA and
   LAR.";
RL EMBO J. 9:2399-2407(1990).
RN [6]
RP FUNCTION. Required for T-cell activation through the antigen
   receptor. The first PTPase domain has enzymatic activity, while
   the second one seems to affect the substrate specificity of the
   first one.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
   tyrosine + phosphate.
CC -!- SUBUNIT: Binds GANAB and PRKCSH (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:

```

CC Event=Alternative splicing; Named isoforms=2;
CC Comment=At least 8 isoforms are produced;
CC Name=1;
CC IsoId=P08575-1; Sequence=displayed;
CC Name=2;
CC IsoId=P08575-2; Sequence=VSP_007780;
CC -1- PPM: Heavily N- and O-glycosylated.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 1/6 subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD45 entry;
CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".

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CC or send an email to license@isb-sib.ch).

DR EMBL: Y00638; CA68669.1; -;
DR EMBL: Y00062; CA68629.1; -;
DR EMBL: M23492; AAD15273.2; -;
DR EMBL: M23496; AAD15273.2; JOINED.
DR EMBL: M23466; AAD15273.2; JOINED.
DR EMBL: M23467; AAD15273.2; JOINED.
DR EMBL: M23468; AAD15273.2; JOINED.
DR EMBL: M23469; AAD15273.2; JOINED.
DR EMBL: M23470; AAD15273.2; JOINED.
DR EMBL: M23471; AAD15273.2; JOINED.
DR EMBL: M23472; AAD15273.2; JOINED.
DR EMBL: M23473; AAD15273.2; JOINED.
DR EMBL: M23474; AAD15273.2; JOINED.
DR EMBL: M23475; AAD15273.2; JOINED.
DR EMBL: M23476; AAD15273.2; JOINED.
DR EMBL: M23477; AAD15273.2; JOINED.
DR EMBL: M23478; AAD15273.2; JOINED.
DR EMBL: M23479; AAD15273.2; JOINED.
DR EMBL: M23480; AAD15273.2; JOINED.
DR EMBL: M23481; AAD15273.2; JOINED.
DR EMBL: M23482; AAD15273.2; JOINED.
DR EMBL: M23483; AAD15273.2; JOINED.
DR EMBL: M23484; AAD15273.2; JOINED.
DR EMBL: M23485; AAD15273.2; JOINED.
DR EMBL: M23486; AAD15273.2; JOINED.
DR EMBL: M23487; AAD15273.2; JOINED.
DR EMBL: M23488; AAD15273.2; JOINED.
DR EMBL: M23489; AAD15273.2; JOINED.
DR EMBL: M23490; AAD15273.2; JOINED.
DR EMBL: M23491; AAD15273.2; JOINED.
DR PIR: A46546; A46546.
DR HSSP: P18031; 1C88.
DR Inactive; P08575; -;
DR Glycosylated; P08575; -;
DR Gene; HGNC:9666; PTPRC.
DR MIM; 151460; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000387; Tyr_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PROSITE; PSS0853; FN3; 2.
DR PROSITE; PSS0083; Tyr_PHOSPHATASE_1; 2.
DR PROSITE; PSS0056; Tyr_PHOSPHATASE_2; 2.
DR PROSITE; PSS0055; Tyr_PHOSPHATASE_PP; 2.
KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;

KM Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
KM Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 1304
FT DOMAIN 24 575
FT TRANSMEM 576 597
FT DOMAIN 598 1304
FT DOMAIN 390 478
FT DOMAIN 482 570
FT DOMAIN 670 919
FT DOMAIN 961 1235
FT ACT_SITE 851 851
FT ACT_SITE 1167 1167
FT CARBOHYD 78 78
FT CARBOHYD 90 90
FT CARBOHYD 95 95
FT CARBOHYD 184 184
FT CARBOHYD 190 190
FT CARBOHYD 197 197
FT CARBOHYD 232 232
FT CARBOHYD 260 260
FT CARBOHYD 270 270
FT CARBOHYD 276 276
FT CARBOHYD 335 335
FT CARBOHYD 378 378
FT CARBOHYD 419 419
FT CARBOHYD 468 468
FT CARBOHYD 488 488
FT CARBOHYD 529 529
FT VARSPPLIC 32 192
FT MUTAGEN 851 851
FT CONFLICT 650 650
FT CONFLICT 1207 1207
SQ SEQUENCE 1304 AA; 147253 MW; A08FC2D6069BAF7 CRC64;
Query Match 100.0%; Score 61; DB 1; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQYQYTNMSV 10
Db 1116 YQYQYTNMSV 1125

RESULT 5
ID 06ED62 PRELIMINARY; PRT; 1303 AA.
AC 06ED62;
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE CD45.
OS Aotus nigriceps (Black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15245371;
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RT "Comparative analysis of CD45 protein in primate context: owl monkeys
RT vs. human.";
RL Tissue Antigens 64:165-172(2004).
DR EMBL; AY445816; AAS06901.1; -;
DR GO; GO:004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003959; PTPC motif.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.

```

DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTRYPHPTASE.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00194; PTPc; 2.
DR SMART: SM00404; PTPc_motif; 2.
DR PROSITE: PS00853; FN3; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
SO SEQUENCE. 1303 AA; 146586 MW; 98B023BBF4EC1165 CRC64;

Query Match
Best Local Similarity 93.4%; Score 57; DB 2; Length 1303;
Matches 9; Conservative 100.0%; Pred. No. 1.3;
Mismatches 0; Indels 0; Gaps 0,

OY 1 YOXOYTNW 9
|||
1115 YOXOYTNW 1123

Db 1115 YOXOYTNW 1123

RESULT 6
PT21_PTYPL STANDARD; PRT; 115 AA.
ID PT21_PTYPL
AC P28213;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase 21 (EC 3.1.3.48) (Fragment).
GN Name=STY 21;
OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Styelidae; Styela.
-0X NCBI_TaxID=7726;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139172; PubMed=1704870;
RA Matthews R.J., Flores E., Thomas M.L.;
RT "Protein tyrosine phosphatase domains from the protochordate Styela
RL plicata.";
CC Immunogenetics 33:33-41(1991).
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -----
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CC -----
CC EMBL: M38006; AAA29839.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; PARTIAL.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; PARTIAL.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Protein phosphatase.
FT NON_TER 1
FT NON_TER 1
SO SEQUENCE 115 AA; 13489 MW; D7B0818BCC8613B5 CRC64;

Query Match
Best Local Similarity 80.3%; Score 49; DB 1; Length 115;
Matches 7; Conservative 87.5%; Pred. No. 2.3;
Mismatches 1; Indels 0; Gaps 0,
OY 1 YOXOYTNW 8
|||||
74 YOXOYTNW 81

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ID	Q7OCW4	PRELIMINARY;	PRT;	730 AA.
DT	01-MAR-2004 (TREMBLrel. 26, Created)			
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	AGCP1784 (Fragment).			
DN	Name=agCG51869; ORFNames=ENSANGG0000013695;			
OS	Anopheles gambiae str. PEST.			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.			
OK	NCBI_TaxID=180454;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PEST;			
RA	Anopheles Genome Sequencing Consortium;			
RL	Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.			
CC	-1- CAUTION: The sequence shown here is derived from an			
CC	EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is			
CC	preliminary data.			
DR	EMBL; AAAH01008659; EAA07762.1; -.			
DR	HSSP; p18052; 1p15.			
DR	GO; GO:0016787; F:hydrolase activity; IEA.			
DR	GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.			
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.			
DR	InterPro; IPR000387; Tyr phosphatase.			
DR	InterPro; IPR000242; Tyr Pp.			
DR	Pfam; PF00102; Y.phosphatase; 2.			
DR	PRINTS; PR00700; PRYPHPTASE			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.			
KW	Hydrolase.			
FT	NON TER	1	1	
FT	NON TER	730	730	
SQ	SEQUENCE	730 AA;	82134 MW;	18AF5A1371A1A9C CRC64;
QY	1 YQYQTNM 8			
DB	226 YQYHTNM 233			
RESULT 8				
Q9VAL3	PRELIMINARY;	PRT;	1226 AA.	
ID	Q9VAL3			
AC	Q9VAL3			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	CG2005-PA.			
CN	Name=Pyg99A; ORFNames=CG2005;			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
CC	Ephyrdoidea; Drosophilidae; Drosophila.			
OK	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,			
RA	Abtli J.F., Agbayani A., An H.-J., Andrews-Plamkoch C., Baldwin D.,			

RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegam C.,
 RA Jatalai M., Kalush F., Kaepfen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodagel, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195 (2000).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frisze E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gbbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence,"
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frisze E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective,"
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Maira S., Crosby M.A., Mungall C.J., Matthews B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Battecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review,"
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003769; AAP56891.3; -
 DR HSSP; P18052; 1YFO.
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 DR GO; GO:0007415; P:deafferentiation of motor neuron; IGI.
 DR GO; GO:0008045; P:motor axon guidance; IGI.
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 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR001005; MyD_DNA_binding.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PRTYPHTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolyase.
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 Best Local Similarity 87.5%; Pred. No. 34;
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 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Abmayyan A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegam C.,
 RA Jatalai M., Kalush F., Kaepfen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleib J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheller F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
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RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleib J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirekas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirekas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochick S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG Playbase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
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RG Playbase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR HSSP; P18031; IKAV.
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DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
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DR InterPro; IPR008957; FN_III-like
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DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR SMART; SM00060; FN3; 2.
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DR SMART; SM00404; PTPC_motif; 2.

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DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolase.
SQ SEQUENCE 1241 AA; 138694 MW; 901457A63DE30797 CRC64;
Query Match 78.7%; Score 48; DB 2; Length 1241;
Best Local Similarity 87.5%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YQYQXTNW 8
DB 656 YQYHTNW 663
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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG2005-PB.
GN Name=Pp99A; ORFNames=CG2005;
OS *Drosophila melanogaster* (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abriil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cheriy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mewklow G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleib J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheller F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]

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 RA Ceiniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Fritse E., Hodgson A.,
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 RA Pacלב J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
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 RA Weinrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
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 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Fritse E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceiniker S.E.;
 RT "the transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Beriman B.P.,
 RA Bettencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
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 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN HSSP; P18052; 1YFO.
 DR HSSP: FBgn0004369; Ptp99A.
 DR GO; GO:0007415; P:decalculation of motor neuron; IGI.
 DR GO; GO:0008045; P:motor axon guidance; IGI.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR001005; MYD DNA binding.
 DR InterPro; IPR000387; TYR phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00041; FN3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PTPYPHPTASE.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PSS0853; FN3; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrolase.
 SO SEQUENCE 1297 AA, 145061 MW, 68020754CMA0A5602 CRC64;

Query Match 78.7%; Score 48; DB 2; Length 1297;
 Best Local Similarity 87.5%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQYQYTNW 8
 DB 641 YQYHTNM 648

RESULT 11
 ID PTP9_DROME STANDARD; PRT; 1301 AA.
 AC P35832;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein-tyrosine phosphatase 99A precursor (EC 3.1.3.48) (Receptor-
 DE linked protein-tyrosine phosphatase 99A).
 OS Name=Ptp99A;
 GN Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
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 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC TISSUE=Eye imaginal disk;
 RX MEDLINE=92107930; PubMed=1662390;
 RA Hartharan I.K., Chuang P.-T., Rubin G.M.;
 RT "Cloning and characterization of a receptor-class phosphotyrosine
 RT phosphatase gene expressed on central nervous system axons in
 RT Drosophila melanogaster.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11266-11270(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RC TISSUE=Embryo;
 RX MEDLINE=92034989; PubMed=1657402; DOI=10.1016/0092-8674(91)90063-5;
 RA Tian S.-S., Tsoulfas P., Zinn K.;
 RT "Three receptor-linked protein-tyrosine phosphatases are selectively
 RT expressed on central nervous system axons in the Drosophila embryo.";
 RL Cell 67:675-685(1991).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Embryo;
 RX MEDLINE=92034988; PubMed=1657401; DOI=10.1016/0092-8674(91)90062-4;
 RA Yang X., Seow K.T., Bahri S.M., Oon S.H., Chia W.;
 RT "Two Drosophila receptor-like tyrosine phosphatase genes are expressed
 RT in a subset of developing axons and pioneer neurons in the embryonic
 RT CNS.";
 RL Cell 67:661-673(1991).
 CC -1- FUNCTION: May play a key role in signal transduction and growth
 CC control.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=Long;
 CC IsoId=P35832-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P35832-2; Sequence=VSP_005142;
 CC -1- TISSUE SPECIFICITY: Selectively expressed in a subset of axons and
 CC pioneer neurons in the embryo.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class subfamily.
 CC -1- SIMILARITY: Contains 3 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M81795; AAA28483.1; -
 DR EMBL; M80539; AAA28485.1; -
 DR EMBL; M80464; AAA28486.1; -
 DR PIR; A41622; A41622.
 DR HSSP; P18052; 1YFO.
 DR FlyBase; FBgn0004369; Ptp99A.


```

DR GO:0007415; P: defasciculation of motor neuron; IGI.
DR GO:0008045; P: motor axon guidance; IGI.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRYHPHTASE.
DR SMART: SM00060; FNC; 2.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00853; FNC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00055; TYR_PHOSPHATASE_2; 1.
DR Alternative splicing; Hydrolase; Protein phosphatase; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 1301 Protein-tyrosine phosphatase 99A.
FT DOMAIN 30 394 Extracellular (Potential).
FT TRANSMEM 395 415 Potential.
FT DOMAIN 416 1301 Cytoplasmic (Potential).
FT DOMAIN 168 168 Fibronectin type-III 1.
FT DOMAIN 169 268 Fibronectin type-III 2.
FT DOMAIN 269 368 Fibronectin type-III 3.
FT DOMAIN 497 747 Protein-tyrosine phosphatase 1.
FT DOMAIN 748 975 Protein-tyrosine phosphatase 2.
FT ACT_SITE 682 682 Phosphocysteine intermediate (By similarity).
FT DOMAIN 1076 1091 Poly-Gln.
FT CARBOHYD 33 33 N-linked (GLCNAC:...) (Potential).
FT CARBOHYD 176 176 N-linked (GLCNAC:...) (Potential).
FT CARBOHYD 212 212 N-linked (GLCNAC:...) (Potential).
FT CARBOHYD 278 278 N-linked (GLCNAC:...) (Potential).
FT CARBOHYD 322 322 N-linked (GLCNAC:...) (Potential).
FT CARBOHYD 336 336 N-linked (GLCNAC:...) (Potential).
FT VARSPLIC 1050 1119 Missing (in isoform Short).
FT FT P->R (in Ref. 2 and 3).
FT CONFLICT 586 586 N->H (in Ref. 3).
FT CONFLICT 1205 1205 N->H (in Ref. 3).
FT SEQUENCE 1301 AA; 14536 MW; 824133E19A4CA5BD CRC64;

Query Match      78.7%; Score 48; DB 1; Length 1301;
Best Local Similarity 87.5%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQYQYTNW 8
Db 641 YQYHYNW 648

RESULT 12
Q9GHP8 PRELIMINARY; PRT; 511 AA.
AC Q9GHP8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Maturease.
GN Name=matk;
OS Alettris glabra.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Nartheciaceae;
OC Alettris.
NCBI_TaxID=119988;
OX NCBI_TaxID=119988;
RN [1]
RP SEQUENCE FROM N.A.
RA Fuse S., Tamura M.N.;
RT "A phylogenetic analysis of the plastid matk gene with emphasis on
RT Melanthiaceae sensu lato."
RL Plant Biol. 2:415-427(2000).
DR EMBL; AB040165; BAB16773.1; -.

```

```

DR GO:0009507; C: chloroplast; IEA.
DR GO:0008380; P: RNA splicing; IEA.
DR InterPro: IPR008998; Agglutinin.
DR InterPro: IPR00442; Intron_mature2.
DR InterPro: IPR002866; MatK_N.
DR Pfam: PF01348; Intron_mature2; 1.
DR Pfam: PF01824; MatK_N; 1.
DR Chloroplast.
KW SEQUENCE 511 AA; 60962 MW; 8582DFB4932B2977 CRC64;

Query Match      72.1%; Score 44; DB 2; Length 511;
Best Local Similarity 55.6%; Pred. No. 62;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNW 9
Db 186 YERYSNW 194

RESULT 13
Q9GHP9 PRELIMINARY; PRT; 511 AA.
AC Q9GHP9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Maturease.
GN Name=matk;
OS Alettris glabra.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Nartheciaceae;
OC Alettris.
NCBI_TaxID=119988;
RN [1]
RP SEQUENCE FROM N.A.
RA Fuse S., Tamura M.N.;
RT "A phylogenetic analysis of the plastid matk gene with emphasis on
RT Melanthiaceae sensu lato."
RL Plant Biol. 2:415-427(2000).
DR EMBL; AB040164; BAB16772.1; -.
DR GO:0009507; C: chloroplast; IEA.
DR GO:0008380; P: RNA splicing; IEA.
DR InterPro: IPR008998; Agglutinin.
DR InterPro: IPR00442; Intron_mature2.
DR InterPro: IPR002866; MatK_N.
DR Pfam: PF01348; Intron_mature2; 1.
DR Pfam: PF01824; MatK_N; 1.
DR Chloroplast.
KW SEQUENCE 511 AA; 60992 MW; 9EC8A6FE80357544 CRC64;

Query Match      72.1%; Score 44; DB 2; Length 511;
Best Local Similarity 55.6%; Pred. No. 62;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNW 9
Db 186 YERYSNW 194

RESULT 14
PT18 STYPL STANDARD; PRT; 115 AA.
AC PT18 STYPL;
DT 01-DEC-1992 (rel. 24, Created)
DT 01-DEC-1992 (rel. 24, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (Fragment).
GN Name=STY 18;
OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7726;

```



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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139172; PubMed=1704870;
RA Matthews R.J., Flores E., Thomas M.L.;
RT "Protein tyrosine phosphatase domains from the protochordate Styela
   plicata.";
RL Immunogenetics 33:33-41(1991).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
   tyrosine + phosphate.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M38003; AAA29836.1; -.
DR HSSP; Q06124; 2SHP.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; PARTIAL.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KM Hydrolyase; Protein phosphatase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 115 AA; 13577 MW; 727E14A73667A001 CRC64;

Query Match 70.5%; Score 43; DB 1; Length 115;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQYQYTNW 8
   :|||  ||
Db 74 FQYQYTNW 81

RESULT 15
PT19_STYPL STANDARD; PRT; 115 AA.
AC P28211;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase 19 (EC 3.1.3.48) (Fragment).
GN Name=STY 19;
OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7726;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139172; PubMed=1704870;
RA Matthews R.J., Flores E., Thomas M.L.;
RT "Protein tyrosine phosphatase domains from the protochordate Styela
   plicata.";
RL Immunogenetics 33:33-41(1991).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
   tyrosine + phosphate.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M38004; AAA29837.1; -.
DR HSSP; P18031; 1C88.

```

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DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; PARTIAL.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KM Hydrolyase; Protein phosphatase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 115 AA; 13602 MW; 84E18CBFC139123 CRC64;

Query Match 70.5%; Score 43; DB 1; Length 115;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQYQYTNW 8
   :|||  ||
Db 74 FQYQYTNW 81

Search completed: May 3, 2005, 06:02:12
Job time : 45.5946 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 06:50:33 ; Search time 46.3158 Seconds
(without alignments)
83.505 Million cell updates/sec

Title: US-10-003-983C-16

Perfect score: 61

Sequence: 1 YQYQYTNMSV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	10	5	ABG31986 Human CD4
2	61	100.0	260	8	ADJ92685 Human Leu
3	61	100.0	273	7	ADJ22989 Human pro
4	61	100.0	764	8	ABO84454 Human can
5	61	100.0	960	8	ADQ39377 Human myo
6	61	100.0	1114	6	ABU05246 Human exp
7	61	100.0	1114	6	ABU05239 Human exp
8	61	100.0	1143	6	ABU05240 Human exp
9	61	100.0	1143	6	ABU05245 Human exp
10	61	100.0	1143	7	ADL16232 Human pro
11	61	100.0	1143	8	ADQ18845 Human sof
12	61	100.0	1149	6	AAM41048 Human pol
13	61	100.0	1149	6	ABU05242 Human exp
14	61	100.0	1192	8	ADQ39378 Human kin
15	61	100.0	1219	8	ADQ39378 Human kin
16	61	100.0	1256	8	ADM67187 Human myo
17	61	100.0	1256	8	ADP12966 Human e
18	61	100.0	1258	8	ADQ39376 Human myo
19	61	100.0	1267	8	ADQ39379 Human myo
20	61	100.0	1304	6	ABU05243 Human exp
21	61	100.0	1304	6	ABU05241 Human exp
22	61	100.0	1304	6	ABU05244 Human exp
23	61	100.0	1304	7	ADL16230 Human pro
24	61	100.0	1304	7	ADP65158 Human pro
25	61	100.0	1304	8	ADM67209 Human adi

26	61	100.0	1304	8	ABO84455 Human can
27	61	100.0	1304	8	ADQ39380 Human myo
28	61	100.0	1306	8	ADQ39375 Human myo
29	48	78.7	257	4	AAB59369 Drosophi1
30	48	78.7	313	4	AAG78267 Drosophi1
31	48	78.7	1214	4	ABBS8751 Drosophi1
32	44	72.1	474	6	ADA34437 Acinetoba
33	43	70.5	35	2	AAR40060 H1b OMP P
34	43	70.5	415	7	ABO73646 Pseudomon
35	43	70.5	459	6	ABU30230 Protein e
36	43	70.5	646	6	ABU01782 S. pneumo
37	43	70.5	646	6	ABP81411 Streptoco
38	43	70.5	646	6	ADM92180 S pneumon
39	42	68.9	179	8	ADO57594 Actinobac
40	42	68.9	443	6	ABU39250 Protein e
41	41	67.2	254	4	AAB59386 Yeast pro
42	41	67.2	312	4	AAG78284 Fission y
43	41	67.2	760	2	AAY28884 Drosophi1
44	41	67.2	760	4	ABB64881 Drosophi1
45	41	67.2	760	6	ABR61842 Drosophi1

ALIGNMENTS

RESULT 1	ABG31986	standard, peptide, 10 AA.
ID	ABG31986	
XX	AC	ABG31986;
XX	XX	
DT	05-NOV-2002	(first entry)
XX	XX	
DE	Human CD45 HLA-binding peptide, huCD45/1116.	
XX	XX	
XX	Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;	
KW	antigen-presenting cell; APC; major histocompatibility complex; MHC;	
KW	antigen; allogenic; T cell receptor; TCR; cancer; tumour;	
KW	allogenic stem cell transplantation; CFU-GM; leukaemia;	
KW	colony forming unit-granulocyte macrophage; immunotherapeutic;	
KW	haematopoietic; malignant.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	PN	WO200244207-A1.
PD	PD	06-JUN-2002.
XX	XX	
PF	30-NOV-2000;	2000WO-GB004566.
XX	XX	
PR	30-NOV-2000;	2000WO-GB004566.
XX	XX	
PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.	
XX	XX	
PI	Stauss HJ, Amrolia PJ;	
DR	WPI, 2002-599413/64.	
XX	XX	
PT	Novel peptide comprising leukocyte antigen binding peptide of human CD45	
PT	polypeptide, useful for producing activated cytotoxic T lymphocytes, for	
PT	killing cancerous cells e.g. leukemia.	
PS	Claim 2, Page 38; 56pp; English.	
XX	XX	
CC	The invention discloses a peptide comprising the human leukocyte antigen	
CC	(HLA)-binding peptide of human CD45 polypeptide, its portion or variant,	
CC	provided that the peptide is not the intact human CD45 polypeptide. The	
CC	peptides are useful for producing activated cytotoxic T lymphocyte (CTL)	
CC	in vitro which involves contracting the CTL with an antigen-presenting	
CC	cell, where its major histocompatibility complex (MHC) class I molecules	
CC	are loaded with the peptide, to activate, in an antigen specific manner,	
CC	where the CTL and the antigen presenting cell are allogenic with respect	
CC	to the class I MHC molecule that is presenting peptides of CD45. The	

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animals models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, hucd45/1116,
CC comprising an HLA-binding peptide of human CD45
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 61; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
1 YQYQYTNMSV 10

RESULT 2
ADD292685
ID ADJ92685 standard; protein; 260 AA.
XX
AC ADJ92685;

DT 06-MAY-2004 (first entry)

XX Human leukocyte common antigen (LCA) phosphatase domain (PD) 2.

XX Receptor-type protein tyrosine phosphatase; RPTP;
KW phosphotyrosine phosphatase; cancer; diabetes; human;
KW leukocyte common antigen; LCA; phosphatase domain; PD.

OS Homo sapiens.

XX US6682905-B1.

PN 27-JAN-2004.

PD 29-MAR-1999; 99US-00280597.

XX 11-JUL-1990; 90US-00551270.

PR 26-FEB-1991; 91US-00654188.

PR 10-FEB-1993; 93US-00015985.

PR 23-MAY-1995; 95US-00448288.

XX (UYNV) UNIV NEW YORK STATE.

XX Schlessinger J, Sap JM;

XX MPI; 2004-118574/12.

PT Identifying a compound that modulates the phosphotyrosine phosphatase
PT activity of a polypeptide by incubating the compound with the
PT polypeptide, which is in pure form, in a membrane preparation or in a
PT whole cell.

XX Example; SEQ ID NO 10; 52pp; English.

XX The invention relates to receptor-type protein tyrosine phosphatase
CC (RPTP) and its corresponding nucleic acid. The invention also relates to
CC a method for identifying a compound that modulates the phosphotyrosine

CC phosphatase activity. The method is useful for identifying a compound
CC that modulates the phosphotyrosine phosphatase activity of a polypeptide
CC and for identifying susceptibility to cancer, diabetes or other diseases
CC associated with alterations in cellular phosphotyrosine metabolism. The
CC present sequence is human leukocyte common antigen (LCA) phosphatase
CC domain (PD) 2. This sequence is used to illustrate the method of the
CC invention.
XX

SQ Sequence 260 AA;

Query Match 100.0%; Score 61; DB 8; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
151 YQYQYTNMSV 160

RESULT 3
ADD22989

ID ADD22989 standard; protein; 273 AA.

XX ADD22989;

DT 15-JAN-2004 (first entry)

XX Human protein tyrosine phosphatase, CD45-D2.

XX Human; enzyme; protein tyrosine phosphatase; PTPH; cytosolic;
KW gene therapy; retroviral vector; phosphotyrosine; pp60(v-src);
KW breast cancer; leukaemia; CD45-D2.

XX Homo sapiens.

XX US2003113294-A1.

PN 19-JUN-2003.

PD 12-NOV-2002; 2002US-00293231.

XX 14-MAR-1990; 90US-00494036.

PR 01-MAR-1991; 91US-00663579.

PR 16-AUG-1993; 93US-00107420.

PR 04-DEC-1996; 96US-00759536.

PR 22-JAN-1999; 99US-00235251.

PR 03-MAY-2001; 2001US-00848294.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Tonks NK;

XX MPI; 2003-810871/76.

PT New isolated RNA encoding protein tyrosine phosphatase designated as
PT PTPH1 useful for treating malignancies such as breast cancer, leukemia.
PT Disclosure; Fig 4B; 12pp; English.

XX The invention relates to an isolated RNA encoding a protein tyrosine
CC phosphatase designated as PTPH1 appearing as ADD22982. Also included is a
CC retroviral vector comprising the RNA. The RNA is useful for treating or
CC preventing a condition in which abnormally high levels of phosphotyrosine
CC occur in a mammalian cell (which involves introducing into the mammalian
CC cell and agent which comprises DNA or RNA encoding all or a portion of a
CC PTPH1, under conditions sufficient to express PTPH1 where the polypeptide
CC can catalyze dephosphorylation of tyrosyl residues that are
CC phosphorylated through action of a protein tyrosine kinase. The RNA is
CC also useful for reversing a malignant phenotype of a mammalian cell which
CC is associated with tyrosyl phosphorylation catalysed by a protein
CC tyrosine kinase. The DNA or RNA is delivered via a recombinant retrovirus
CC or a recombinant vaccinia virus. At least one tyrosyl residue that is
CC dephosphorylated by the protein tyrosine phosphatase polypeptide can be

CC aberrantly phosphorylated by p60(V-src). The RNA is useful for treating
CC or preventing malignancies such as breast cancer and leukaemia. The
CC present sequence is a PTP similar to PRPH1.
XX
SQ Sequence 273 AA;
Query Match 100.0%; Score 61; DB 7; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YQYQYTNMSV 10
Db 151 YQYQYTNMSV 160
RESULT 4
ABO84454 standard; protein; 764 AA.
XX
AC ABO84454;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP13-011.1.
XX
KM Human; cancer-associated protein; cytostatic; cancer; leukaemia;
XX lymphoma; CAP.
XX
OS Homo sapiens.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
XX
PR 14-MAR-2003; 2003US-00388838.
XX
PR 15-APR-2003; 2003US-00417375.
XX
PR 13-JUN-2003; 2003US-00461862.
XX
PR 15-SEP-2003; 2003US-00663431.
XX
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
DR WPI; 2004-652914/63.
XX
DR N-PSDB; ABO32625.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer;
XX
PS claim 18; seqid 145; 310pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an

CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 764 AA;
Query Match 100.0%; Score 61; DB 8; Length 764;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YQYQYTNMSV 10
Db 576 YQYQYTNMSV 585
RESULT 5
ADQ39377 standard; protein; 960 AA.
XX
ID ADQ39377
XX
AC ADQ39377;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1040.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiac; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-UTL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
XX
PR 10-MAR-2003; 2003US-0453135P.
XX
PR 30-APR-2003; 2003US-0466412P.
XX
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JT, Iakubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PSDB; ADQ38549.
XX
PT Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1040; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX SQ Sequence 960 AA;

Query Match 100.0%; Score 61; DB 8; Length 960;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YQYQYTNMSV 10
DB 772 YQYQYTNMSV 781

RESULT 6
ABU05246

ID ABU05246 standard; protein; 1114 AA.

XX AC ABU05246;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1912.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.

XX PS Example 2; SEQ ID NO 1912; 134dp; English.

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1114 AA;

Query Match 100.0%; Score 61; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YQYQYTNMSV 10
DB 926 YQYQYTNMSV 935

RESULT 7
ABU05239

ID ABU05239 standard; protein; 1114 AA.

XX AC ABU05239;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1905.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.

```
XX PS Example 2; SEQ ID NO 1905; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SO Sequence 1114 AA;

Query Match          100.0%; Score 61; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
Db 926 YQYQYTNMSV 935

RESULT 8
ID ABU05240 standard; protein; 1143 AA.
XX AC ABU05240;
XX DT 29-JUN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1906.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
```

```
XX PS Example 2; SEQ ID NO 1906; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SO Sequence 1143 AA;

Query Match          100.0%; Score 61; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
Db 955 YQYQYTNMSV 964

RESULT 9
ID ABU05245 standard; protein; 1143 AA.
XX AC ABU05245;
XX DT 29-JUN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1911.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
```

XX Example 2; SEQ ID NO 1911; 134pp; English.
PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents a
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SO Sequence 1143 AA;

Query Match 100.0%; Score 61; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
|||
DB 955 YQYQYTNMSV 964

RESULT 10

ID ADL16232 standard; protein; 1143 AA.

ADL16232;

DT 06-MAY-2004 (first entry)

DE Human protein tyrosine phosphatase #27.

XX cytosolic; immunosuppressive; antiallergic;
XX protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
XX inducible signalling pathway; cell proliferation; cancer;
XX guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX cell-cycle abnormality; enzyme.
OS
XX Homo sapiens.
XX
XX WO2003068984-A2.
XX
XX 21-AUG-2003.
XX
XX 13-FEB-2003; 2003WO-EP001446.
XX
XX 13-FEB-2002; 2002US-0356810P.
XX
XX 12-FEB-2003; 2003US-0036547.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX (CEPT-) CEPTYR INC.
XX
XX Tonke NK, Tzu-Ching M. Cool DB;
XX
XX WPI; 2003-712572/67.
XX
XX N-PSDB; ADL16231.
XX
XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX screening for specific modulators, potential agents for treating e.g.
XX cancer or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 81; 238pp; English.
XX

CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulphydryl-reactive agent (ii) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune disease; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX

SO Sequence 1143 AA;

Query Match 100.0%; Score 61; DB 7; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
|||
DB 955 YQYQYTNMSV 964

RESULT 11

ID ADQ18845 standard; protein; 1143 AA.

ADQ18845;

DT 26-AUG-2004 (first entry)

DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.

XX soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human.
XX
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnick A;
XX
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX

PS Example 2; SEQ ID NO 1664; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX

Sequence 1143 AA;

Query Match 100.0%; Score 61; DB 8; Length 1143;

Best Local Similarity 100.0%; Pred. No. 0.6;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10

Db 955 YQYQYTNMSV 964

RESULT 12

AAM41048

ID AAM41048 standard; protein; 1149 AA.

XX AAM41048;

XX 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 5979.

XX

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

XX peripheral nervous system; neuropathy; central nervous system; CNS;

XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

XX chemokine; thrombolytic; drug screening; arthritis; inflammation;

XX leukemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US034263.

XX

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX

XX (HYSE-) HYSEQ INC.

XX

PA

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa;

PI Zhou P, Goodrich R, Drmanac RT;

XX

XX WPI; 2001-442253/47.

DR N-PSDB; AAI60204.

XX

XX

PT Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.

XX

PS Example 2; SEQ ID NO 5979; 10078bp; English.

XX

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AAM38642-AAM4213) with nootropic

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

Sequence 1149 AA;

Query Match 100.0%; Score 61; DB 4; Length 1149;

Best Local Similarity 100.0%; Pred. No. 0.6;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10

Db 961 YQYQYTNMSV 970

RESULT 13

ABU05242

ID ABU05242 standard; protein; 1149 AA.

XX

AC ABU05242;

XX

DE 29-JUN-2003 (first entry)

XX

DE Human expressed protein tag (EPT) #1908.

XX

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX protease; proteinase inhibitor; transporter; cytoskeletal protein;

XX receptor; transcription factor; cancer; MHC;

XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;

XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX

OS Homo sapiens.

XX

PN WO200278524-A2.

XX

PD 10-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-US009671.

XX

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX

PA (ZYCO-) ZYCO INC.

XX

PI Chicx RM, Tomlinson AJ, Urban RG;

PI WPI; 2003-040607/03.

XX

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.

XX

XX

XX Example 2; SEQ ID NO 1908; 134pp; English.

XX

XX The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, proteinase inhibitor,

CC transporter, cytoskeletal protein, receptor or transcription factor. The

CC polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified

CC polypeptide. The purified polypeptide, or the antibody that binds to this

CC polypeptide, is useful for treating cancer. The polypeptide is also

CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIP0 at
CC ftp.wip0.int/pub/published_ppt_sequences
XX
SQ Sequence 1149 AA;
Query Match 100.0%; Score 61; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQYQYTNMSV 10
DB 961 YQYQYTNMSV 970
RESULT 14
ID ADR39747 standard; protein; 1192 AA.
XX
AC ADR39747;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.
XX
XX human; kinase and phosphatase protein; KPP; enzyme; cytosolic;
XX antiarteriosclerotic; anti-HIV; antiallergic; antiinflammatory;
XX chemoprotective; anticonvulsant; nootropic; neuroprotective;
XX thymomimetic; gene therapy; cell proliferative disorder; cancer;
XX atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
XX stroke; immune disorder; inflammatory disorder; AIDS; allergy;
XX developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX KPP-20.
XX
OS Homo sapiens.
XX
XX WO2004074453-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005092.
XX
PR 20-FEB-2003; 2003US-0449059P.
XX
PR 19-MAR-2003; 2003US-0456932P.
XX
PR 28-MAR-2003; 2003US-0458844P.
XX
PR 09-APR-2003; 2003US-0461678P.
XX
PR 17-APR-2003; 2003US-0463937P.
XX
XX
XX (INCY-) INCYTE CORP.
XX
PI Rankumar J, Margulis JP, Swarnakar A, Chawla NK, Tran UK;
PI Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;
PI Jackson AA, Yang J, Gorvad AE;
XX
XX WPI; 2004-635568/61.
XX
DR N-PSDB; ADR39793.
XX
XX
XX New human kinases and phosphatases (KPP) for diagnosing, treating and
XX preventing diseases or conditions associated with aberrant KPP expression
XX e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX
XX Claim 1; SEQ ID NO 20; 239pp; English.
XX
XX The present sequence represents the human kinase and phosphatase protein
XX (KPP), designated KPP-20. The human KPP sequences from the present
XX invention have cytosolic, antiarteriosclerotic, anticonvulsant,
XX nootropic, neuroprotective, chemoprotective, anti-HIV, antiallergic,
XX antiinflammatory and thymomimetic activities, and can be used in gene

CC therapy. The human KPP proteins and polynucleotides can be used in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KPP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They can also be used in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
XX
SQ Sequence 1192 AA;
Query Match 100.0%; Score 61; DB 8; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQYQYTNMSV 10
DB 1004 YQYQYTNMSV 1013
RESULT 15
ID ADQ39378 standard; protein; 1219 AA.
XX
XX ADQ39378;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiac; gene therapy; human.
XX
XX
XX Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX
XX 15-JUL-2004.
XX
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX
XX 20-DEC-2002; 2002US-0434778P.
XX
XX 10-MAR-2003; 2003US-0453135P.
XX
XX 30-APR-2003; 2003US-0466412P.
XX
XX 23-SEP-2003; 2003US-0504955P.
XX
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JU, Iakoubova O;
XX
XX WPI; 2004-533949/51.
XX
XX DR N-PSDB; ADQ38550.
XX
XX
XX Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
XX
XX Claim 10; SEQ ID NO 1041; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide

comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiac activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 1219 AA;

Query Match 100.0%; Score 61; DB 8; Length 1219;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
 |||||
Db 1031 YQYQYTNMSV 1040

RESULT 16
ADM67187
ID ADM67187 standard; protein; 1256 AA.
XX ADM67187;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human adipocyte specific PTPase receptor type C protein SegID 541.
XX
KW human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW anti-diabetic; hypotensive; PTPase receptor type C.
XX
OS Homo sapiens.
XX
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGCE-) HMGCE INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR MPI; 2004-143846/14.
XX
DR N-PSDB; ADM66908.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Disclosure; SEQ ID NO 541; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and

is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMGI-C^{-/-}, ob/ob, or HMGI-C^{-/-} ob/ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were identified that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, hypertension and cardiovascular disease, as well as screening for compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, anti-diabetic and hypotensive activities. This polypeptide sequence is a human homologue of a murine adipocyte specific protein sequence of the invention.

Sequence 1256 AA;

Query Match 100.0%; Score 61; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
 |||||
Db 1068 YQYQYTNMSV 1077

RESULT 17
ADP12966
ID ADP12966 standard; protein; 1256 AA.
XX ADP12966;
XX
DT 12-AUG-2004 (first entry)
XX
DE Protein encoding reference mRNA sequence #51.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR MPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2975; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring

CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein encoded by an mRNA sequence of the invention which show altered
CC expression in renal transplantation and expression.

CC Sequence 1256 AA;

Query Match 100.0%; Score 61; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
Db 1068 YQYQYTNMSV 1077

RESULT 18
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.

AC ADQ39376;
DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.

KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin JT, Iakubova O;

DR MPI; 2004-533949/51.

DR N-PSDB; ADQ38548.

XX Claim 10; SEQ ID NO 1039; 145pp; English.

PT Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

XX The invention relates to a novel method for identifying an individual who

XX has an altered risk for developing myocardial infarction. The method

XX comprises detecting a single nucleotide polymorphism (SNP) in any one of

XX the nucleotide sequences given in the specification in the individual's

XX nucleic acids, where the presence of the SNP is correlated with an

XX altered risk for myocardial infarction in the individual. The invention

XX further comprises: an isolated nucleic acid molecule comprising at least

XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in

XX the specification or its complement and encoding any one of the amino

XX acid sequences given in the specification; an isolated polypeptide

XX comprising an amino acid sequence given in the specification; an antibody

XX that specifically binds to the polypeptide or its antigen-binding

XX fragment; an amplified polynucleotide containing an SNP given in the

XX specification and which is between about 16 and 1000 nucleotides in

XX length; a kit for detecting a SNP in a nucleic acid, comprising the

XX polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a

XX nucleic acid molecule; a method of detecting a variant polypeptide; and a

CC method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiant activity.

CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or

CC decreased risk for developing myocardial infarction and for preparing a

CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-

CC associated gene containing one or more SNPs of the invention. Note: This

CC sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.

QY 1 YQYQYTNMSV 10
Db 1070 YQYQYTNMSV 1079

RESULT 19
ADQ39379
ID ADQ39379 standard; protein; 1267 AA.

AC ADQ39379;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.

KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KW cardiant; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

PR 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin JT, Iakubova O;

DR MPI; 2004-533949/51.

DR N-PSDB; ADQ38551.

XX Claim 10; SEQ ID NO 1042; 145pp; English.

PT Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

XX The invention relates to a novel method for identifying an individual who

XX has an altered risk for developing myocardial infarction. The method

XX comprises detecting a single nucleotide polymorphism (SNP) in any one of

XX the nucleotide sequences given in the specification in the individual's

XX nucleic acids, where the presence of the SNP is correlated with an

XX altered risk for myocardial infarction in the individual. The invention

XX further comprises: an isolated nucleic acid molecule comprising at least

XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in

XX the specification or its complement and encoding any one of the amino

XX acid sequences given in the specification; an isolated polypeptide

XX comprising an amino acid sequence given in the specification; an antibody

XX that specifically binds to the polypeptide or its antigen-binding

CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 61; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQYQYTNMSV 10
DB 1116 YQYQYTNMSV 1125
XX
RESULT 22
ABU05244
ID ABU05244 standard; protein; 1304 AA.
XX
AC ABU05244;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1910.
XX
KW Translational profiling; expressed protein tag; EPT, kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1910, 134pp; English.
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,

CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 61; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQYQYTNMSV 10
DB 1116 YQYQYTNMSV 1125
XX
RESULT 23
ADL16230
ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #26.
XX
KW cytosolic; immunosuppressive; anti-allergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-0036547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI (CEPT-) CEPT INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-PSDB; ADL16229.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 79; 238pp; English.
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulphydryl-reactive agent (ii) that

irreversibly modifies the thiol group of an invariant Cys in the active site of PTP; and (iii) determining, under reducing conditions, the level of dephosphorylation, caused by PTP, of a labelled substrate (III), where dephosphorylation indicates that an active PTP is present. . No details of tests for these activities are given. The method is used to identify reversibly oxidized PTP, also to identify agents that: (a) reversibly modify such PTP, or (b) alter inducible signalling pathways in which PTP are involved. These agents are potentially useful, in human or veterinary medicine, for treating abnormal cell proliferation or growth (cancer); guest vs. host disease; autoimmune diseases; allergy or other immunosuppressed states; metabolic disorders and cell-cycle abnormalities. This sequence represents one of the PTP enzyme of the invention.

SO Sequence 1304 AA;

Query Match 100.0%; Score 61; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
|||
Db 1116 YQYQYTNMSV 1125

RESULT 24
ADP65158
ID ADP65158 standard; protein; 1304 AA.
XX
AC ADP65158;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
XX
KW autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;
KW antiarthritic; osteopathic; anti-gout; anti-inflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
OS Homo sapiens.
XX
PN MO2003072827-A1.
XX
PD 04-SEP-2003.
XX
PF 31-OCT-2002; 2002MO-US035433.
XX
PR 31-OCT-2001; 2001US-0336220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thorton SL;
XX
DR WPI, 2003-712740/67.
XX
DR GENBANK; NP_002829.
XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
XX Disclosure; Page; 56pp; English.
XX
XX The invention relates to a novel method for diagnosing and analyzing
XX autoimmune disease or arthritis. The method comprises obtaining a
XX patient sample containing mRNA, analyzing gene expression using the mRNA
XX that results in a gene expression signature of the mRNA, and using that
XX gene expression signature to diagnose or analyse the autoimmune disease
XX or arthritis in the patient, where gene expression of at least 60% of
XX the genes correlates with that of the gene signature. The invention

further comprises: a treatment of rheumatoid arthritis; identification of CC genes for targeting in the treatment of rheumatoid arthritis in a mammal; an CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an CC array or gene chip, specific for rheumatoid arthritis; diagnosis or CC analyses of autoimmune disease or rheumatoid arthritis; screening the CC efficacy of a candidate drug in vitro for the treatment of collagen- CC induced arthritis; and reducing the symptoms associated with collagen- CC induced arthritis. The compositions of the invention have the following CC activities: immunosuppressive, anti-rheumatic, antiarthritic, osteopathic, CC anti-gout, anti-inflammatory, dermatological, and immunomodulatory. The CC methods and compositions of the present invention are useful for CC diagnosing and treating autoimmune disease or arthritis, such as CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an CC immune disease caused by an infectious agent. This sequence represents a CC protein sequence relating to the genes used in the analysis and treatment CC of autoimmune diseases or arthritis. Note: This sequence is not shown CC in the specification. It has been supplied in an electronic format from CC WIPO.

SO Sequence 1304 AA;

Query Match 100.0%; Score 61; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQYQYTNMSV 10
|||
Db 1116 YQYQYTNMSV 1125

RESULT 25
ADM67209
ID ADM67209 standard; protein; 1304 AA.
XX
AC ADM67209;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human adipocyte specific leukocyte common antigen protein SegID 563.
XX
KW human; adipocyte specific; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; leukocyte common antigen.
XX
OS Homo sapiens.
XX
PN MO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
XX
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMG-) HMGNE INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR WPI, 2004-143846/14.
XX
DR N-PSDB; ADM65930.
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
XX Disclosure; SEQ ID NO 563; 91pp; English.
XX
XX This invention relates to a novel method for identifying genes that are
XX over-expressed in adipose tissue and as such it provides targets for anti

-obesity pharmaceutical compositions. Specifically, it refers to a high CC mobility group I-C protein (HMG-C) that is associated with obesity and CC is epistatic to leptin, furthermore, it refers to the ob gene where an CC autosomal recessive trait is linked to obesity and diabetes. The present CC invention describes performing differential gene expression analysis CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT) CC of any two different mice selected from a group consisting of wild-type, CC HMG-C -/-, ob/ob, or HMG-C -/- ob/ob genotype mice. Accordingly, using CC this method novel nucleotides and the encoded proteins thereof were CC identified that are adipocyte specific, and as such can be used for CC preventing adipogenesis, diagnosing and treating diabetes, obesity, CC hypertension and cardiovascular disease, as well as screening for CC compounds that can modulate or prevent adipogenesis and treat diabetes or CC obesity. These compositions exhibit anorectic, anti-diabetic and CC hypotensive activities. This polypeptide sequence is a human homologue of CC a murine adipocyte specific protein sequence of the invention.

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 61; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.69; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 YQYQYTNMSV 10
1116 YQYQYTNMSV 1125

DB 1116 YQYQYTNMSV 1125

RESULT 26
ABO84455 standard; protein; 1304 AA.
XX AC ABO84455;
XX 18-NOV-2004 (first entry)
XX Human cancer-associated protein HPI3-011.2.
XX Human cancer-associated protein; cytosolic; cancer; leukaemia;
XX lymphoma; CAP.
XX Homo sapiens.
XX OS
XX PN WO2004074320-A2.
XX PD 02-SEP-2004.
XX 17-FEB-2004; 2004WO-US004730.
XX 14-FEB-2003; 2003US-00367094.
XX 14-MAR-2003; 2003US-00388838.
XX 15-APR-2003; 2003US-00417375.
XX 13-JUN-2003; 2003US-00461862.
XX 15-SEP-2003; 2003US-00663431.
XX 15-DEC-2003; 2003US-00737318.
XX (SAGR-) SAGRES DISCOVERY INC.
XX PI Morris DW, Morris DW, Malandro MS;
XX WPI; 2004-652914/63.
XX DR N-PSDB; ABD32626.
XX New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.
XX claim 18; seqid 147; 310pp; English.
XX The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
XX in the specification, or its complement. The nucleic acids encode cancer-
XX associated proteins. Also included are an expression vector comprising

CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual), a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1304 AA;

Query Match 100.0%; Score 61; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 0.69; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 YQYQYTNMSV 10
1116 YQYQYTNMSV 1125

DB 1116 YQYQYTNMSV 1125

RESULT 27
ADQ39380 standard; protein; 1304 AA.
XX AC ADQ39380;
XX 18-NOV-2004 (first entry)
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
XX DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiac; gene therapy; human.
XX OS
XX PN WO2004058052-A2.
XX PD 15-JUL-2004.
XX 22-DEC-2003; 2003WO-US040978.
XX 20-DEC-2002; 2002US-0434778P.
XX 10-MAR-2003; 2003US-0453135P.
XX 30-APR-2003; 2003US-0466412P.
XX 23-SEP-2003; 2003US-0504955P.
XX (APPL-) APPLERA CORP.
XX PI Cargill M, Devlin JY, Iakobova O;
XX WPI; 2004-533949/51.
XX DR N-PSDB; ADQ38552.
XX

PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.

PS Claim 10; SEQ ID NO 1043; 145pp; English

CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement; and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

SQ Sequence 1304 AA;

Query Match	100.0%	Score 61	DB 8	Length 1304
Best Local Similarity	100.0%	Pred. NO.	0.69	
Matches 10	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 YQYQYTNMSV 10

Db 1116 YQYQYTNWSV 1125

RESULT 28

ID ADQ39375 standard; protein; 1306 AA.

AC ADQ39375;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.

KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;

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PR 10-MAR-2003; 2003US-0453135P

PR 23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

PI Cargill M, Devlin JJ, Iakubova O;

DR WPI; 2004-533949/51.

XX

PT

PT the individual's nucleic acids.

PS Claim 10; SEQ ID NO 1038; 145pp; English

CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

SQ Sequence 1306 AA;

Query Match	100.0%	Score 61	DB 8	Length 1306
Best Local Similarity	100.0%	Pred. NO. 0.69		
Matches 10	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 YQYQYTNMSV 10

Db 1118 YQYQYTNWSV 1127

Search completed: May 3, 2005, 07:31:14

Job time : 60.3158 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-3

Perfect score: 43

Sequence: 1 KLFYAKLV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	100.0	72	2	06QIN1	06qin1 homo sapien
2	43	100.0	72	2	06QIM9	06qim9 gorilla gorilla
3	43	100.0	72	2	06QINO	06qino pan troglod
4	43	100.0	77	2	06QIM4	06qim4 colobus gus
5	43	100.0	77	2	06QIM5	06qim5 cercopithec
6	43	100.0	77	2	06QIM6	06qim6 macaca nem
7	43	100.0	756	2	06PUK7	06puk7 homo sapien
8	43	100.0	1290	2	06ED60	06ed60 actus vocif
9	43	100.0	1303	2	06ED61	06ed61 actus nancy
10	43	100.0	1303	2	06ED62	06ed62 actus nigril
11	43	100.0	1304	1	CD45_HUMAN	P08575 homo sapien
12	38	88.4	72	2	06QIM8	06qim8 pongo pygma
13	37	86.0	285	2	097UH7	097uh7 sulfolobus
14	36	83.7	77	2	06QIM7	06qim7 hylolobus
15	36	83.7	489	2	06MDS3	06mds3 parschlamy
16	35	81.4	701	2	08K4K9	08k4k9 rattus norv
17	34	79.1	172	2	09FZF7	09fzf7 arabidopsis
18	34	79.1	248	2	08I7M5	08i7m5 caenorhabdi
19	34	79.1	309	2	069Z57	069z57 mus musculu
20	34	79.1	479	2	096E49	096e49 homo sapien
21	34	79.1	538	2	080YX5	080yx5 mus musculu
22	34	79.1	735	2	08TF49	08tf49 homo sapien
23	34	79.1	871	2	07Z6B9	07z6b9 homo sapien
24	33	76.7	392	2	034539	034539 bacillus su
25	33	76.7	678	1	RNB_VIBCH	09k1e1 vibrio chol
26	33	76.7	814	2	06C5X1	06c5x1 yarrowia li
27	33	76.7	898	2	07TIP6	07tip6 raja erinac
28	33	76.7	1240	2	06H8S0	06h8s0 yarrowia li
29	32	74.4	212	2	0647F4	0647f4 thermoprote
30	32	74.4	274	1	PERA_ECO27	P43459 escherichia
31	32	74.4	274	2	Q47074	Q47074 escherichia

32	32	74.4	274	2	Q7ISM4	Q7ism4 escherichia
33	32	74.4	274	2	Q9APE6	Q9ape6 escherichia
34	32	74.4	274	2	Q9EZ03	Q9ez03 escherichia
35	32	74.4	274	2	Q9F871	Q9f871 escherichia
36	32	74.4	274	2	Q9F872	Q9f872 escherichia
37	32	74.4	274	2	Q9F873	Q9f873 escherichia
38	32	74.4	274	2	Q9F877	Q9f877 escherichia
39	32	74.4	274	2	Q9F878	Q9f878 escherichia
40	32	74.4	274	2	Q9F882	Q9f882 escherichia
41	32	74.4	274	2	Q9F884	Q9f884 escherichia
42	32	74.4	338	2	Q63IS8	Q63is8 burkholderi
43	32	74.4	381	2	Q814M1	Q814m1 caenorhabdi
44	32	74.4	540	2	Q70XZ4	Q70xz4 amborella t
45	32	74.4	578	2	Q73M41	Q73m41 treponema d

ALIGNMENTS

RESULT 1	06QIN1	PRELIMINARY;	PRT;	72 AA.
ID	06QIN1			
AC	06QIN1			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DE	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	CD45 (Fragment).			
GN	Name=PTPRC;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15014144; DOI=10.1093/molbev/msh111;			
RA	Philip L.C., Mundy N.I.;			
RT	"Rapid Evolution by Positive Darwinian Selection in the Extracellular			
RT	Mol. Biol. Evol. 21:1504-1511(2004)."			
DR	EMBL; AY539691; AAS46946.1; -.			
FT	NON TER			
FT	NON TER			
SQ	SEQUENCE	72 AA;	8003 MW;	2EAC73A3A290D4E4 CRC64;
Query Match				
Best Local Similarity		100.0%;	Score 43;	DB 2; Length 72;
Matches	9;	Conservative	0;	Pred. No. 0.1;
			Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1 KLFYAKLV 9			
Db	17 KLFYAKLV 25			
RESULT 2	06QIM9	PRELIMINARY;	PRT;	72 AA.
ID	06QIM9			
AC	06QIM9			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	CD45 (Fragment).			
GN	Name=PTPRC;			
OS	Gorilla gorilla (gorilla).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.			
OX	NCBI_Taxid=9593;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15014144; DOI=10.1093/molbev/msh111;			
RA	Philip L.C., Mundy N.I.;			
RT	"Rapid Evolution by Positive Darwinian Selection in the Extracellular			
RT	Mol. Biol. Evol. 21:1504-1511(2004)."			

DR EMBL: AY539693; AAS46948.1; -.
FT NON_TER 1
FT NON_TER 72
SQ SEQUENCE 72 AA; 8063 MW; 42AC733A3297AD52 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
DB 17 KLFYAKLV 25

RESULT 3

QOQIM0 PRELIMINARY; PRT; 72 AA.
AC QOQIM0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL: AY539692; AAS46947.1; -.
FT NON_TER 1
FT NON_TER 72
SQ SEQUENCE 72 AA; 8063 MW; 42AC733A3297AD52 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
DB 17 KLFYAKLV 25

RESULT 4

QOQIM4 PRELIMINARY; PRT; 77 AA.
AC QOQIM4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
OX NCBI_TaxID=3548;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL: AY539698; AAS46953.1; -.
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 8789 MW; 5F58DB11E1DC818C CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
DB 17 KLFYAKLV 25

RESULT 5

QOQIM5 PRELIMINARY; PRT; 77 AA.
AC QOQIM5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Cercopithecus neglectus (De Brazza's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_TaxID=36227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL: AY539697; AAS46952.1; -.
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 8815 MW; 6DDDE13DEDEB1184 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
DB 17 KLFYAKLV 25

RESULT 6

QOQIM6 PRELIMINARY; PRT; 77 AA.
AC QOQIM6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15014144; DOI=10.1093/molbev/msh111;
RA Filip L.C., Mundy N.I.;
RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
RL Mol. Biol. Evol. 21:1504-1511(2004).
DR EMBL: AY539696; AAS46951.1; -.
FT NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 8918 MW; D82A0CB0CEB6758 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 2; Length 77;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLFATKLVN 9
| | | | |
Db 17 KLFATKLVN 25

RESULT 7

Q6PJK7 PRELIMINARY; PRT; 756 AA.

AC Q6PJK7 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
PR PTPRC protein (Fragment).

GN Name=PTPRC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Helen F.,

RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ueding T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimmett J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalusz D.E., Schermer A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.L.

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC014239; AAHL14239.1; -.

DR HSSP: P18031; 1AAX.

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR003961; FN III.

DR InterPro: IPR008957; FN_III-like.

DR InterPro: IPR000242; Tyr_PP.

DR Pfam: PF00061; fn3; 2.

DR Pfam: PF00102; Y_PTPHPTASE.

DR PRINTS: PR00700; PRTYPHPTASE.

DR SMART: SM00060; FNC3; 2.

DR SMART: SM00194; PTPC; 1.

DR PROSITE: PS50853; FNC3; 2.

DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.

FT NON_TER 756

SQ SEQUENCE 756 AA; 85430 MW; 8A9A63827BD69E6 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 756;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLFATKLVN 9
| | | | |
Db 196 KLFATKLVN 204

RESULT 8

Q6ED60 PRELIMINARY; PRT; 1290 AA.

AC Q6ED60 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

CD 45.

OS Actus vociferans (Spix's owl monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=57176;

RN [1]

SEQUENCE FROM N.A.

RA PubMed=15245371;

RT "Comparative analysis of CD45 protein in primate context: owl monkeys

vs. human.";

RL Tissue Antigens 64:165-172(2004).

DR EMBL: AY445818; AAS06903.1; -.

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR003961; FN III.

DR InterPro: IPR003955; PTPC_motif.

DR InterPro: IPR00387; TYR_phosphatase.

DR InterPro: IPR000242; Tyr_PP.

DR Pfam: PF00041; fn3; 2.

DR PRINTS: PR00700; PRTYPHPTASE.

DR SMART: SM00060; FNC3; 2.

DR SMART: SM00194; PTPC; 2.

DR PROSITE: PS50853; FNC3; 2.

DR PROSITE: PS50383; TYR_PHOSPHATASE_1; 2.

DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

KW Hydrolase.

SQ SEQUENCE 1290 AA; 145616 MW; 99E810C75D932824 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 1290;

Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLFATKLVN 9
| | | | |
Db 235 KLFATKLVN 243

RESULT 9

Q6ED61 PRELIMINARY; PRT; 1303 AA.

AC Q6ED61 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

CD 45.

OS Actus nancyanae (Ma's night monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=37293;

RN [1]

SEQUENCE FROM N.A.

RA PubMed=15245371;

RT "Comparative analysis of CD45 protein in primate context: owl monkeys

vs. human.";

RL Tissue Antigens 64:165-172(2004).

DR EMBL: AY445817; AAS06902.1; -.

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003585; PTPC_motif.
 DR InterPro: IPR00387; TYR_phosphatase.
 DR InterPro: IPR00242; TYR_PP.
 DR Pfam: PFO0041; fn3; 2.
 DR Pfam: PFO0102; Y_phosphatase; 2.
 DR PRINTS: PRO0700; PRTPHPTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 2.
 DR SMART: SM00404; PTPC_motif; 2.
 DR PROSITE: PS00853; FN3; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR HydroLase.
 KW SEQUENCE 1303 AA; 146929 MW; DOBBOC640D1D1788 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 1303;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
 |||||
 DB 244 KLFYAKLV 252

RESULT 10
 ID 06ED62 PRELIMINARY; PRT; 1303 AA.
 AC 06ED62;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE CD45.
 OS Aotus nigricaps (Black-headed owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 RT vs. human";
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL: AY445816; AAS06901.1;
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003585; PTPC_motif.
 DR InterPro: IPR00387; TYR_phosphatase.
 DR InterPro: IPR00242; TYR_PP.
 DR Pfam: PFO0041; fn3; 2.
 DR Pfam: PFO0102; Y_phosphatase; 2.
 DR PRINTS: PRO0700; PRTPHPTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPC; 2.
 DR SMART: SM00404; PTPC_motif; 2.
 DR PROSITE: PS00853; FN3; 2.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR HydroLase.
 KW SEQUENCE 1303 AA; 146586 MW; 98B023EBF4BC1165 CRC64;

Query Match 100.0%; Score 43; DB 2; Length 1303;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
 |||||

DB 244 KLFYAKLV 252

RESULT 11
 ID CD45 HUMAN STANDARD; PRT; 1304 AA.
 AC P08575; O16614; O9H0Y6;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Leukocyte common antigen precursor (p3.1.3.48) (IL-CA) (CD45 antigen) (T200).
 GN Name=PTPRC; Synonyms=CD45;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=88061067; PubMed=2824653;
 RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
 RT "Differential usage of three exons generates at least five different
 RT mRNAs encoding human leukocyte common antigens";
 RL J. Exp. Med. 166:1548-1566(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.
 RX MEDLINE=87275816; PubMed=2956090;
 RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;
 RT "Structural variants of human T200 glycoprotein (leukocyte-common
 RT antigen)";
 RL EMBO J. 6:1251-1257(1987).
 RN [3]
 RP SEQUENCE OF 191-1304 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=89009812; PubMed=2971730;
 RA Hall L.R., Streuli M., Schlossman S.F., Saito H.;
 RT "Complete exon-intron organization of the human leukocyte common
 RT antigen (CD45) gene";
 RL J. Immunol. 141:2781-2787(1988).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=89017162; PubMed=2845400;
 RA Chabouneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
 RT "The leukocyte common antigen (CD45): a putative receptor-linked
 RT protein tyrosine phosphatase";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
 RN [5]
 RP MUTAGENESIS.
 RX MEDLINE=90316093; PubMed=1695146;
 RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
 RT "Distinct functional roles of the two intracellular phosphatase like
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and
 RT LAR";
 RL EMBO J. 9:2399-2407(1990).
 CC -1- FUNCTION: Required for T-cell activation through the antigen
 CC receptor. The first PTPase domain has enzymatic activity, while
 CC the second one seems to affect the substrate specificity of the
 CC first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2O) = protein
 CC tyrosine + phosphate.
 CC -1- SUBUNIT: Binds GANAB and PRKSH (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=At least 8 isoforms are produced;
 CC Name=1;
 CC Name=2;
 CC Name=1; IsoId=P08575-1; Sequence=Displayed;
 CC Name=2; IsoId=P08575-2; Sequence=VSP_007780;
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 1/6 subfamily.

CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD45 entry;
 WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Y00638; CA68669.1; -;
 DR EMBL; Y00638; CA68669.1; -;
 DR EMBL; M23492; AAD15273.2; -;
 DR EMBL; M23492; AAD15273.2; -;
 DR EMBL; M23496; AAD15273.2; JOINED.
 DR EMBL; M23496; AAD15273.2; JOINED.
 DR EMBL; M23467; AAD15273.2; JOINED.
 DR EMBL; M23467; AAD15273.2; JOINED.
 DR EMBL; M23468; AAD15273.2; JOINED.
 DR EMBL; M23468; AAD15273.2; JOINED.
 DR EMBL; M23469; AAD15273.2; JOINED.
 DR EMBL; M23470; AAD15273.2; JOINED.
 DR EMBL; M23471; AAD15273.2; JOINED.
 DR EMBL; M23472; AAD15273.2; JOINED.
 DR EMBL; M23473; AAD15273.2; JOINED.
 DR EMBL; M23474; AAD15273.2; JOINED.
 DR EMBL; M23475; AAD15273.2; JOINED.
 DR EMBL; M23476; AAD15273.2; JOINED.
 DR EMBL; M23477; AAD15273.2; JOINED.
 DR EMBL; M23478; AAD15273.2; JOINED.
 DR EMBL; M23479; AAD15273.2; JOINED.
 DR EMBL; M23480; AAD15273.2; JOINED.
 DR EMBL; M23481; AAD15273.2; JOINED.
 DR EMBL; M23482; AAD15273.2; JOINED.
 DR EMBL; M23483; AAD15273.2; JOINED.
 DR EMBL; M23484; AAD15273.2; JOINED.
 DR EMBL; M23485; AAD15273.2; JOINED.
 DR EMBL; M23486; AAD15273.2; JOINED.
 DR EMBL; M23487; AAD15273.2; JOINED.
 DR EMBL; M23488; AAD15273.2; JOINED.
 DR EMBL; M23489; AAD15273.2; JOINED.
 DR EMBL; M23490; AAD15273.2; JOINED.
 DR EMBL; M23491; AAD15273.2; JOINED.
 DR PIR; A46546; A46546.
 DR HSP; P18031; 1C88.
 DR ITCAC; P08575; -;
 DR GlycosylatedB; P08575; -;
 DR Genew; HGNC:9666; PTPRC.
 DR MIM; 151460; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PTPRHPTASE.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PP; 2.
 KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;
 KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 KW Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 1304
 FT DOMAIN 24 575
 FT TRANSMEM 576 597
 FT DOMAIN 598 1304
 FT DOMAIN 390 478
 FT DOMAIN 482 570

FT DOMAIN 670 919
 FT DOMAIN 961 1235
 FT ACT_SITE 851 851
 FT ACT_SITE 1167 1167
 FT CARBOHYD 78 78
 FT CARBOHYD 90 90
 FT CARBOHYD 95 95
 FT CARBOHYD 184 184
 FT CARBOHYD 190 190
 FT CARBOHYD 197 197
 FT CARBOHYD 232 232
 FT CARBOHYD 260 260
 FT CARBOHYD 270 270
 FT CARBOHYD 276 276
 FT CARBOHYD 335 335
 FT CARBOHYD 378 378
 FT CARBOHYD 419 419
 FT CARBOHYD 468 468
 FT CARBOHYD 488 488
 FT CARBOHYD 529 529
 FT VARSPLIC 32 192
 FT MUTAGEN 851 851
 FT CONFLICT 650 650
 FT CONFLICT 1207 1207
 SQ SEQUENCE 1304 AA; 147253 MW; A08FC22D606BAFZ CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 43; DB 1; Length 1304;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEPTAKLV 9
 Db 244 KLEPTAKLV 252
 ID 06QIM8 PRELIMINARY; PRT; 72 AA.
 AC 06QIM8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CD45 (Fragment).
 GN Name=PTPRC;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed:15014144; DOI=10.1093/molbev/meh111;
 RA Filip L.C., Mundy N.I.;
 RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
 RT Domain of the Abundant Lymphocyte Protein CD45 in Primates."
 RL Mol. Biol. Evol. 21:1504-1511(2004).
 DR EMBL; AF539694; AAS46949.1; -;
 DR FT NON TER 1 1
 DR FT NON TER 72 72
 SQ SEQUENCE 72 AA; 8303 MW; B4AAAFB3D47C5A42 CRC64;
 Query Match
 Best Local Similarity 88.4%; Score 38; DB 2; Length 72;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KLEPTAKLV 9
 Db 17 KLEPTAKLV 25
 RESULT 13
 Q97UH7

ID 097UH7 PRELIMINARY; PRT; 285 AA.
 AC 097UH7;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=SS03041;
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 NCBI_TaxID=2287;
 RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awayez M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Efraim G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006895; AAK43142.1; -.
 DR PTR; G90485; G90485.
 DR InterPro; IPR005511; SMP-30.
 DR Pfam; PF03758; SMP-30; 1.
 DR PRINTS; PR01790; SMP30FAMILY.
 DR KMP complete proteome; Hypothetical protein.
 SQ SEQUENCE 285 AA; 32805 MW; 416D9E8FA6446ED CRC64;

Query Match 86.0%; Score 37; DB 2; Length 285;
 Best Local Similarity 66.7%; Pred. No. 9.4;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLFYAKLV 9
 Db 267 RLFTAKMNI 275

RESULT 14
 O6QIM7 PRELIMINARY; PRT; 77 AA.
 ID 06QIM7;
 AC 06QIM7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CD45 (Fragment).
 GN Name=PTPRC;
 OS Hylobates muelleri (Mueller's gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 NCBI_TaxID=9588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15014144; DOI=10.1093/molbev/msh111;
 RA Filip L.C., Mundy N.I.;
 RT "Rapid Evolution by Positive Darwinian Selection in the Extracellular
 RT Domain of the Abundant Lymphocyte Protein CD45 in Primates.";
 RL Mol. Biol. Evol. 21:1504-1511(2004).
 DR EMBL; AY539695; AAS46950.1; -.
 FT NON_TER 1
 FT NON_TER 77
 SQ SEQUENCE 77 AA; 8782 MW; 65B19539596D7CA CRC64;

Query Match 83.7%; Score 36; DB 2; Length 77;
 Best Local Similarity 88.9%; Pred. No. 4.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KLFYAKLV 9
 Db 17 KEFTAKLV 25

RESULT 15
 Q6MDS3 PRELIMINARY; PRT; 489 AA.
 ID Q6MDS3;
 AC Q6MDS3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative outer membrane protein, component of multidrug efflux
 DE systems.
 GN Name=oprK; OrderedLocustNames=pc0552;
 OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
 OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
 NCBI_TaxID=264201;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
 RA Fartmann B., Brandt P., Nyakatura G.J., Droge M., Frishman D.,
 RA Rattei T., Mewes H.-W., Wagner M.;
 RT "Genome sequence of an amoeba symbiont and its use for reconstructing
 RT the evolutionary history of chlamydiae.";
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BX908798; CAF23276.1; -.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003423; OEP.
 DR InterPro; IPR010131; RND_outter_NodT.
 DR Pfam; PF02321; OEP; 2.
 DR TIGRFAMs; TIGR01845; RND_outter_NodT; 1.
 DR KMP complete proteome.
 SQ SEQUENCE 489 AA; 54357 MW; DB227548C1FF2B17 CRC64;

Query Match 83.7%; Score 36; DB 2; Length 489;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLFYAKLV 9
 Db 444 KLFYAKLV 452

Search completed: May 3, 2005, 05:58:48
 Job time : 49.1351 secs

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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:29:40 ; Search time 50 Seconds
(without alignments)
77.352 Million cell updates/sec

Title: US-10-003-983C-10

Perfect score: 51

Sequence: 1 TLILDVPCGV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	5 ABG31980	Abg31980 Human CD4
2	51	100.0	19	2 AAR26823	Aar26823 Cell adhe
3	51	100.0	20	2 AAR30900	Aar30900 Cell adhe
4	51	100.0	553	2 AAW35856	Aaw35856 Human CD4
5	51	100.0	553	6 ABU07335	Abu07335 Human exp
6	51	100.0	641	4 AAM23689	Aam23689 Human EST
7	51	100.0	641	6 ABU07333	Abu07333 Human exp
8	51	100.0	664	4 AAM39262	Aam39262 Human pol
9	51	100.0	664	6 ABU07334	Abu07334 Human exp
10	51	100.0	1114	6 ABU05246	Abu05246 Human exp
11	51	100.0	1114	6 ABU05239	Abu05239 Human exp
12	51	100.0	1143	6 ABU05240	Abu05240 Human exp
13	51	100.0	1143	6 ABU05245	Abu05245 Human exp
14	51	100.0	1143	7 ADL16232	Adl16232 Human pro
15	51	100.0	1143	8 ADQ18845	Adq18845 Human pro
16	51	100.0	1149	4 AAM41048	Aam41048 Human sol
17	51	100.0	1149	6 ABU05242	Abu05242 Human exp
18	51	100.0	1192	8 ADR39747	Adr39747 Human kin
19	51	100.0	1219	8 ADQ39378	Adq39378 Human myo
20	51	100.0	1256	8 ADM67187	Adm67187 Human adi
21	51	100.0	1256	8 ADP12966	Adp12966 Protein e
22	51	100.0	1258	8 ADQ39376	Adq39376 Human myo
23	51	100.0	1267	8 ADQ39379	Adq39379 Human myo
24	51	100.0	1304	6 ABU05243	Abu05243 Human exp
25	51	100.0	1304	6 ABU05241	Abu05241 Human exp

26	51	100.0	1304	6 ABU05244	Abu05244 Human exp
27	51	100.0	1304	7 ADL16230	Adl16230 Human pro
28	51	100.0	1304	7 ADP65158	Adp65158 Human pro
29	51	100.0	1304	8 ADM67209	Adm67209 Human adi
30	51	100.0	1304	8 ABQ84455	Abq84455 Human can
31	51	100.0	1304	8 ADQ39380	Adq39380 Human myo
32	51	100.0	1306	8 ADQ39375	Adq39375 Human myo
33	46	90.2	140	5 ABG31979	Abg31979 Human CD4
34	41	80.4	140	4 AAU59723	Aau59723 Propionib
35	41	80.4	140	6 ABM56242	Abm56242 Propionib
36	39	76.5	354	6 ABM73414	Abm73414 Staphyloc
37	37	76.5	354	7 ABR62803	Abm62803 Methicill
38	38	74.5	185	7 ABQ73710	Abq73710 Pseudomon
39	38	74.5	243	4 AAB96190	Aab96190 Putative
40	38	74.5	257	6 ABU38869	Abu38869 Protein e
41	38	74.5	381	7 ABQ61639	Abq61639 Klebsiell
42	38	74.5	528	8 ADS44221	Ads44221 Bacterial
43	37	72.5	212	6 ABU50501	Abu50501 Protein e
44	37	72.5	248	8 ADN47276	Adn47276 Thermococ
45	37	72.5	266	3 AAG48634	Aag48634 Arabidops

ALIGNMENTS

RESULT 1
ABG31980
ID ABG31980 standard; peptide; 10 AA.

AC ABG31980;

DT 05-NOV-2002 (first entry)

DE Human CD45 HLA-binding peptide, huCD45/292.

XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;

XX antigen-presenting cell; APC; major histocompatibility complex; MHC;

XX antigen; allogenic; T cell receptor; TCR; cancer; tumour;

XX allogenic stem cell transplantation; CFU-GM; leukaemia;

XX colony forming unit-granulocyte macrophage; immunotherapeutic;

XX haematopoietic; malignant.

XX Homo sapiens.

OS WO200244207-A1.

PN 06-JUN-2002.

PD 30-NOV-2000; 2000WO-GB004566.

PF 30-NOV-2000; 2000WO-GB004566.

PR 30-NOV-2000; 2000WO-GB004566.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Stausas HJ, Amrolia PJ;

PI WPI; 2002-599413/64.

DR Novel peptide comprising leukocyte antigen binding peptide of human CD45

XX polypeptide, useful for producing activated cytotoxic T lymphocytes, for

PT killing cancerous cells e.g. leukemia.

XX Claim 2; Page 38; 56pp; English.

PS The invention discloses a peptide comprising the human leukocyte antigen

XX (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,

CC provided that the peptide is not the intact human CD45 polypeptide. The

CC peptides are useful for producing activated cytotoxic T lymphocyte (CTL)

CC in vitro which involves contacting the CTL with an antigen-presenting

CC cell, where its major histocompatibility complex (MHC) class I molecules

CC are loaded with the peptide, to activate, in an antigen specific manner,

CC where the CTL and the antigen presenting cell are allogenic with respect

CC to the class I MHC molecule that is presenting peptides of CD45. The

Query Match	100.0%	Score 51	DB 5	Length 10
Best Local Similarity	100.0%	Pred. NO. 0.044		
Matches 10; Conservative	0	Mismatches 0	Indels 0	Gaps 0

RESULT 2	
AA26823	
ID	AA26823 standard; peptide; 19 AA

KM MOLT-4; human; lymphoblastic leukaemia; A375-SW; metastatic; melanoma
 KM H1080; fibrosarcoma; LDV; LDV; IDA; inflammatory disease;
 KM rheumatoid arthritis; asthma; sepsis; graft rejection; reperfusion.
 XX Synthetic.
 OS

PN MO9213887-A1.
XX
PD 20-AUG-1992.
XX-
PF 06-FEB-1992; -92MO-GB000226.
XX-
PR 07-FEB-1991; 91GB-00002655.
XX 08-FEB-1991; 91GB-00002818.
PA (UYMA-) UNIV VICTORIA MANCHESTER

PI	Humphries MJ;
XX	
DR	WPI; 1992-299

PT New cell adhesion (poly) peptide(s) modifying cell adhesive properties -
PT useful in treating inflammatory conditions e.g. rheumatoid arthritis,
PT asthma, inflammatory bowel disease, sepsis, etc.

PS Disclosure; Page 4; 23pp; English.

CC The peptide is an example of a cell adhesion polypeptide contg. the amino
CC sequence X-Asp-Y-(A)n-Phe, where X and Y = Ala, Leu, Ile or Val, A= any
CC amino acid and n = 3-10. At least a subsequence of the polypeptide is
CC adherent for MOLT-4 human lymphoblastic leukaemia, A375-SM human
CC metastatic melanoma or H1080 human fibrosarcoma cells. The cell adhesion

Sequence 19 AA;

Query Match	100.0%	Score 51;	DB 2;	length 19;
Best Local Similarity	100.0%;	Pred. No. 0.087;		
Matches	10;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps	0

```
QY      1 TLILDVPPGV 10  
         |||||  
Db      5 TLILDVPPGV 14
```

```

RESULT 3
AAR30900
ID    AAR30900 standard; peptide; 20 AA.

```

AC	AAR30900;	
XX		
DT	25-MAR-2003	(revised)
DT	09-FEB-1993	(first entry)
XX		
DE	Cell adhesion polypeptide	

Cell adhesion polypeptide CD45.

KM MOLT-4; human; lymphoblastic leukaemia; A375-SM; metastatic; melanoma
KM H1080; fibrosarcoma; LDV, LDL; IDA; inflammatory disease;
KM rheumatoid arthritis; aschma; sepsis; graft rejection; reperfusion.

OS	Synthetic.
XX	
PN	W09213887-A1.

PD 20-AUG-1992.

06-FEB-1992; 92WO-GB000226.

07-FEB-1991; 91GB-000002655.

PR 08-FEB-1991; 91GB-00002818.

PA (UYMA-) UNIV VICTORIA MANCHESTER.

PI Humphries MJ;

DR WPI; 1992-299988/36.

PT New cell adhesion (poly)peptide(s) modifying cell adhesive properties -
PT useful in treating inflammatory conditions e.g. rheumatoid arthritis,
PT asthma, inflammatory bowel disease, sepsis, etc.

PS Disclosure; Page 11; 23pp; English.

The peptide is an example of a cell adhesion polypeptide contg. the amino acid sequence X-Asp⁻-Y-(A)n-Phe, where X and Y = Ala, Leu, Ile or Val, A = any amino acid and n = 3-10. At least a subsequence of the polypeptide is adherent for MOLT-4 human lymphoblastic leukaemia, A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells. The cell adhesion peptides are used to modify or control the adhesive properties of cells, e.g. in treatment of inflammatory conditions such as rheumatoid arthritis, asthma, sepsis, graft rejection, inflammatory bowel disease, reperfusion of cardiac tissue after myocardial infarction, and coagulatory disorders. They are selective antagonists of cell adhesion, e.g. they promote adhesion of the specified cells but inhibit adhesion to the natural adhesion protein contg. the adhesive sequence. See also MAR26821-30 and MAR30887-903. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 AA;
SQ Query Match 100.0%; Score 51; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLILDVPPGV 10
DB 6 TLILDVPPGV 15
RESULT 4
AAW35856
ID AAW35856 standard; protein; 553 AA.
XX AAW35856;
AC AAW35856;
DT 27-APR-1998 (first entry).
XX 27-APR-1998 (first entry).
DE Human CD45 for use in T lymphocyte veto molecule.
XX Human; CD45; T lymphocyte veto molecule; chimeric molecule;
KW targeting polypeptide; suppression; immune response; treatment;
KM autoimmune disease; allergy; immunological disorder;
KM transplant rejection.
XX Homo sapiens.
OS Homo sapiens.
XX MO9737687-A1.
PN MO9737687-A1.
PD 16-OCT-1997.
XX 16-OCT-1997.
PF 10-APR-1997; 97MO-US005943.
XX 10-APR-1997; 97MO-US005943.
PR 10-APR-1996; 96US-00630172.
XX 10-APR-1996; 96US-00630172.
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Staerz UD;
XX Staerz UD;
DR WPI; 1997-512419/47.
XX WPI; 1997-512419/47.
PT T lymphocyte veto molecule comprising response cell activating protein -
PT linked to molecule that targets stimulator cell marker, used for
PT selective suppression of immune response, e.g. prevention of graft
PT rejection or treatment of auto-immune disease.
XX T lymphocyte veto molecule comprising response cell activating protein -
PS Claim 37; Page 70-72; 309pp; English.
XX Claim 37; Page 70-72; 309pp; English.
XX A novel T lymphocyte veto molecule is a chimeric molecule comprising a
CC protein, e.g. the present sequence, linked to a targeting polypeptide
CC that binds a molecule, which differentiates a host cell from a tissue
CC graft cell, or selectively targets a stimulator cell involved in the
CC autoimmune response. A veto molecule, in which the protein binds a
CC molecule that targets stimulator cells, can be used to suppress an immune
CC response and therefore treat autoimmune diseases, e.g. systemic lupus
CC erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent
CC diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune
CC thyroiditis, Addison's or Grave's diseases and rheumatoid arthritis,
CC allergies and other immunological disorders. Where the protein binds a
CC molecule that differentiates graft and host cells, the veto molecule can
CC be used to reduce transplant rejection. The veto molecule provides
CC specific regulation of particular stimulator cells that can kill graft
CC cells or respond to autoantigens, but leave other stimulator cells
CC unaffected, e.g. CD4 or CD8 positive cells can be regulated without one
CC affecting the other. The veto molecule can be administered locally to
CC minimise generalised immunosuppression
XX minimise generalised immunosuppression
SQ Sequence 553 AA;
Query Match 100.0%; Score 51; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 3;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLILDVPPGV 10
DB 269 TLILDVPPGV 278
RESULT 5
ABU07335
ID ABU07335 standard; protein; 553 AA.
XX ABU07335;
AC ABU07335;
DT 29-JAN-2003 (first entry)
XX 29-JAN-2003 (first entry)
DE Human expressed protein tag (EPT) #2036.
XX Human expressed protein tag (EPT) #2036.
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
OS Homo sapiens.
XX MO200278524-A2.
PN MO200278524-A2.
PD 10-OCT-2002.
XX 10-OCT-2002.
PF 28-MAR-2002; 2002MO-US009671.
XX 28-MAR-2002; 2002MO-US009671.
PR 28-MAR-2001; 2001US-0279495P.
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
XX 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
XX 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
XX 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
XX 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX 20-FEB-2002; 2002US-0358985P.
PA (ZYCO-) ZYCO INC.
XX (ZYCO-) ZYCO INC.
PI Chicz RM, Tomlinson AJ, Urban RG;
XX Chicz RM, Tomlinson AJ, Urban RG;
DR WPI; 2003-040607/03.
XX WPI; 2003-040607/03.
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
PS Example 2; SEQ ID NO 2036; 134pp; English.
XX Example 2; SEQ ID NO 2036; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 553 AA;
Query Match 100.0%; Score 51; DB 6; Length 553;
Best Local Similarity 100.0%; Pred. No. 3;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPPGV 10
| | | | | | | | | |
XX 269 TLILDVPPGV 278

RESULT 6

AA023689 standard; protein; 641 AA.

AC AAM23689;

DT 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1214.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KM diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

XX Homo sapiens.

PN WO200154477-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US002687.

PR 25-JAN-2000; 2000US-00491404.

PR 17-JUL-2000; 2000US-00617746.

PR 03-SEP-2000; 2000US-00631451.

PR 15-SEP-2000; 2000US-0063870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.

DR N-PSDB; AAH98348.

XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use.

PS Claim 20; Page 875-876; 1275PP; English.

XX The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensic, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention

XX Sequence 641 AA;

Query Match 100.0%; Score 51; DB 4; Length 641;

Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPPGV 10
| | | | | | | | | |
DB 133 TLILDVPPGV 142

RESULT 7

AB007333 standard; protein; 641 AA.

AC ABO07333;

XX 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #2034.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KM protease; protease inhibitor; transporter; cytoskeletal protein;

KM receptor; transcription factor; cancer; MHC;

KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;

XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX Homo sapiens.

PN WO200278524-A2.

DT 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

PF 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicz RM, Tomlinson AJ, Urban RG,

PI WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

PT leukemia.

XX Example 2; SEQ ID NO 2034; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,

CC transporter, cytoskeletal protein, receptor or transcription factor. The

CC polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified

CC polypeptide. The purified polypeptide, or the antibody that binds to this

CC polypeptide, is useful for treating cancer. The polypeptide is also

CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing

CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukemia. These are also useful for screening agents for

CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 641 AA;

Query Match 100.0%; Score 51; DB 6; Length 641;

Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPPGV 10
| | | | | | | | | |
DB 133 TLILDVPPGV 142

RESULT 8

AA039262 standard; protein; 664 AA.

AC AAM39262;

XX 22-OCT-2001 (first entry)
XX
XX
DE Human polypeptide SEQ ID NO 2407.
XX
XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukemia.
XX Homo sapiens.
XX OS
XX WO200153312-A1.
XX PN
XX 26-JUL-2001.
XX PD
XX 26-DEC-2000; 2000WO-US034263.
XX PF
XX 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-0052317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX PA
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI Zhou F, Goodrich R, Dymnac KT;
XX
XX WPI; 2001-442253/47.
XX DR N-PSDB; AAI58418.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 2407; 10078pp; English.
XX PS
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA038642-AA042213) with nootropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX SQ Sequence 664 AA;

Query Match 100.0%; Score 51; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPGV 10
| | | | | | | | | |
| | | | | | | | | |
Db 133 TLILDVPGV 142

RESULT 9
ABU07334

ID ABU07334 standard; protein; 664 AA.
XX
XX AC ABU07334;
XX
XX 29-JAN-2003 (first entry)
XX DT
XX DE Human expressed protein tag (EPT) #2035.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX WO200278524-A2.
XX PN
XX 10-OCT-2002.
XX PD
XX 28-MAR-2002; 2002WO-US009671.
XX PF
XX 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX PA
XX Chicx RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX DR
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 2035; 134pp; English.
XX PS
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 664 AA;

Query Match 100.0%; Score 51; DB 6; Length 664;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPGV 10
| | | | | | | | | |
| | | | | | | | | |
Db 133 TLILDVPGV 142

RESULT 10
ABU05246

ID ABU05246 standard; protein; 1114 AA.
XX
AC ABU05246;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1912.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1912; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;
XX
Query Match 100.0%; Score 51; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
ABU05239

ID ABU05239 standard; protein; 1114 AA.
XX
AC ABU05239;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1905.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1905; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;
XX
Query Match 100.0%; Score 51; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
ABU05240

ID ABU05240 standard; protein; 1143 AA.
XX
AC ABU05240;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1906.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1906; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;
XX
Query Match 100.0%; Score 51; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPGV 10
|||
Db 131 TLILDVPGV 140

RESULT 13
ABU05245

ID ABU05245 standard; protein; 1143 AA.
XX
AC ABU05245;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1911.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1911; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;
XX
Query Match 100.0%; Score 51; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPGV 10
|||
Db 131 TLILDVPGV 140

RESULT 14
ADL16232

ID ADL16232 standard; protein; 1143 AA.
 AC ADL16232;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 XX
 DE Human protein tyrosine phosphatase #27.
 KW cytosolic; immunosuppressive; antiallergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signalling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003068984-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-EP001446.
 XX
 PR 13-FEB-2002; 2002US-0356810P.
 PR 12-FEB-2003; 2003US-00366547.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (CEPT-) CEPTYR INC.
 XX
 PI Tonks NK, Tzu-Ching M, Cool DE;
 PI WPI; 2003-712572/67.
 DR N-PSDB; ADL16231.
 XX
 PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 81; 238bp; English.
 XX
 CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (1)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulphydryl-reactive agent (iii) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
 CC dephosphorylation indicates that an active PTP is present. . No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 CC
 SQ Sequence 1143 AA;
 XX
 XX
 Query Match 100.0%; Score 51; DB 7; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLILDVPPGV 10
 |||||
 |||||
 DB 131 TLILDVPPGV 140
 |||||
 |||||
 RESULT 15
 ADQ18845
 ID ADQ18845 standard; protein; 1143 AA.
 XX

AC ADQ18845;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.
 XX
 KW soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038193.
 XX
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Ginsburg WM, Zlotnick A;
 PI WPI; 2004-441208/41.
 DR
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 PS Example 2; SEQ ID NO 1664; 210bp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytosolic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 CC
 SQ Sequence 1143 AA;
 XX
 XX
 Query Match 100.0%; Score 51; DB 8; Length 1143;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLILDVPPGV 10
 |||||
 |||||
 DB 131 TLILDVPPGV 140
 |||||
 |||||
 RESULT 16
 AAM41048
 ID AAM41048 standard; protein; 1149 AA.
 XX
 AC AAM41048;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 5979.
 XX
 KW Human; nocrotropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX

OS	Homo sapiens.
XX	
XX	WO200153312-A1.
XX	
XX	26-JUL-2001.
XX	
XX	26-DEC-2000; 2000WO-US034263.
PF	
XX	
XX	23-DEC-1999; 99US-00471275.
XX	21-JAN-2000; 2000US-00488725.
XX	25-APR-2000; 2000US-00552317.
XX	20-JUN-2000; 2000US-00598042.
XX	19-JUL-2000; 2000US-00620312.
XX	03-AUG-2000; 2000US-00653450.
XX	14-SEP-2000; 2000US-00662191.
XX	19-OCT-2000; 2000US-00693036.
XX	29-NOV-2000; 2000US-00727344.
XX	
XX	(HUSE-) HUSEQ INC.
XX	
XX	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Qa;
XX	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
XX	Zhou P, Goodrich R, Drmanac RT;
XX	
XX	WPI; 2001-442253/47.
XX	N-PSDB; AA160204.
XX	
XX	Novel nucleic acids and polypeptides, useful for treating disorders such
XX	as central nervous system injuries.
XX	
XX	Example 2; SEQ ID NO 5979; 10078bp; English.
XX	
XX	The invention relates to human nucleic acids (AA157798-AA161369) and the
XX	encoded polypeptides (AAW38642-AAW42213) with neurotrophic,
XX	immunosuppressant and cytostatic activity. The polynucleotides are useful
XX	in gene therapy. A composition containing a polypeptide or polynucleotide
XX	of the invention may be used to treat diseases of the peripheral nervous
XX	system, such as peripheral nervous injuries, peripheral neuropathy and
XX	localised neuropathies and central nervous system diseases, such as
XX	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX	utilisation of the activities such as: Immune system suppression,
XX	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX	assays for receptor activity, arthritis and inflammation, leukaemias and
XX	C.N.S disorders. Note: The sequence data for this patent did not form
XX	part of the printed specification
XX	
XX	Sequence 1149 AA;
XX	
XX	Query Match 100.0%; Score 51; DB 4; Length 1149;
XX	Best Local Similarity 100.0%; Pred. No. 6.5;
XX	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	
XX	1 TLIDVPGV 10
XX	
XX	136 TLIDVPGV 145
XX	
XX	RESULT 17
XX	ABU05242
XX	ID ABU05242 standard; protein; 1149 AA.
XX	XX
XX	ABU05242;
XX	
XX	29-JAN-2003 (first entry)
XX	
XX	Human expressed protein tag (EPT) #1908.
XX	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX	protease; protease inhibitor; transporter; cytoskeletal protein;
XX	receptor; transcription factor; cancer; MHC;
XX	major histocompatibility complex; myeloma; colon cancer; gastric cancer;

KM		adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX		
OS	Homo sapiens.	
XX		
PN	WO200278524-A2.	
XX		
PD	10-OCT-2002.	
XX		
PJ	28-MAR-2002; 2002WO-US009671.	
XX		
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX		
PA	(ZYCO-) ZYCOS INC.	
XX		
PI	Chicz RM, Tomlinson AJ, Urban RG;	
XX		
DR	WPI, 2003-040607/03.	
XX		
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
PT	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PS	leukemia.	
XX		
PS	Example 2; SEQ ID NO 1908; 134pp; English.	
XX		
CC	The invention describes a purified polypeptide, which comprises a	
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	
CC	mammal an immunogenic response directed against any of the purified	
CC	polypeptide. The purified polypeptide, or the antibody that binds to this	
CC	polypeptide, is useful for treating cancer. The polypeptide is also	
CC	useful for identifying compounds that binds to a naturally processed	
CC	class I or class II MHC-binding polypeptide. The polypeptides and	
CC	polynucleotides are particularly useful for treating or preventing	
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,	
CC	lymphoma or leukaemia. These are also useful for screening agents for	
CC	treating the above mentioned diseases. This sequence represents an	
CC	expressed protein tag (EPT) isolated from human tissue for translational	
CC	profiling. Note: This sequence does not appear in the printed	
CC	specification but was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 1149 AA;	
Query Match	100.0%; Score 51; DB 6; Length 1149;	
Best Local Similarity	100.0%; Prod. No. 6.5;	
Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 TLILDVPPGV 10 	
DB	136 TLILDVPPGV 145	
RESULT 18		
ID	ADR39747	
AD	ADR39747 standard; protein; 1192 AA.	
XX		
AC	ADR39747;	
XX		
DT	18-NOV-2004 (first entry)	
XX		
DE	Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.	
XX		
KW	human; kinase and phosphatase protein; KPP; enzyme; cytostatic;	
KW	antiartherosclerotic; anticonvulsant; nootropic; neuroprotective;	
KW	cerebroprotective; anti-HIV; antiallergic; antiinflammatory;	
KW	thyromimetic; gene therapy; cell proliferative disorder; cancer;	

CC The present sequence represents the human xanin kinase and phosphatase protein
CC (KXP), designated KXP-20. The human KXP sequences from the present
CC invention have cytosolic, antiarteriosclerotic, anticonvulsant,
CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thyromimetic activities, and can be used in gene
CC therapy. The human KXP proteins and polynucleotides can be used in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KXP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They can also be used in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KXP. The KXP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
XX Sequence 1192 AA;

```
Qy      1 TLILDVPPGV 10
         |||||
Db      180 TLILDVPPGV 189
```

RESULT 19	
ADQ39378	
ID	ADQ39378 standard; protein, 1219 AA.
XX	
XX	
AC	ADQ39378;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Human myocardial infarction-associated gene derived protein, SEQ ID 1041

PS Claim 10; SEQ ID NO 1041; 145pp; English.

CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

SQ Sequence 1219 AA;

Query Match	100.0%	Score 51;	DB 8;	Length 1219;
Best Local Similarity	100.0%	Pred. NO. 6.9;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY      1 TLILDVPPGV 10
          |||||
Db      207 TLILDVPPGV 216
```

RESULT	20
ADM67187	
ID	ADM67187 standard; protein; 1256 AA
XX	
AC	ADM67187;

XX 03-JUN-2004 (first entry)
DT Human adipocyte specific PTPase receptor type C protein Segid 541.
XX
DE human; adipocyte specific; adipose tissue; anti-obesity;
XX high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;
KM adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive; PTPase receptor type C.
XX
OS Homo sapiens.
XX
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
XX
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMG1-C) HMG1-C INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
PI WPI; 2004-143846/14.
DR N-PSDB; ADM66908.
DR
XX
XX Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
XX Disclosure, SEQ ID NO 541; 91pp; English.
XX
XX This invention relates to a novel method for identifying genes that are
XX over-expressed in adipose tissue and as such it provides targets for anti-
XX -obesity pharmaceutical compositions. Specifically, it refers to a high
XX mobility group I-C protein (HMG1-C) that is associated with obesity and
XX is epistatic to leptin, furthermore, it refers to the ob gene where an
XX autosomal recessive trait is linked to obesity and diabetes. The present
XX invention describes performing differential gene expression analysis
XX between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
XX of any two different mice selected from a group consisting of wild-type,
XX HMG1-C -/-, ob/ob, or HMG1-C -/-ob/ob genotype mice. Accordingly, using
XX this method novel nucleotides and the encoded proteins thereof were
XX identified that are adipocyte specific, and as such can be used for
XX preventing adipogenesis, diagnosing and treating diabetes, obesity,
XX hypertension and cardiovascular disease, as well as screening for
XX compounds that can modulate or prevent adipogenesis and treat diabetes or
XX obesity. These compositions exhibit anorectic, antidiabetic and
XX hypotensive activities. This polypeptide sequence is a human homologue of
XX a murine adipocyte specific protein sequence of the invention.
XX
SQ Sequence 1256 AA;
XX
XX
Query Match 100.0%; Score 51; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TLILDVPGV 10
DB 244 TLILDVPGV 253

DE Protein encoding reference mRNA sequence #51.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
XX Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
XX
PR 24-APR-2002; 2002US-00313831.
XX
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
PI WPI; 2004-400724/37.
DR
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 65; SEQ ID NO 2975; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprises detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX protein encoded by an mRNA sequence of the invention which show altered
XX expression in renal transplantation and expression.
XX
SQ Sequence 1256 AA;
XX
XX
Query Match 100.0%; Score 51; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TLILDVPGV 10
DB 244 TLILDVPGV 253

RESULT 22
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.
XX
XX ADQ39376;
XX
DT 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KM cardiac; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2004058052-A2.
XX
XX

PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003MO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 XX 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin J, Iakubova O;
 XX
 DR WPI: 2004-533949/51.
 DR N-PSDB; ADQ38548.
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1039; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1258 AA;
 Query Match 100.0%; Score 51; DB 8; Length 1258;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLILDVPGV 10
 DB 246 TLILDVPGV 255
 RESULT 23
 ADQ39379
 ID ADQ39379 standard; protein; 1267 AA.
 XX
 AC ADQ39379;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human.

XX
 OS Homo sapiens.
 XX
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003MO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 XX 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin J, Iakubova O;
 XX
 DR WPI: 2004-533949/51.
 DR N-PSDB; ADQ38551.
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1042; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1267 AA;
 Query Match 100.0%; Score 51; DB 8; Length 1267;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLILDVPGV 10
 DB 255 TLILDVPGV 264
 RESULT 24
 ABU05243
 ID ABU05243 standard; protein; 1304 AA.
 XX
 AC ABU05243;
 XX
 DT 29-JAN-2003 (first entry)

XX		Human expressed protein tag (EPT) #1909.
DE		
XX		
KW		Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM		protease; protease inhibitor; transporter; cytoskeletal protein;
KX		receptor; transcription factor; cancer; MHC;
KV		major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW		adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX		
OS	Homo sapiens.	
XX		
PN	WO200278524-A2.	
PD		
BD	10-OCT-2002.	
PF		
PE	28-MAR-2002; 2002WO-US009671.	
PR		
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
PA	(ZYCO-) ZYCOS INC.	
P1	Chicz RM, Tomlinson AJ, Urban RG;	
XX		
DR	WPI; 2003-040607/03.	
PT		
FT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
PT	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
XX	leukemia.	
PS		
XX		
Example 2; SEQ ID NO 1909; 134pp; English.		
XX		
CC	The invention describes a purified polypeptide, which comprises a	
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	
CC	mammal an immunogenic response directed against any of the purified	
CC	polypeptide. The purified polypeptide, or the antibody that binds to this	
CC	polypeptide, is useful for treating cancer. The polypeptide is also	
CC	useful for identifying compounds that binds to a naturally processed	
CC	class I or class II MHC-binding polypeptide. The polypeptides and	
CC	polynucleotides are particularly useful for treating or preventing	
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,	
CC	lymphoma or leukemia. These are also useful for screening agents for	
CC	treating the above mentioned diseases. This sequence represents an	
CC	expressed protein tag (EPT) isolated from human tissue for translational	
CC	profiling. Note: This sequence does not appear in the printed	
CC	specification but was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 1304 AA:	
Query Match	100.0%; Score 51; DB 6; Length 1304;	
Best Local Similarity	100.0%; Pred. No. 7.4;	
Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
OY	1 TLILDVPPGV 10 	
DB	292 TLILDVPPGV 301	
RESULT 25		
ID	ABU05241	
AC	ABU05241 standard; protein; 1304 AA.	
XX		
XX	ABU05241;	
XX		
DT	29-JAN-2003 (first entry)	

XX		Human expressed protein tag (EPT) #1907.
DE		
KX		
KM		Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KV		protease; protease inhibitor; transporter; cytoskeletal protein;
KW		receptor; transcription factor; cancer; MHC;
KM		major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KN		adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XK		
OS	Homo sapiens.	
XX		
PJ	WO200278524-A2.	
PD		
EP	10-OCT-2002.	
PF		
PR	28-MAR-2002; 2002WO-US009671.	
PP		
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
PA	(ZYCO-) ZYCOS INC.	
PI	Chicz RM, Tomlinson AJ, Urban RG;	
DR	WPI; 2003-040607/03.	
XX		
PS	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
PT	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PT	leukemia.	
XX		
PS	Example 2; SEQ ID NO 1907; 134pp; English.	
CC	The invention describes a purified polypeptide, which comprises a	
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	
CC	mammal an immunogenic response directed against any of the purified	
CC	polypeptide. The purified polypeptide, or the antibody that binds to this	
CC	polypeptide, is useful for treating cancer. The polypeptide is also	
CC	useful for identifying compounds that bind to a naturally processed	
CC	class I or class II MHC-binding polypeptide. The polypeptides and	
CC	polynucleotides are particularly useful for treating or preventing	
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,	
CC	lymphoma or leukemia. These are also useful for screening agents for	
CC	treating the above mentioned diseases. This sequence represents an	
CC	expressed protein tag (EPT) isolated from human tissue for translational	
CC	profiling. Note: This sequence does not appear in the printed	
CC	specification but was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
SQ	Sequence 1304 AA:	
OY	Query Match	100.0%; Score 51; DB 6; Length 1304;
ID	Best Local Similarity	100.0%; Pred. No. 7.4;
MATCHES	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
DB	1 TLIDVPVG 10 	
	292 TLIIDVPEGV 301	
RESULT 26		
ABU05244		
ID	ABU05244 standard; protein; 1304 AA.	
AC	ABU05244;	
JT	29-JAN-2003 (first entry)	

XX DE Human expressed protein tag (EPT) #1910.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS Homo sapiens.
PN WO200278524-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCO INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX Example 2; SEQ ID NO 1910; 134bp; English.
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1304 AA;
Query Match 100.0%; Score 51; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLILDVPGV 10
DB 292 TLILDVPGV 301

RESULT 27
ADL16230
ID ADL16230 standard; protein; 1304 AA.
AC ADL16230;
XX 06-MAY-2004 (first entry)
DT XX

XX DE Human protein tyrosine phosphatase #26.
XX KW cytosolic; immunosuppressive; antiallergic;
XX KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
XX KW inducible signalling pathway; cell proliferation; cancer;
XX KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX KW cell-cycle abnormality; enzyme.
OS Homo sapiens.
PN WO2003068984-A2.
XX 21-AUG-2003.
XX 13-FEB-2003; 2003WO-EP001446.
XX 13-FEB-2002; 2002US-0356810P.
XX 12-FEB-2003; 2003US-0036547.
XX (COLD-) COLD SPRING HARBOR LAB.
XX (CEPT-) CEPTIR INC.
XX PA Tonks NK, Tzu-Ching M, Cool DE;
XX PI WPI; 2003-712572/67.
XX DR N-PSDB; ADL16229.
XX PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX PT screening for specific modulators, potential agents for treating e.g.
XX PT cancer or autoimmune disease.
XX PS Disclosure; SEQ ID NO 79; 238bp; English.
XX The invention relates to a method for identifying a protein tyrosine
XX phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX subjecting a sample, including a cell that contains at least one PTP, to
XX conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX anaerobically, in presence of a sulfhydryl-reactive agent (II) that
XX irreversibly modifies the thiol group of an invariant Cys in the active
XX site of PTP; and (iii) determining, under reducing conditions, the level
XX of dephosphorylation, caused by PTP, of a labeled substrate (III), where
XX dephosphorylation indicates that an active PTP is present. No details
XX of tests for these activities are given. The method is used to identify
XX reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX are involved. These agents are potentially useful, in human or veterinary
XX medicine, for treating abnormal cell proliferation or growth (cancer);
XX guest vs. host disease; autoimmune diseases; allergy or other
XX immunosuppressed states; metabolic disorders and cell-cycle
XX abnormalities. This sequence represents one of the PTP enzyme of the
XX invention.
SQ Sequence 1304 AA;
Query Match 100.0%; Score 51; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TLILDVPGV 10
DB 292 TLILDVPGV 301

RESULT 28
ADP65158
ID ADP65158 standard; protein; 1304 AA.
AC ADP65158;
XX 12-AUG-2004 (first entry)
DT XX Human protein tyrosine phosphatase, receptor type, C, isoform 1.
DE XX

XX autoimmune disease; arthritis; gene expression analysis;
KM rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KM antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;
KM immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KM fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KM immune; human.
XX Homo sapiens.
OS
PN WO2003072827-A1.
XX
PD 04-SEP-2003.
XX
PF 31-OCT-2002; 2002WO-US035433.
XX
PR 31-OCT-2001; 2001US-0336220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thornton SL,
XX
DR WPI; 2003-712740/67.
XX
DR GENBANK; NP_002829.
XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
XX
PS Disclosure; Page; 56pp; English.
XX
CC The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritis, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
SQ Sequence 1304 AA;
XX
XX
Query Match 100.0%; Score 51; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TLILDVPPGV 10
Db 292 TLILDVPPGV 301

RESULT 29
ADM67209
ID ADM67209 standard; protein; 1304 AA.

XX
AC ADM67209;
XX
DT 03-JUN-2004 (first entry)
XX
XX Human adipocyte specific leukocyte common antigen protein Segid 563.
DE
XX
XX human; adipocyte specific; adipose tissue; anti-obesity;
KM high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KM adipogenesis; hypertension; cardiovascular disease; anorectic;
KM antidiabetic; hypotensive; leukocyte common antigen.
XX
XX Homo sapiens.
OS
PN WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
XX
PR 12-JUN-2003; 2003US-0478206P.
XX
PA (HMGCR-) HMGCR INC.
XX
PI Chada K, Chouinard R, Ashar H, Sayed AMD;
XX
DR WPI; 2004-143846/14.
XX
DR N-PSDB; ADM66930.
XX
XX
PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
XX
PS Disclosure; SEQ ID NO 563; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of
CC a murine adipocyte specific protein sequence of the invention.
XX
XX
SQ Sequence 1304 AA;
XX
XX
Query Match 100.0%; Score 51; DB 8; Length 1304;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TLILDVPPGV 10
Db 292 TLILDVPPGV 301

RESULT 30
AB084455
ID AB084455 standard; protein; 1304 AA.
XX
AC AB084455;
XX

DT 18-NOV-2004 (first entry)
 XX Human cancer-associated protein HP13-011.2.
 DE Human; cancer-associated protein; cytosolic; cancer; leukaemia;
 KW Lymphoma; CAP.
 XX Homo sapiens.
 OS
 XX WO2004074320-A2.
 PN
 XX 02-SEP-2004.
 PD
 XX 17-FEB-2004; 2004WO-US004730.
 PF
 XX 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Morrie DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABD32626.
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 XX claim 18; seqid 147; 310pp; English.
 PS
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 1304 AA;
 Query Match 100.0%; Score 51; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLILDVPGV 10
 DB 292 TLILDVPGV 301
 RESULT 31
 ADQ39380
 ID ADQ39380 standard; protein; 1304 AA.
 XX
 XX ADQ39380;
 AC
 XX
 DT 18-NOV-2004 (first entry)
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiac; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004058052-A2.
 PD
 XX 15-JUL-2004.
 PD
 XX 22-DEC-2003; 2003WO-US040978.
 PF
 XX 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JT, Iakoubova O;
 XX
 DR WPI; 2004-533949/51.
 DR N-PSDB; ADQ38552.
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 XX Claim 10; SEQ ID NO 1043; 145pp; English.
 PS
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiac activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.

SQ Sequence 1304 AA;
 Query Match 100.0%; Score 51; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLILDVPPGV 10
 |||||
 DB 292 TLILDVPPGV 301
 RESULT 32
 ADQ39375
 ID ADQ39375 standard; protein; 1306 AA.
 XX
 AC ADQ39375;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
 XX
 KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KM cardiant; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Gargill M, Devlin JJ, Iakubova O;
 XX
 DR WPI; 2004-533949/51.
 DR N-PSDB; ADQ38547.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1038; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1306 AA;
 Query Match 100.0%; Score 51; DB 8; Length 1306;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLILDVPPGV 10
 |||||
 DB 294 TLILDVPPGV 303
 Search completed: May 3, 2005, 07:36:40
 Job time : 76 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:31:22 ; Search time 48 seconds
(without alignments)
72.518 Million cell updates/sec

Title: US-10-003-983C-9

Perfect score: 46

Sequence: 1 LILDVPPGV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	5 ABG31979	Abg31979 Human CD4
2	46	100.0	10	5 ABG31980	Abg31980 Human CD4
3	46	100.0	19	2 AAR26823	Aar26823 Cell adhe
4	46	100.0	20	2 AAR30900	Aar30900 Cell adhe
5	46	100.0	553	2 AAW35856	Aaw35856 Human CD4
6	46	100.0	553	6 ABU07335	Abu07335 Human exp
7	46	100.0	641	4 AAM23689	Aam23689 Human EST
8	46	100.0	641	6 ABU07333	Abu07333 Human exp
9	46	100.0	664	4 AAM39282	Aam39282 Human pro
10	46	100.0	664	6 ABU07334	Abu07334 Human exp
11	46	100.0	1114	6 ABU05246	Abu05246 Human exp
12	46	100.0	1114	6 ABU05239	Abu05239 Human exp
13	46	100.0	1143	6 ABU05240	Abu05240 Human exp
14	46	100.0	1143	6 ABU05245	Abu05245 Human exp
15	46	100.0	1143	7 ADI16232	Adi16232 Human pro
16	46	100.0	1143	8 ADQ18845	Adq18845 Human sot
17	46	100.0	1149	6 AAM41048	Aam41048 Human pol
18	46	100.0	1149	6 ABU05242	Abu05242 Human exp
19	46	100.0	1192	8 ADR39747	Adr39747 Human kin
20	46	100.0	1219	8 ADQ39378	Adq39378 Human myo
21	46	100.0	1256	8 ADM67187	Adm67187 Human adi
22	46	100.0	1256	8 ADP12966	Adp12966 Protein e
23	46	100.0	1258	8 ADQ39376	Adq39376 Human myo
24	46	100.0	1267	8 ADQ39379	Adq39379 Human myo
25	46	100.0	1304	6 ABU05243	Abu05243 Human exp

26	46	100.0	1304	6 ABU05241	Abu05241 Human exp
27	46	100.0	1304	6 ABU05244	Abu05244 Human exp
28	46	100.0	1304	7 ADI16230	Adi16230 Human pro
29	46	100.0	1304	7 ADP65158	Adp65158 Human pro
30	46	100.0	1304	8 ADM67209	Adm67209 Human adi
31	46	100.0	1304	8 AB084455	Ab084455 Human can
32	46	100.0	1304	8 ADQ39380	Adq39380 Human myo
33	46	100.0	1306	8 ADQ39375	Adq39375 Human myo
34	46	100.0	140	4 AAM59723	Aam59723 Prolionib
35	41	89.1	140	6 AAM56242	Am56242 Prolionib
36	39	84.8	354	6 ABM73414	Abm73414 Staphyloc
37	38	84.8	354	7 ABR62803	AbR62803 Methicill
38	38	82.6	243	4 AAB36190	Aab36190 Putative
39	38	82.6	257	6 ABU38869	Abu38869 Protein e
40	38	82.6	381	7 AB061639	Ab061639 Kiebsell
41	37	80.4	248	8 ADN47276	Adn47276 Thermococ
42	37	80.4	266	3 AAG48634	Aag48634 Arabidops
43	37	80.4	266	3 AAG08777	Aag08777 Arabidops
44	37	80.4	270	7 AB072309	Ab072309 Pseudomon
45	37	80.4	282	5 AAM50930	Aam50930 Arabidops

ALIGNMENTS

RESULT 1	ABG31979	standard, peptide, 9 AA.
ID	ABG31979	
XX	AC	ABG31979;
XX	DT	05-NOV-2002 (first entry)
DE	Human CD45 HLA-binding peptide, huCD45/293.	
XX	Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;	
KW	antigen-presenting cell; APC; major histocompatibility complex; MHC;	
KW	antigen; allogenic; T cell receptor; TCR; cancer; tumour;	
KW	allogenic stem cell transplantation; CFU-GM; leukaemia;	
KW	colony forming unit-granulocyte macrophage; immunotherapeutic;	
KW	haematopoietic; malignant.	
OS	Homo sapiens.	
XX	WO200244207-A1.	
XX	PD	06-JUN-2002.
XX	PF	30-NOV-2000; 2000MO-GB004566.
XX	PR	30-NOV-2000; 2000MO-GB004566.
XX	PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX	PI	Staus HJ, Amrolia PJ;
XX	DR	WPI, 2002-599413/64.
XX	PT	Novel peptide comprising leukocyte antigen binding peptide of human CD45
XX	PT	polypeptide, useful for producing activated cytotoxic T lymphocytes, for
XX	PT	killing cancerous cells e.g. leukemia.
XX	PS	Claim 2; Page 38; 56pp; English.
XX	XX	The invention discloses a peptide comprising the human leukocyte antigen
XX	XX	(HLA)-binding peptide of human CD45 polypeptide, its portion or variant,
XX	XX	provided that the peptide is not the intact human CD45 polypeptide. The
XX	XX	peptides are useful for producing activated cytotoxic T lymphocyte (CTL)
XX	XX	in vitro which involves contacting the CTL with an antigen-presenting
XX	XX	cell, where its major histocompatibility complex (MHC) class I molecules
XX	XX	are loaded with the peptide, to activate, in an antigen specific manner,
XX	XX	where the CTL and the antigen presenting cell are allogenic with respect
XX	XX	to the class I MHC molecule that is presenting peptides of CD45. The

CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR),
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animals models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/293,
CC comprising an HLA-binding peptide of human CD45
CC
CC
SQ Sequence 9 AA;

Query Match 100.0%; Score 46; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LILDVPGV 9
Db 1 LILDVPGV 9

RESULT 2
ABG31980
ID ABG31980 standard; peptide; 10 AA.

AC ABG31980;

DT 05-NOV-2002 (first entry)

DE Human CD45 HLA-binding peptide, huCD45/292.

XX Human, CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;
KW antigen-presenting cell; APC; major histocompatibility complex; MHC;
KW antigen; allogeneic; T cell receptor; TCR; cancer; tumour;
KW allogeneic stem cell transplantation; CFU-GM; leukaemia;
KW colony forming unit-granulocyte macrophage; immunotherapeutic;
KW haematopoietic; malignant.

XX Homo sapiens.

XX WO200244207-A1.

PD 06-JUN-2002.

PF 30-NOV-2000; 2000WO-GB004566.

PR 30-NOV-2000; 2000WO-GB004566.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Stausas HJ, Amrolia PJ;

DR WPI; 2002-599413/64.

XX Novel peptide comprising leukocyte antigen binding peptide of human CD45
PT polypeptide, useful for producing activated cytotoxic T lymphocytes, for
PT killing cancerous cells e.g. leukemia.

XX Claim 2; Page 38; 56pp; English.

XX The invention discloses a peptide comprising the human leukocyte antigen
CC (HLA)-binding peptide of human CD45 polypeptide, its portion or variant,
CC provided that the peptide is not the intact human CD45 polypeptide. The
CC peptides are useful for producing activated cytotoxic T lymphocyte (CTL)

CC in vitro which involves contacting the CTL with an antigen-presenting
CC cell, where its major histocompatibility complex (MHC) class I molecules
CC are loaded with the peptide, to activate, in an antigen specific manner,
CC where the CTL and the antigen presenting cell are allogeneic with respect
CC to the class I MHC molecule that is presenting peptides of CD45. The
CC antigen-presenting cell contains an expression vector including the
CC polynucleotides encoding the CD45 peptides. The activated CTLs are useful
CC for killing, and in the manufacture of a medicament for, target cells
CC expressing the CD45 peptides in a patient. A T cell receptor (TCR)
CC recognising cells expressing the CD45 peptides, is useful for killing
CC target cells (cancer cells) in a patient which involves obtaining CTLs
CC from the patient, introducing into the CTLs the polynucleotide encoding
CC the TCR and then introducing the cells thus produced into the patient who
CC has undergone an allogeneic stem cell transplantation. Tumour reactive
CC CTLs have been shown to mediate tumour regression in animals models by
CC the inhibition of colony forming unit-granulocyte macrophage (CFU-GM)
CC colony formation. The cancer is leukaemia which expresses the CD45
CC polypeptide. The method is useful as an immunotherapeutic for treating a
CC patient with haematopoietic malignancy or to target and kill cells which
CC express the CD45 polypeptide. The advantage this method provides is that
CC the CTLs destroy the malignant haematopoietic cells but not the
CC transplanted cells. The sequence presented is the peptide, huCD45/292,
CC comprising an HLA-binding peptide of human CD45
CC
CC
SQ Sequence 10 AA;

Query Match 100.0%; Score 46; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LILDVPGV 9
Db 2 LILDVPGV 10

RESULT 3
AAR26823
ID AAR26823 standard; peptide; 19 AA.

AC AAR26823;

DT 25-MAR-2003 (revised)

DT 09-FEB-1993 (first entry)

DE Cell adhesion polypeptide.

XX MOLF-4; human; lymphoblastic leukaemia; A375-SM; metastatic; melanoma;
KW H1080; fibrosarcoma; LDV; LDL; IDA; inflammatory disease;
KW rheumatoid arthritis; asthma; sepsis; graft rejection; reperfusion.

XX Synthetic.

XX WO9213887-A1

PD 20-AUG-1992.

PF 06-FEB-1992; 92WO-GB000226.

PR 07-FEB-1991; 91GB-00002655.

XX 08-FEB-1991; 91GB-00002818.

XX (UMMA-) UNIV VICTORIA MANCHESTER.

XX Humphries MJ;

DR WPI; 1992-299988/36.

XX New cell adhesion (poly)peptide(s) modifying cell adhesive properties -
PT useful in treating inflammatory conditions e.g. rheumatoid arthritis,
PT asthma, inflammatory bowel disease, sepsis, etc.

XX Disclosure; Page 4; 23pp; English.

The peptide is an example of a cell adhesion polypeptide contg. the amino acid sequence X-Asp-Y-(A)-n-Phe, where X and Y = Ala, Leu, Ile or Val, A= any amino acid and n= 3-10. At least a subsequence of the polypeptide is adherent for MOLT-4 human lymphoblastic leukaemia, A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells. The cell adhesion peptides are used to modify or control the adhesive properties of cells, e.g. in treatment of inflammatory conditions such as Rheumatoid arthritis, asthma, sepsis, graft rejection, inflammatory bowel disease, reperfusion of cardiac tissue after Myocardial infarction, and coagulatory disorders. They are selective antagonists of cell adhesion, e.g. they promote adhesion of the specified cells but inhibit adhesion to the natural adhesion protein concg. the adhesive sequence. See also PAR26621-30 and PAR30887-903. (updated on 25-MAR-2003 to correct FN field.)

Sequence 19 AA;

Query Match	100.0%	Score 46	DB 2	Length 19
Best Local Similarity	100.0%	Pred. NO	0.56	
Matches	9	Conservative	0	Mismatches 0; Indels 0; Gaps 0

QY	1 LILDVPPGV 9
Db	6 LILDVPPGV 14

RESULT 4
AAR30900
ID AAR30900 standard; peptide; 20 AA

AC	AAR30900;	
XX		
DT	25-MAR-2003	(revised)
DT	09-FEB-1993	(first entry)

Cell adhesion polypeptide CD45.

KW MOLT-4; human, lymphoblastic leukaemia; A375-SM; metastatic; melanoma
KW H1080; fibrosarcoma; LDV; LDL; IDA; inflammatory disease;
KW rheumatoid arthritis; ascemia; sepsis; graft rejection; reperfusion.

OS Synthetic.

PN MO9213887-A1.

PD 20-AUG-1992

PF 06-FEB-1992; 92WO-GB000226

PR 07-FEB-1991; 91GB-00002655

PR 08-FEB-1991; 91GB-00002818

PA (UYMA-) UNIV VICTORIA MANCHESTER

PI Humphries MJ;

DR WPI; 1992-299988/36.

PT New cell adhesion (poly)peptide(s) modifying cell adhesive properties -
PT useful in treating inflammatory conditions e.g. rheumatoid arthritis,
PT asthma, inflammatory bowel disease, sepsis, etc.

PS Disclosure; Page 11; 23pp; English

The peptide is a cell adhesion polypeptide contg. the amino acid sequence X-Asp-Y-(A)n-Phe where X and Y = Ala, Leu, Ile or Val, A = any amino acid and n = 3-10. At least a subsequence of the polypeptide is adherent for MOLT-4 human lymphoblastic leukaemia, A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells. The cell adhesion peptides are used to modify or control the adhesive properties of cells, e.g. in treatment of inflammatory conditions such as Rheumatoid arthritis, asthma, sepsis, graft rejection, inflammatory bowel disease, reperfusion of cardiac tissue after myocardial infarction, and

CC conjugatory disorders. They are selective antagonists of cell adhesion,
e.g. they promote adhesion of the specified cells but inhibit adhesion
CC to the natural adhesion protein contg. the adhesive sequence. See also
CC AA226821-30 and AA300867-903. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
Sequence 20 AA;

Query Match	100.0%	Score 46	DB 2	Length 20
Best Local Similarity	100.0%	Pred. No. 0.59		
Matches 9	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	LILDVPEGV	9
Db	7	LILDVPEGV	15

RESULT 5
AAW35856
ID AAW35856 standard; protein; 553 AA

AC	AAW35856;
XX	
DT	27-APR-1998 (first entry)

DE Human CD45 for use in T lymphocyte veto molecule

KM Human; CD45, T lymphocyte veto molecule; chimeric molecule;
 KM targeting polypeptide; suppression; immune response; treatment;
 KM autoimmune disease; allergy; immunological disorder;
 KM transplant rejection.

OS Homo sapiens

PN WO9737687-A1

PD 16-OCT-1997.

PF 10-APR-1997; 97WO-US005943

PR 10-APR-1996; 96US-00630172

PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY

PI Staerz UD

DR WPI; 1997-512419/47

PT T lymphocyte veto molecule comprising response cell activating protein -
PT linked to molecule that targets stimulator cell marker, used for
PT selective suppression of immune response, e.g. prevention of graft
PT rejection or treatment of auto-immune disease.

PS Claim 37; Page 70-72; 309pp; English

A novel lymphocyte veto molecule is a chimeric molecule comprising a protein, e.g. the present sequence, linked to a targeting polypeptide that binds a molecule, which differentiates a host cell from a tissue graft cell, or selectively targets a stimulator cell involved in the autoimmune response. A veto molecule, in which the protein binds a molecule that targets stimulator cells, can be used to suppress an immune response and therefore treat autoimmune diseases, e.g. systemic lupus erythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune thyroiditis, Addison's or Grave's diseases and rheumatoid carditis, allergies and other immunological disorders. Where the protein binds a molecule that differentiates graft and host cells, the veto molecule can be used to reduce transplant rejection. The veto molecule provides specific regulation of particular stimulator cells that can kill graft cells or respond to autoantigens, but leave other stimulator cells unaffected, e.g. CD4 or CD8 positive cells can be regulated without one affecting the other. The veto molecule can be administered locally to minimise generalised immunosuppression

SO	Sequence	553 AA;	100.0%;	Score 46;	DB 2;	Length 553;	
Query Match			100.0%;	Pred. No. 18;			
Best Local Similarity			100.0%;				
Matches	9;	Conservative	0;	Mismatches	0;	Indels	0
OY	1	LILDVPGV	9				
Db	270	LILDVPGV	278				
RESULT 6							
ID	ABU07335	standard; protein;	553 AA.				
AC	ABU07335;						
XX							
DT	29-JAN-2003	(first entry)					
DE		Human expressed protein tag (EPT) #2036.					
XX							
KW		Translational profiling; expressed protein tag; EPT; kinase; phosphatase;					
KW		protease; protease inhibitor; transporter; cytoskeletal protein;					
KW		receptor; transcription factor; cancer; MHC;					
KW		major histocompatibility complex; myeloma; colon cancer; gastric cancer;					
KW		adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.					
OS		Homo sapiens.					
XX							
PN	WO200278524-A2.						
PD	10-OCT-2002.						
PF	28-MAR-2002; 2002WO-US009671.						
PR	28-MAR-2001; 2001US-0279495P.						
PR	21-MAY-2001; 2001US-0292544P.						
PR	08-AUG-2001; 2001US-0310801P.						
PR	04-OCT-2001; 2001US-0326370P.						
PR	01-DEC-2001; 2001US-0336780P.						
PR	20-FEB-2002; 2002US-0358985P.						
PA	(ZYCO-) ZYCOs INC.						
PI	Chicz RM, Tomlinson AJ, Urban RG;						
XX							
DR	WPI, 2003-040607/03.						
XX							
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,						
PT	cytoskeletal proteins, receptors or transcription factors), useful for						
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or						
PT	leukemia.						
XX							
XX	Example 2, SEQ ID NO 2036; 134pp; English.						
XX							
CC	The invention describes a purified polypeptide, which comprises a						
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,						
CC	transporter, cytoskeletal protein, receptor or transcription factor. The						
CC	polypeptide is useful as an immunogenic composition for eliciting in a						
CC	mammal an immunogenic response directed against any of the purified						
CC	polypeptide. The purified polypeptide, or the antibody that binds to this						
CC	polypeptide, is useful for treating cancer. The polypeptide is also						
CC	useful for identifying compounds that binds to a naturally processed						
CC	class I or class II MHC-binding polypeptide. The polypeptides and						
CC	polynucleotides are particularly useful for treating or preventing						
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,						
CC	lymphoma or leukaemia. These are also useful for screening agents for						
CC	treating the above mentioned diseases. This sequence represents an						
CC	expressed protein tag (EPT) isolated from human tissue for translational						
CC	profiling. Note: This sequence does not appear in the printed						
CC	specification but was obtained in electronic format directly from WIPO at						
CC	ftp.wipo.int/pub/published_pct_sequences						

Query Match	Best Local Similarity	Score	DB	Length	553;
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1 LILDVPPGV 9	270 LILDVPPGV 278				
<p>RESULT 7</p> <p>AA023689</p> <p>AA023689 standard; protein; 641 AA.</p> <p>AA023689;</p> <p>12-OCT-2001 (first entry)</p> <p>Human EST encoded protein SEQ ID NO: 1214.</p> <p>Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.</p> <p>Homo sapiens.</p> <p>WO200154477-A2.</p> <p>02-AUG-2001.</p> <p>25-JAN-2001; 2001WO-US002687.</p> <p>25-JAN-2000; 2000US-00491404.</p> <p>17-JUL-2000; 2000US-00617746.</p> <p>03-AUG-2000; 2000US-00631451.</p> <p>15-SEP-2000; 2000US-00663870.</p> <p>(HYSE-) HYSEQ INC.</p> <p>Tang Y, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V; Cao Y, Dmanac RA, Zhang J, Werhman T; MPI; 2001-476164/51.</p> <p>N-PSDB; AA098348.</p> <p>Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.</p> <p>Claim 20; Page 875-876; 1275pp; English.</p> <p>The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention</p> <p>Sequence 641 AA;</p> <p>Query Match 100.0%; Score 46; DB 4; Length 641;</p> <p>Best Local Similarity 100.0%; Pred. No. 21;</p> <p>Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>1 LILDVPPGV 9</p> <p>270 LILDVPPGV 278</p>					

```
RESULT 8
ABU07333
ID ABU07333 standard; protein; 641 AA.
XX
AC ABU07333;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2034.
XX
KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protein inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MEC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCO INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2034; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 641 AA;
XX
Query Match 100.0%; Score 46; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 9
AAM39262
ID AAM39262 standard; protein; 664 AA.
XX
AC AAM39262;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2407.
XX
KM Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KM leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Dymnac RT;
XX
DR WPI; 2001-442253/47.
XX
DR N-PSDB; AAI58418.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2407; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 664 AA;
XX
Query Match 100.0%; Score 46; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

DB 134 LILDVPGV 142

RESULT 10
ABU07334
ID ABU07334 standard; protein; 664 AA.
XX
XX ABU07334;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #2035.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW processase; process inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX Homo sapiens.
OS
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 2035; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 664 AA;
SQ

Query Match 100.0%; Score 46; DB 6; Length 664;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LILDVPGV 9
|||||

DB 134 LILDVPGV 142

RESULT 11
ABU05246
ID ABU05246 standard; protein; 1114 AA.
XX
XX ABU05246;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1912.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW processase; process inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX Homo sapiens.
OS
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1912; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1114 AA;
SQ

Query Match 100.0%; Score 46; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LILDVPGV 9
|||||

Db 103 LILDVPGV 111

RESULT 12
ABU05239
ID ABU05239 standard; protein; 1114 AA.
XX
XX AC ABU05239;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1905.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1905; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1114 AA;

Query Match 100.0%; Score 46; DB 6; Length 1114;

Best Local Similarity 100.0%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPGV 9
|||||||

Db 103 LILDVPGV 111

RESULT 13
ABU05240
ID ABU05240 standard; protein; 1143 AA.
XX
XX AC ABU05240;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1906.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN MO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1906; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1143 AA;

Query Match 100.0%; Score 46; DB 6; Length 1143;

Best Local Similarity 100.0%; Pred. No. 38; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPGV 9
|||||||

Db 132 LILDVPGV 140

RESULT 14

ABU05245 ID ABU05245 standard; protein; 1143 AA.

AC ABU05245;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1911.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX processase; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCOS INC.

PI Chicz RM, Tomlinson AJ, Urban RG;

DR MPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

PS Example 2; SEQ ID NO 1911; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1143 AA;

Query Match 100.0%; Score 46; DB 6; Length 1143;

Best Local Similarity 100.0%; Pred. No. 38; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LILDVPGV 9

|||||

Db 132 LILDVPGV 140

RESULT 15

ADL16232 ID ADL16232 standard; protein; 1143 AA.

AC ADL16232;

DT 06-MAY-2004 (first entry)

DE Human protein tyrosine phosphatase #27.

XX cytosolic; immunosuppressive; antiallergic;
XX protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
XX inducible signalling pathway; cell proliferation; cancer;
XX guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX cell-cycle abnormality; enzyme.

OS Homo sapiens.

PN WO2003068984-A2.

PD 21-AUG-2003.

PF 13-FEB-2003; 2003WO-EP001446.

PR 13-FEB-2002; 2002US-0356810P.

PR 12-FEB-2003; 2003US-0036547.

PR (COLD-) COLD SPRING HARBOR LAB.

PA (CEPT-) CEPTYR INC.

PI Tonks NK, Tzu-Ching M, Cool DE;

DR MPI; 2003-712572/67.

DR N-PSDB; ADL16231.

XX Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX screening for specific modulators, potential agents for treating e.g.
XX cancer or autoimmune disease.

PS Disclosure; SEQ ID NO 81; 238pp; English.

XX The invention relates to a method for identifying a protein tyrosine
XX phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
XX subjecting a sample, including a cell that contains at least one PTP, to
XX conditions that cause reversible oxidation of PTP; (ii) isolating PTP
XX anaerobically, in presence of a sulphydryl-reactive agent (II) that
XX irreversibly modifies the thiol group of an invariant Cys in the active
XX site of PTP; and (iii) determining, under reducing conditions, the level
XX of dephosphorylation, caused by PTP, of a labelled substrate (III), where
XX dephosphorylation indicates that an active PTP is present. . No details
XX of tests for these activities are given. The method is used to identify
XX reversibly oxidized PTP, also to identify agents that: (a) reversibly
XX modify such PTP; or (b) alter inducible signalling pathways in which PTP
XX are involved. These agents are potentially useful, in human or veterinary
XX medicine, for treating abnormal cell proliferation or growth (cancer);
XX guest vs. host disease; autoimmune diseases; allergy or other
XX abnormalities. This sequence represents one of the PTP enzyme of the
XX invention.

SQ Sequence 1143 AA;

Query Match 100.0%; Score 46; DB 7; Length 1143;

Best Local Similarity 100.0%; Pred. No. 38; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LILDVPGV 9

|||||

Db 132 LILDVPGV 140

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0356985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DR MPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1908; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide, is useful for treating cancer. The polypeptide binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1149 AA;
 XX
 QY Query Match 100.0%; Score 46; DB 6; Length 1149;
 DB Best Local Similarity 100.0%; Pred. No. 38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 LILDVPGV 9
 |||||
 137 LILDVPGV 145
 |||||
 RESULT 19
 ID ADR39747 standard; protein; 1192 AA.
 XX ADR39747;
 AC ADR39747;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.

XX human; kinase and phosphatase protein; KPP; enzyme; cytostatic;
 KW antihistaminic; anticonvulsant; neurotropic; neuroprotective;
 KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
 KW thymomimetic; gene therapy; cell proliferative disorder; cancer;
 KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
 KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
 KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
 KW KPP-20.
 XX
 OS Homo sapiens.
 PN WO2004074453-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 20-FEB-2004; 2004WO-US005092.
 XX
 PR 20-FEB-2003; 2003US-0449059P.
 PR 19-MAR-2003; 2003US-0456932P.
 PR 28-MAR-2003; 2003US-0458844P.
 PR 09-APR-2003; 2003US-0461678P.
 PR 17-APR-2003; 2003US-0463937P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Rankumar J, Margis JP, Swarnakar A, Chawla NK, Tran UK;
 PI Becha SD, Lee SY, Hafalla AJA, Richardson TW, Khare R, Jiang X;
 PI Jackson AA, Yang J, Gorvad AE;
 XX
 DR MPI; 2004-635568/61.
 DR N-PSDB; ADR39793.
 XX
 PT New human kinases and phosphatases (KPP) for diagnosing, treating and
 PT preventing diseases or conditions associated with aberrant KPP expression
 PT e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
 XX
 PS Claim 1; SEQ ID NO 20; 299pp; English.
 XX
 CC The present sequence represents the human kinase and phosphatase protein
 CC (KPP), designated KPP-20. The human KPP sequences from the present
 CC invention have cytostatic, antihistaminic, anticonvulsant,
 CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
 CC antiinflammatory and thymomimetic activities, and can be used in gene
 CC therapy. The human KPP proteins and polynucleotides can be used in
 CC diagnosing, treating and preventing diseases or conditions associated
 CC with the decreased expression or overexpression of KPP, such as cell
 CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
 CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
 CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
 CC disorders, or infections. They can also be used in assessing the effects
 CC of exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of KPP. The KPP or its fragments are useful in screening
 CC compounds for effectiveness as agonist or antagonist of the polypeptides,
 CC or in altering the expression of the target polynucleotide and compounds
 CC that specifically bind to or modulate the activity of the polypeptide.
 XX
 SQ Sequence 1192 AA;
 XX
 QY Query Match 100.0%; Score 46; DB 8; Length 1192;
 DB Best Local Similarity 100.0%; Pred. No. 39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 LILDVPGV 9
 |||||
 181 LILDVPGV 189
 |||||
 RESULT 20
 ID ADR39378 standard; protein; 1219 AA.
 XX ADR39378;
 AC ADR39378;

XX 18-NOV-2004 (first entry)
 DT Human myocardial infarction-associated gene derived protein, SEQ ID 1041.
 DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human.
 XX
 OS Homo sapiens.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PF 22-DEC-2003; 2003WO-US040978.
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin JJ, Iakubova O;
 DR WPI: 2004-533949/51.
 DR N-PSDB; ADQ38550.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1041; 145bp; English.

XX The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1219 AA;

Query Match 100.0%; Score 46; DB 8; Length 1219;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 9
 |||||
 DB 208 LILDVPPGV 216

RESULT 21
 ADM67187
 ID ADM67187 standard; protein; 1256 AA.
 XX
 AC ADM67187;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human adipocyte specific PTPase receptor type C protein Seqid 541.
 KW human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; PTPase receptor type C.
 XX
 OS Homo sapiens.
 PN WO2004011618-A2.
 PD '05-FEB-2004.
 PF 29-JUL-2003; 2003WO-US023684.
 PR 29-JUL-2002; 2002US-0398785P.
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMGF-) HMGF INC.
 PI Chada K, Chouinard R, Ashar H, Sayed AMD;
 DR WPI: 2004-143846/14.
 DR N-PSDB; ADM66908.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 XX mice of different genotypes.
 XX
 PS Disclosure; SEQ ID NO 541; 91bp; English.

XX This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C^{-/-}, ob/ob, or HMGI-C^{-/-} ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.
 XX
 SQ Sequence 1256 AA;

Query Match 100.0%; Score 46; DB 8; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 9
 |||||
 DB 245 LILDVPPGV 253

RESULT 22
 ADP12966
 ID ADP12966 standard; protein; 1256 AA.

XX ADP12966;
AC
XX 12-AUG-2004 (first entry)
DT
XX Protein encoding reference mRNA sequence #51.
DE
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS Homo sapiens.
PN WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
PF
XX 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M,
PI Rosenberg S;
XX
XX MPI; 2004-400724/37.
DR
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 65; SEQ ID NO 2975; 1762pp; English.
PS
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprising detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection, in an
CC xenotransplant or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein encoded by an mRNA sequence of the invention which show altered
CC expression in renal transplantation and expression.
XX
SQ Sequence 1256 AA;
QY
Query Match 100.0%; Score 46; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 LILDVPGV 9
245 LILDVPGV 253
RESULT 23
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.
XX
XX ADQ39376;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
DE
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.

XX Homo sapiens.
OS
XX
XX WO2004058052-A2.
PN
XX
XX 15-JUL-2004.
PD
XX
XX 22-DEC-2003; 2003WO-US040978.
PF
XX
XX 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
PA
PI Cargill M, Devlin JJ, Iakubova O;
PI
XX MPI; 2004-533949/51.
DR
XX N-PSDB; ADQ38548.
DR
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1039; 145pp; English.
PS
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1258 AA;
QY
Query Match 100.0%; Score 46; DB 8; Length 1258;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 LILDVPGV 9
247 LILDVPGV 255
RESULT 24
ADQ39379
ID ADQ39379 standard; protein; 1267 AA.
XX
XX ADQ39379;
AC
XX
XX 18-NOV-2004 (first entry)
DT

ID	ABU05241 standard; protein; 1304 AA.
XX	
AC	ABU05241;
XX	
DT	29-JAN-2003 (first entry)
XX	
DE	Human expressed protein tag (EPT) #1907.
XX	
KM	Translational profiling; expressed protein tag; EPT; kinase, phosphatase,
KW	protease; protease inhibitor; transporter; cytoskeletal protein;
KV	receptor; transcription factor; cancer; MHC;
RK	major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS	
MS	Homo sapiens.
PN	WO200278524-A2.
XX	
PD	10-OCT-2002.
XX	
PF	28-MAR-2002; 2002MO-US0009671.
XX	
PR	28-MAR-2001; 2001US-0279495P.
PR	21-MAY-2001; 2001US-0292544P.
PR	08-AUG-2001; 2001US-0310801P.
PR	01-OCT-2001; 2001US-0326370P.
PR	04-DEC-2001; 2001US-0336780P.
PR	20-FEB-2002; 2002US-0358985P.
XX	
PA	(ZYCO-) ZYCOS INC.
PI	Chicz RM, Tomlinson AJ, Urban RG,
XX	
DR	WPI; 2003-040607/03.
XX	
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT	cytoskeletal proteins, receptors or transcription factors), useful for
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT	leukemia.
XX	
P8	Example 2; SEQ ID NO 1907; 134bp; English.
CC	The invention describes a purified polypeptide, which comprises a
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,
CC	transporter, cytoskeletal protein, receptor or transcription factor. The
CC	polypeptide is useful as an immunogenic composition for eliciting in a
CC	mammal an immunogenic response directed against any of the purified
CC	polypeptide. The purified polypeptide, or the antibody that binds to this
CC	polypeptide, is useful for treating cancer. The polypeptide is also
CC	useful for identifying compounds that binds to a naturally processed
CC	class I or class II MHC-binding polypeptide. The polypeptides and
CC	polynucleotides are particularly useful for treating or preventing
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC	lymphoma or leukemia. These are also useful for screening agents for
CC	treating the above mentioned diseases. This sequence represents an
CC	expressed protein tag (EPT) isolated from human tissue for translational
CC	profiling. Note: This sequence does not appear in the printed
CC	specification but was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 1304 AA:
Query Match	100.0%; Score 46; DB 6; Length 1304;
Best Local Similarity	100.0%; Pred. No. 43;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XY	1 LILDVPPGV 9
DB	293 LILDVPPGV 301

RESULT 2
ABU05244

ID	ABU05244	standard; protein; 1304 AA.
XX		
XX	ABU05244;	
AC		
XX		
DT	29-JAN-2003	(first entry)
XX		
DE	Human expressed protein tag (EPT) #1910.	
XX		
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	
XX	protease; protease inhibitor; transporter; cytoskeletal protein;	
XX	receptor; transcription factor; cancer; MHC;	
XX	major histocompatibility complex; myeloma; colon cancer; gastric cancer;	
XX	adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.	
OS	Homo sapiens.	
XX		
XX	WO200278524-A2.	
XX		
PD	10-OCT-2002.	
XX		
XX	28-MAR-2002; 2002WO-US009671.	
XX		
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX		
PA	(ZYCO-) ZYCO INC.	
XX		
PI	Chicz RM, Tomlinson AJ, Urban RG;	
XX		
XX	WPI; 2003-040607/03.	
XX		
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
PT	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PT	leukemia.	
XX		
PS	Example 2; SEQ ID NO 1910; 134pp; English.	
XX		
CC	The invention describes a purified polypeptide, which comprises a	
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	
CC	mammal an immunogenic response directed against any of the purified	
CC	polypeptide. The purified polypeptide, or the antibody that binds to this	
CC	polypeptide, is useful for treating cancer. The polypeptide is also	
CC	useful for identifying compounds that binds to a naturally processed	
CC	class I or class II MHC-binding polypeptide. The polypeptides and	
CC	polynucleotides are particularly useful for treating or preventing	
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,	
CC	lymphoma or leukemia. These are also useful for screening agents for	
CC	treating the above mentioned diseases. This sequence represents an	
CC	expressed protein tag (EPT) isolated from human tissue for translational	
CC	profiling. Note: This sequence does not appear in the printed	
CC	specification but was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
XX	Sequence 1304 AA;	
XX		
XX	Query Match	100.0%; Score 46; DB 6; Length 1304;
XX	Best Local Similarity	100.0%; Pred. No. 43;
XX	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX		
QY	1 LILDVPGV 9	
XX		
XX		
XX		
DB	293 LILDVPGV 301	

RESULT 28
ADL16230

ID ADL16230 standard; protein; 1304 AA.
XX
AC ADL16230;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human protein tyrosine phosphatase #26.
XX
KW cytosolic; immunosuppressive; anti-allergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
OS Homo sapiens.
XX
PN MO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003MO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
XX
PR 12-FEB-2003; 2003US-00366547.
XX
PA (CEPR-) COLD SPRING HARBOR LAB.
XX
PI (CEPR-) CEPR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-PSDB; ADL16229.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 79; 238bp; English.
XX
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. . No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 46; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. NO. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ADP65158;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
XX
KW autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
OS Homo sapiens.
XX
PN MO2003072827-A1.
XX
PD 04-SEP-2003.
XX
PF 31-OCT-2002; 2002MO-US035433.
XX
PR 31-OCT-2001; 2001US-0336220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thornton SL;
XX
DR WPI; 2003-712740/67.
XX
DR GENBANK; NP_002829.
XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
PS Disclosure; Page; 56pp; English.
XX
CC The invention relates to a novel method for diagnosing and analyzing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
SQ Sequence 1304 AA;
XX
Query Match 100.0%; Score 46; DB 7; Length 1304;
Best Local Similarity 100.0%; Pred. NO. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30

ADM67209

ID ADM67209 standard; protein; 1304 AA.

AC ADM67209;

DT 03-JUN-2004 (first entry)

DE Human adipocyte specific leukocyte common antigen protein SegID 563.

KW human; adipocyte specific; adipose tissue; anti-obesity;

KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;

KW adipogenesis; hypertension; cardiovascular disease; anorectic;

KW antidiabetic; hypotensive; leukocyte common antigen.

OS Homo sapiens.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

PA (HMG-) HMGENCE INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

PI MPI: 2004-143846/14.

DR N-PSDB; ADM66930.

PT Identifying adipocyte specific genes, useful for treating obesity or

PT diabetes, and for identifying drug targets, by differential gene

PT expression analysis between adipose tissue or stromal vascular tissue of

PT mice of different genotypes.

PS Disclosure; SEQ ID NO 563; 91pp; English.

This invention relates to a novel method for identifying genes that are over-expressed in adipose tissue and as such it provides targets for anti-obesity pharmaceutical compositions. Specifically, it refers to a high mobility group I-C protein (HMGI-C) that is associated with obesity and is epistatic to leptin, furthermore, it refers to the ob gene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were identified that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, hypertension and cardiovascular disease, as well as screening for compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, antidiabetic and hypotensive activities. This polypeptide sequence is a human homologue of a murine adipocyte specific protein sequence of the invention.

SQ Sequence 1304 AA;

Query Match 100.0%; Score 46; DB 8; Length 1304;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILVDPGV 9

Db 293 LILVDPGV 301

RESULT 31

ABO84455

ID ABO84455 standard; protein; 1304 AA.

AC ABO84455;

DT 18-NOV-2004 (first entry)

DE Human cancer-associated protein HP13-011.2.

KW Human; cancer-associated protein; cytosstatic; cancer; leukaemia;

KW lymphoma; CAP.

OS Homo sapiens.

PN WO2004074320-A2.

PD 02-SEP-2004.

PF 17-FEB-2004; 2004WO-US004730.

PR 14-FEB-2003; 2003US-00367094.

PR 15-APR-2003; 2003US-00388838.

PR 13-JUN-2003; 2003US-00417375.

PR 15-SEP-2003; 2003US-00461862.

PR 15-SEP-2003; 2003US-00663431.

PR 15-DEC-2003; 2003US-00737318.

PA (SAGR-) SAGRES DISCOVERY INC.

PI Morris DW, Morris DW, Malandro MS;

PI MPI: 2004-652914/63.

DR N-PSDB; ABD32626.

PT New isolated cancer-associated polynucleotides and polypeptides useful

PT for diagnosing, preventing or treating cancer, especially lymphoma and

PT leukemia, or in screening for agents that modulate cancer.

PS claim 18; seqid 147; 310pp; English.

The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer-associated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above recombinant nucleic acid or expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above-mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a CA sequence selected from any of the 95 polynucleotide sequences as mentioned in the specification, or its complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above antibody and a pharmaceutical excipient, a kit for detecting cancer cells (comprising the antibody cited above, methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual), a method for inhibiting growth of cancer cells in an individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above polynucleotide or polypeptide (or their fragments), methods of screening for anticancer activity or for a bioactive agent capable of modulating the activity of a CA protein (CAP), methods for detecting cancer associated with expression of a polypeptide in a test cell sample, a method for treating cancer and a method for inhibiting the expression of CA gene in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancer, especially lymphoma and leukaemia. These may also be used in screening for agents that modulate cancer. The present sequence is a human CAP protein sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1304 AA;
 Query Match 100.0%; Score 46; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 L1LDVPPGV 9
 Db 293 L1LDVPPGV 301
 RESULT 32
 ADQ39380
 ID ADQ39380 standard; protein; 1304 AA.
 XX
 AC ADQ39380;
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
 XX
 KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KM cardiant; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN MO2004058052-A2.
 PD 15-UTL-2004.
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JT, Iakubova O;
 DR N-PSDB; ADQ38552.
 DR
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1043; 145pp; English.
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 1304 AA;
 Query Match 100.0%; Score 46; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 L1LDVPPGV 9
 Db 293 L1LDVPPGV 301
 RESULT 33
 ADQ39375
 ID ADQ39375 standard; protein; 1306 AA.
 XX
 AC ADQ39375;
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
 XX
 KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KM cardiant; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN MO2004058052-A2.
 PD 15-UTL-2004.
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JT, Iakubova O;
 DR N-PSDB; ADQ38547.
 DR
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 10; SEQ ID NO 1038; 145pp; English.
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction.
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
xx

SQ Sequence 1306 AA;

Query Match 100.0%; Score 46; DB 8; Length 1306;

Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LILDVPPGV 9
|||||

Db 295 LILDVPPGV 303

Search completed: May 3, 2005, 07:37:15
Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 7.43243 Seconds

(without alignments)
129.455 Million cell updates/sec

Title: US-10-003-983C-15

Perfect score: 49
Sequence: 1 KLAFFGPAFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	1304	1 A46546	leukocyte common a
2	43	87.8	24	2 I57644	transmembrane glyco
3	43	87.8	183	2 A28335	leukocyte common a
4	43	87.8	1291	1 A28334	protein-tyrosine-p
5	42	85.7	1237	2 A54080	protein-tyrosine-p
6	39	79.6	213	2 S73011	hypothetical prote
7	39	79.6	336	2 G87202	hypothetical prote
8	38	77.6	347	2 G90444	probable membrane
9	37	75.5	253	2 T30928	hypothetical prote
10	36	73.5	481	2 T23729	hypothetical prote
11	36	73.5	721	2 AH3417	hypothetical prote
12	35	71.4	351	2 C64646	lipid protein (impo
13	35	71.4	351	2 E71935	dihydroorotate deh
14	35	71.4	478	2 C97708	cell cycle protein
15	35	71.4	1132	2 T03844	telomerase catalyt
16	35	71.4	1447	2 T15200	hypothetical prote
17	35	71.4	2273	2 I46477	calcium channel BI
18	35	71.4	2326	2 B47447	calcium channel BI
19	35	71.4	2424	2 I46480	calcium channel BI
20	34	69.4	198	2 A71801	hypothetical prote
21	34	69.4	220	2 D64717	hypothetical prote
22	34	69.4	256	2 F89955	conserved hypothet
23	34	69.4	259	2 H69445	conserved hypothet
24	34	69.4	321	2 AC0658	peptide transport
25	34	69.4	321	2 F90862	peptide transport
26	34	69.4	321	2 C85756	peptide transport
27	34	69.4	321	2 H64877	peptide transport
28	34	69.4	321	2 S39586	peptide transport
29	34	69.4	335	2 G71867	hypothetical prote

30	34	69.4	335	2 B64572	hypothetical prote
31	34	69.4	355	2 F96020	probable iron ABC
32	34	69.4	391	2 F82259	D-alanyl-D-alanine
33	34	69.4	430	2 B95892	probable ABC trans
34	34	69.4	482	2 T43885	cytochrome-c oxida
35	34	69.4	512	2 T09801	cytochrome-c oxida
36	34	69.4	513	2 T11999	cytochrome-c oxida
37	34	69.4	592	2 E70488	cytochrome-c oxida
38	34	69.4	672	2 B84782	probable receptor
39	34	69.4	708	2 T29669	hypothetical prote
40	34	69.4	2212	2 A41098	calcium channel pr
41	33	67.3	98	2 T14136	NADH2 dehydrogenas
42	33	67.3	331	2 AB3372	toluene tolerance
43	33	67.3	372	1 T04157	dihydrokaempferol
44	33	67.3	386	2 C83146	D-ala-D-ala-carbox
45	33	67.3	397	2 C84078	hypothetical prote

ALIGNMENTS

RESULT 1

A46546
leukocyte common antigen long splice form precursor - human
N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprote
N:Contains: leukocyte common antigen intermediate splice form; leukocyte common antigen
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 09-Jul-2004
C/Accession: A46546; B46546; C46546; A29449; B29449; I57658
R/Streuli, M.; Hall, L.R.; Saga, Y.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 166, 1548-1566, 1987
A>Title: Differential usage of three exons generates at least five different mRNAs encod
A:Reference number: A46546; MUID:88061067; PMID:2824653
A:Accession: A46546
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1304 <STR>
A:Cross-references: UNIPROT:P08575; GB:Y00638
A:Experimental source: clone LCA.6/2
A:Accession: B46546
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-32,99-264 <STR>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.111 and clone LCA.260
A:Accession: C46546
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-31,193-264 <STR>
A:Cross-references: GB:Y00638
A:Experimental source: clone LCA.1
R/Ralph, S.J.; Thomas, W.L.; Morton, C.C.; Trowbridge, I.S.
EMBO J. 6, 1251-1257, 1987
A>Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
A:Reference number: A91066; MUID:87275816; PMID:2956090
A:Accession: A29449
A:Molecule type: mRNA
A:Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAI>
A:Cross-references: GB:Y00662; MUID:934275; PIND:CA68269.1; PID:934276
A:Experimental source: clones pHLC-1 and lambdaHNG1
A:Accession: B29449
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 32-192 <RA2>
A:Experimental source: clone HLC-2
R/Tsai, A.Y.; Streuli, M.; Saito, H.
Mol. Cell. Biol. 9, 4550-4555, 1989
A>Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative :
A:Reference number: I57658; MUID:90066468; PMID:2531281
A:Accession: I57658
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 146-192 <RES>

A:Cross-references: GB:M29253; NID:g187020; PIDN:AAA59497.1; PID:g553521
 C:Genetics:
 A:Gene: GDB:PTPRC; CD45
 A:Cross-references: GDB:119768; OMIM:151460
 A:Map position: 1q31-1q32
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:594-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:675-899/Domain: protein-tyrosine-phosphatase homology <PT>
 F:851/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 49; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLLAFGFAL 10
 |||||
 DB 6 KLLAFGFALL 15

RESULT 2
 157644
 transmembrane glycoprotein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: 157644
 R:Saga, Y.; Tung, J.
 Mol. Cell. Biol. 8, 4889-4895, 1988
 A:Title: Organization of the Ly-5 Gene.
 A:Reference number: 157644; MUID:89096862; PMID:3211131
 A:Accession: 157644
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-24 <RES>
 A:Cross-references: UNIPROT:Q61815; GB:M23354; NID:g340890; PIDN:AAA39462.1; PID:g554192
 C:Genetics:
 A:Gene: Ly-5
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 C:Keywords: glycoprotein

Query Match 87.8%; Score 43; DB 2; Length 24;
 Best Local Similarity 90.0%; Pred. No. 0.081;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLLAFGFAL 10
 |||||
 DB 8 KLLAFGFALL 17

RESULT 3
 A28335
 leukocyte common antigen precursor - mouse (fragment)
 N:Alternate names: B220; Ly-5 (B-cell specific)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C:Accession: A28335
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A:Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishin
 A:Reference number: A28335; MUID:87260987; PMID:3037546
 A:Accession: A28335
 A:Molecule type: mRNA
 A:Residues: 1-183 <SAG>
 A:Cross-references: UNIPROT:Q61814; GB:M14342
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-183/Product: leukocyte common antigen, 200K #status predicted <MNT>

Query Match 87.8%; Score 43; DB 2; Length 183;
 Best Local Similarity 90.0%; Pred. No. 0.58;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLLAFGFAL 10
 |||||
 DB 6 KLLAFGFALL 15

RESULT 4
 A28334
 protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse
 N:Alternate names: 200K leukocyte common antigen; B220; CD45; Ly-5 (B-cell specific); PT
 N:Contains: protein-tyrosine-phosphatase (T-cell variant)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A28334; A29381; A61180; A60933; A33522; A29075; I54450; A28335; A23329; I57
 R:Thomas, M.L.; Reynolds, P.J.; Chain, A.; Ben-Neriah, Y.; Trowbridge, I.S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5360-5363, 1987
 A:Title: B-cell variant of mouse T200 (Ly-5): evidence for alternative mRNA splicing.
 A:Reference number: A28334; MUID:87260986; PMID:2955416
 A:Accession: A28334
 A:Molecule type: mRNA
 A:Residues: 1-1291 <THO>
 A:Cross-references: UNIPROT:P06800; UNIPROT:Q61814; UNIPROT:Q61815; UNIPROT:Q61813; GB:M
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6940-6944, 1986
 A:Title: Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.
 A:Reference number: A29381; MUID:86313686; PMID:2944116
 A:Accession: A29381
 A:Molecule type: mRNA
 A:Residues: 1-30,170-517, 'NTT', 521-527, 'G', 529-555, 'S', 557-587, 'S', 589-905, 'Q', 907-930, '
 A:Cross-references: GB:M14342; NID:g198914; PIDN:AAA39458.1; PID:g198915
 R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
 A:Reference number: A61180; MUID:92032882; PMID:1932742
 A:Accession: A61180
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 730-838 <YTA>
 R:Gomez, I.J.; Walker, I.D.; Sandrin, M.S.; McKenzie, I.F.C.
 Immunogenetics 25, 263-266, 1987
 A:Title: High sequence conservation between rat (T200) and mouse (Ly-5) leukocyte common
 A:Reference number: A60933; MUID:87192931; PMID:3570377
 A:Accession: A60933
 A:Molecule type: protein
 A:Residues: 'R', 289-298; '329', 'V', 331-336, 'Y', 'R', 364-370, 'X', 372-375; 595-608; 638-649; 669-
 R:Johnson, N.A.; Meyer, C.M.; Pingel, J.T.; Thomas, M.L.
 J. Biol. Chem. 264, 6220-6229, 1989
 A:Title: Sequence conservation in potential regulatory regions of the mouse and human le
 A:Reference number: A33522; MUID:89197920; PMID:2522930
 A:Accession: A33522
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <JOH>
 A:Cross-references: GB:M22456; NID:g198755; PIDN:ABA46374.1; PID:g554185; GB:J04640; GB:
 R:Saechke, W.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 161-165, 1987
 A:Title: Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lym
 A:Reference number: A29075; MUID:87092355; PMID:2948186
 A:Accession: A29075
 A:Molecule type: mRNA
 A:Residues: 961-1291 <RAS>
 A:Cross-references: GB:M5174; NID:g201105; PIDN:AAA40161.1; PID:g201106
 R:Tung, J.
 Immunogenetics 28, 271-277, 1988
 A:Title: Structural features of Ly-5 glycoproteins of the mouse and counterparts in othe
 A:Reference number: I54450; MUID:88330145; PMID:3417340
 A:Accession: I54450
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 32-73 <RES>
 A:Cross-references: GB:M2241; NID:g340850; PIDN:AAA39460.1; PID:g548174
 R:Saga, Y.; Tung, J.S.; Shen, F.W.; Boyse, E.A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5364-5368, 1987
 A:Title: Alternative use of 5' exons in the specification of Ly-5 isoforms distinguishin

A/Reference number: A28335; MUID:87260987; PMID:3037546
A/Accession: A28335
A/Molecule type: mRNA
A/Residues: 1-30, 74-226 <SN2>
A/Cross-references: GB:M14342
R/Shen, F.W.; Saga, Y.; Litman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boye, E.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 7360-7363, 1985
A/Reference number: A23329; MUID:86042665; PMID:3864163
A/Accession: A23329
A/Molecule type: mRNA
A/Residues: 10-30, 170-263 <SHE>
A/Cross-references: GB:M11934; NID:g198919; PIDN:AAA39461.1; PID:g198920
R/Saga, Y.; Tung, J.
Mol. Cell. Biol. 8, 4889-4895, 1988
A/Title: Organization of the ly-5 Gene.
A/Reference number: 157644; MUID:89096862; PMID:3211131
A/Accession: 157644
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 'MT', 1-22 <RE2>
A/Cross-references: GB:M23354; NID:g340890; PIDN:AAA39462.1; PID:g554192
C/Genetics:
A/Gene: ly-5
C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C/Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-1291/Product: protein-tyrosine-phosphatase (B-cell variant) #status predicted <MT>
F:24-554/Domain: extracellular #status predicted <EXT>
F:24-30, 170-1291/Product: protein-tyrosine-phosphatase (T-cell variant) #status predicte
F:565-586/Domain: transmembrane #status predicted <TM>
F:583-1223/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:587-1291/Domain: intracellular #status predicted <INT>
F:664-888/Domain: protein-tyrosine-phosphatase homology <PTP>
F:64, 150, 161, 207, 211, 218, 253, 258, 290, 311, 322, 347, 416, 427, 457, 489, 520, 556/Binding site: C
F:940/Active site: Cys (phosphotyrosine intermediate) #status predicted
F:846/Binding site: substrate phosphate (Arg) #status predicted

Query Match 87.8%; Score 43; DB 1; Length 1291;
Best Local Similarity 90.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLIAFGFAFL 10
DB 6 KLIAFGFAFL 15

RESULT 5
A54080
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C/Accession: A54080; 150592
R/Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
J. Biol. Chem. 269, 14056-14063, 1994
A/Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in
A/Reference number: A54080; MUID:94245724; PMID:8188666
A/Accession: A54080
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1237 <FAN>
A/Cross-references: UNIPROT:Q91976; EMBL:Z21960; NID:g510510; PIDN:CAA79972.1; PID:g5105
C/Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol
C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:510-834/Domain: protein-tyrosine-phosphatase homology <PTP>
F:786/Active site: Cys (phosphotyrosine intermediate) #status predicted
F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 85.7%; Score 42; DB 2; Length 1237;
Best Local Similarity 90.0%; Pred. No. 5.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLIAFGFAFL 10

DB 6 KLIAFGFAFL 15

RESULT 6
S73011
hypothetical protein L518_C3_195 - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S73011
R/Smith, D.R.; Robison, K.
Submitted to the EMBL Data Library, November 1993
A/Description: Mycobacterium leprae cosmid L518.
A/Reference number: S72591
A/Accession: S73011
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-213 <SMI>
A/Cross-references: UNIPROT:Q49930; EMBL:U00023; NID:g467194; PIDN:AAA17354.1; PID:g467
C/Genetics:
A/Start codon: GTG
C/Superfamily: Mycobacterium leprae hypothetical protein L518_C3_195

Query Match 79.6%; Score 39; DB 2; Length 213;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIAFGFAFL 10
DB 40 LIAFGFAFL 48

RESULT 7
G87202
probable membrane protein [imported] - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: G87202
R/Coile, S.T.; Eigmeier, K.; Parhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duthey, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: G87202
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-336 <STO>
A/Cross-references: UNIPROT:Q69510; GB:AL450380; NID:g13093956; PIDN:CAJ31863.1; GSPDB:
C/Genetics:
A/Gene: ML2347

Query Match 79.6%; Score 39; DB 2; Length 336;
Best Local Similarity 88.9%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LIAFGFAFL 10
DB 40 LIAFGFAFL 48

RESULT 8
G90444
hypothetical protein SSO2702 [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: G90444
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jung, I.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.

Query Match	73.5%	Score 36	DB 2	Length 481
Best Local Similarity	77.8%	Pred. No. 33		
Matches	7	Conservative	1	Indels 0
		Mismatches	1	Gaps 0
QY	2	LIAPGRAFL	10	

RESULT 13
E71935
dihydroorotate dehydrogenase - *Helicobacter pylori* (strain J99)
C:Species: *Helicobacter pylori*
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71935
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, G.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999

A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: E71935
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-351 <ARN>
 A:Cross-references: UNIPROT:Q9ZM11; GB:AE001475; GB:AE001439; NID:g4154939; PIDN:AAD0598
 A:Experimental source: strain 999
 C:Genetics:
 A:Gene: pyrD
 C:Superfamily: dithydroorotate oxidase

Query Match 71.4%; Score 35; DB 2; Length 351;
 Best Local Similarity 66.7%; Pred. No. 37;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LIAFGFAFL 10
 Db 79 LIAFGFGYL 87

RESULT 14

C97708
 cell cycle protein MeuJ [imported] - Rickettsia conorii (strain Malish 7)
 C:Species: Rickettsia conorii
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: C97708
 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
 Science 293, 2093-2098, 2001
 A>Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A:Reference number: A97700; MUID:21442074; PMID:11557893
 A:Accession: C97708
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-478 <KOR>
 A:Cross-references: UNIPROT:Q9ZJK0; GB:AE006914; PIDN:AAL02605.1; PID:g15619104; GSPDB:G
 C:Genetics:
 A:Gene: meuJ

Query Match 71.4%; Score 35; DB 2; Length 478;
 Best Local Similarity 60.0%; Pred. No. 50;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KILAFGAFL 10
 Db 288 KIFGYGAFL 297

RESULT 15

T03844
 telomerase catalytic chain - human
 N:Alternate names: telomerase reverse transcriptase
 C:Species: Homo sapiens (man)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T03844
 R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
 Science 277, 955-959, 1997
 A>Title: Telomerase catalytic subunit homologs from fission yeast and human.
 A:Reference number: Z1511; MUID:97400623; PMID:9252327
 A:Accession: T03844
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1132 <NAK>
 A:Cross-references: UNIPROT:Q14746; EMBL:AF015950; NID:g2330016; PIDN:AACS1672.1; PID:g2
 A:Experimental source: kidney
 C:Genetics:
 A:Gene: TRT
 A:Map position: 5p

Query Match 71.4%; Score 35; DB 2; Length 1132;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LIAFGFAFL 10
 Db 96 LIAFGFAFL 104

Search completed: May 3, 2005, 06:17:22
 Job time : 11.4324 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2005, 07:28:27 ; Search time 38.6757 Seconds
(without alignments)
90.001 Million cell updates/sec

Title: US-10-003-983C-3
Perfect score: 43
Sequence: 1 KLFYAKLVN 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	9	ABG31973	Abg31973 Human CD4
2	43	100.0	553	AAW35856	AAW35856 Human CD4
3	43	100.0	553	ABU07335	ABU07335 Human EXP
4	43	100.0	641	AAW23689	AAW23689 Human EST
5	43	100.0	641	ABU07333	ABU07333 Human EXP
6	43	100.0	664	AAW39262	AAW39262 Human POL
7	43	100.0	664	ABU07334	ABU07334 Human EXP
8	43	100.0	1114	ABU05246	ABU05246 Human EXP
9	43	100.0	1114	ABU05239	ABU05239 Human EXP
10	43	100.0	1143	ABU05240	ABU05240 Human EXP
11	43	100.0	1143	ABU05245	ABU05245 Human EXP
12	43	100.0	1143	ADL16232	ADL16232 Human PRO
13	43	100.0	1143	ADQ18845	ADQ18845 Human SOF
14	43	100.0	1149	AAW41048	AAW41048 Human POL
15	43	100.0	1149	ABU05242	ABU05242 Human EXP
16	43	100.0	1192	ADR39747	ADR39747 Human KIN
17	43	100.0	1219	ADQ39378	ADQ39378 Human MYO
18	43	100.0	1256	ADM67187	ADM67187 Human ADI
19	43	100.0	1256	ADP12966	ADP12966 Protein e
20	43	100.0	1258	ADQ39376	ADQ39376 Human MYO
21	43	100.0	1267	ADQ39379	ADQ39379 Human MYO
22	43	100.0	1304	ABU05243	ABU05243 Human EXP
23	43	100.0	1304	ABU05241	ABU05241 Human EXP
24	43	100.0	1304	ABU05244	ABU05244 Human PRO
25	43	100.0	1304	ADL16230	ADL16230 Human PRO

26	43	100.0	1304	ADP65158	ADP65158 Human PRO
27	43	100.0	1304	ADM67209	ADM67209 Human ADI
28	43	100.0	1304	ABO84455	ABO84455 Human CAN
29	43	100.0	1304	ADQ39380	ADQ39380 Human MYO
30	43	100.0	1306	ADQ39375	ADQ39375 Human MYO
31	35	81.4	461	ABU24704	ABU24704 Protein e
32	34	79.1	548	AAW39463	AAW39463 Human POL
33	34	79.1	558	AAW41249	AAW41249 Human POL
34	34	79.1	725	ADU71182	ADU71182 Human HEA
35	34	79.1	865	ADDO1200	ADDO1200 Human NUC
36	34	79.1	988	ABO84844	ABO84844 Murine CA
37	33	76.7	678	ABU49732	ABU49732 Protein e
38	32	74.4	89	ADH86272	ADH86272 Enterococ
39	32	74.4	141	AAW41484	AAW41484 Lectin po
40	32	74.4	377	ADN21747	ADN21747 Bacterial
41	32	74.4	380	ADN24502	ADN24502 Bacterial
42	31	72.1	129	AAW22613	AAW22613 Zea may
43	31	72.1	140	AAW22612	AAW22612 Zea may
44	31	72.1	168	AAW22611	AAW22611 Zea may
45	31	72.1	226	AAW40561	AAW40561 Maize glu

ALIGNMENTS

RESULT 1
ABG31973 standard; peptide, 9 AA.

AC ABG31973;

DT 05-NOV-2002 (first entry)

DE Human CD45 HLA-binding peptide, huCD45/244.

XX Human; CD45; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL;

KW antigen-presenting cell; APC; major histocompatibility complex; MHC;

KW antigen; allogenic; T cell receptor; TCR; cancer; tumour;

KW allogenic stem cell transplantation; CFU-GM; leukaemia;

XX colony forming unit-granulocyte macrophage; immunotherapeutic;

XX haematopoietic; malignant.

XX Homo sapiens.

OS Homo sapiens.

PN WO200244207-A1.

PD 06-JUN-2002.

XX 30-NOV-2000; 2000MO-GB004566.

PF 30-NOV-2000; 2000MO-GB004566.

PR 30-NOV-2000; 2000MO-GB004566.

XX 30-NOV-2000; 2000MO-GB004566.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Steaus HJ, Amrolia PJ;

PI WPI; 2002-599413/64.

DR Novel peptide comprising leukocyte antigen binding peptide of human CD45

XX polypeptide, useful for producing activated cytotoxic T lymphocytes, for

PT killing cancerous cells e.g. leukemia.

PS Claim 2, Page 38; 56pp; English.

The invention discloses a peptide comprising the human leukocyte antigen (HLA)-binding peptide of human CD45 polypeptide, its portion or variant, provided that the peptide is not the intact human CD45 polypeptide. The peptides are useful for producing activated cytotoxic T lymphocyte (CTL) in vitro which involves contacting the CTL with an antigen-presenting cell, where its major histocompatibility complex (MHC) class I molecules are loaded with the peptide, to activate, in an antigen specific manner, where the CTL and the antigen presenting cell are allogenic with respect to the class I MHC molecule that is presenting peptides of CD45. The

CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 553 AA;

Query Match 100.0%; Score 43; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KLFPAKLNV 9
221 KLFPAKLNV 229

RESULT 4
ID AAM23689 standard; protein; 641 AA.
XX
AC AAM23689;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1214.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSB-) HYSBQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
XX
DR N-PSDB; AAH98348.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 875-876; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 43; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KLFPAKLNV 9
85 KLFPAKLNV 93

RESULT 5
ID ABU07333 standard; protein; 641 AA.
XX
AC ABU07333;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2034.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2034; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 641 AA;
Query Match          100.0%; Score 43; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KLFATKLVN 9
Db 85 KLFATKLVN 93

RESULT 6
ID AAM39262 standard; protein; 664 AA.
AC AAM39262;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2407.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW Leukemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00486725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang Z, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI58418.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2407; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

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CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 664 AA;
Query Match          100.0%; Score 43; DB 4; Length 664;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KLFATKLVN 9
Db 85 KLFATKLVN 93

RESULT 7
ID ABU07334 standard; protein; 664 AA.
AC ABU07334;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #2035.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 2035; 134bp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an

```

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SO Sequence 664 AA;

Query Match 100.0%; Score 43; DB 6; Length 664;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
|||
Db 85 KLFYAKLV 93

RESULT 8
ABU05246
ID ABU05246 standard; protein; 1114 AA.
XX
AC ABU05246;
XX

DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1912.
XX

KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

OS Homo sapiens.
XX

PN WO200278524-A2.
XX

PD 10-OCT-2002.
XX

PF 28-MAR-2002; 2002WO-US009671.
XX

PR 28-MAR-2001; 2001US-0279495P.
XX

PR 21-MAY-2001; 2001US-0292544P.
XX

PR 08-AUG-2001; 2001US-0310801P.
XX

PR 01-OCT-2001; 2001US-0326370P.
XX

PR 04-DEC-2001; 2001US-0336780P.
XX

PR 20-FEB-2002; 2002US-0358985P.
XX

PA (ZYCO-) ZYCO INC.
XX

PI Chicx RM, Tomlinson AJ, Urban RG;
XX

DR WPI; 2003-040607/03.
XX

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX

PS Example 2; SEQ ID NO 1912; 134pp; English.
XX

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SO Sequence 1114 AA;

Query Match 100.0%; Score 43; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLV 9
|||
Db 54 KLFYAKLV 62

RESULT 9
ABU05239
ID ABU05239 standard; protein; 1114 AA.
XX
AC ABU05239;
XX

DT 29-JAN-2003 (first entry)
XX

DE Human expressed protein tag (EPT) #1905.
XX

KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

OS Homo sapiens.
XX

PN WO200278524-A2.
XX

PD 10-OCT-2002.
XX

PF 28-MAR-2002; 2002WO-US009671.
XX

PR 28-MAR-2001; 2001US-0279495P.
XX

PR 21-MAY-2001; 2001US-0292544P.
XX

PR 08-AUG-2001; 2001US-0310801P.
XX

PR 01-OCT-2001; 2001US-0326370P.
XX

PR 04-DEC-2001; 2001US-0336780P.
XX

PR 20-FEB-2002; 2002US-0358985P.
XX

PA (ZYCO-) ZYCO INC.
XX

PI Chicx RM, Tomlinson AJ, Urban RG;
XX

DR WPI; 2003-040607/03.
XX

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX

PS Example 2; SEQ ID NO 1905; 134pp; English.
XX

CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1114 AA;

Query Match 100.0%; Score 43; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLFYAKLVN 9
|||
Db 54 KLFYAKLVN 62

RESULT 10
ABU05240
ID ABU05240 standard; protein; 1143 AA.

XX AC ABU05240;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1906.

XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KM protease; protease inhibitor; transporter; cytoskeletal protein;
XX KM receptor; transcription factor; cancer; MHC;
XX KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.

XX PS Example 2; SEQ ID NO 1906; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1143 AA;

Query Match 100.0%; Score 43; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLFYAKLVN 9
|||
Db 83 KLFYAKLVN 91

RESULT 11
ABU05245
ID ABU05245 standard; protein; 1143 AA.

XX AC ABU05245;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1911.

XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KM protease; protease inhibitor; transporter; cytoskeletal protein;
XX KM receptor; transcription factor; cancer; MHC;
XX KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.

XX PS Example 2; SEQ ID NO 1911; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 1143 AA;

Query Match 100.0%; Score 43; DB 6; Length 1143;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLVN 9
| | | | | | | | | |

Db 83 KLFYAKLVN 91

RESULT 12

ADL16232
ID ADL16232 standard; protein; 1143 AA.

XX ADL16232;

AC ADL16232;

DT 06-MAY-2004 (first entry)

XX Human protein tyrosine phosphatase #27.

DE cytostatic; immunosuppressive; antiallergic;
XX protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KM inducible signaling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
XX cell-cycle abnormality; enzyme.

OS Homo sapiens.

PN WO2003068984-A2.

XX 21-AUG-2003.

PD 13-FEB-2003; 2003WO-EP001446.

PF 13-FEB-2002; 2002US-0356810P.

PR 12-FEB-2003; 2003US-00366547.

XX (COLD-) COLD SPRING HARBOR LAB.

PA (CEPT-) CEPT INC.

PI Tonks NK, Tzu-Ching M, Cool DE;

XX WPI; 2003-712572/67.

DR N-PSDB; ADL16231.

PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
XX screening for specific modulators, potential agents for treating e.g.
XX cancer or autoimmune disease.

PS Disclosure; SEQ ID NO 81; 238bp; English.

XX The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulphydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle

CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.

XX Sequence 1143 AA;

Query Match 100.0%; Score 43; DB 7; Length 1143;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLVN 9
| | | | | | | | | |

Db 83 KLFYAKLVN 91

RESULT 13

ADQ18845
ID ADQ18845 standard; protein; 1143 AA.

XX ADQ18845;

AC ADQ18845;

DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 1664.

DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

PN WO2004048938-A2.

XX 10-JUN-2004.

PD 26-NOV-2003; 2003WO-US038193.

PR 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

PA Aziz N, Ginsburg WM, Zlotnick A;

PI WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.

PS Example 2; SEQ ID NO 1664; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 1143 AA;

Query Match 100.0%; Score 43; DB 8; Length 1143;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYAKLVN 9
| | | | | | | | | |

Db 83 KLFYAKLVN 91

RESULT 14
AA041048
ID AA041048 standard; protein; 1149 AA.
XX
XX
XX
AC AA041048;
XX
XX
DT 22-OCT-2001 (first entry)
XX
XX
DE Human polypeptide SEQ ID NO 5979.
XX
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200153312-A1.
XX
XX PD 26-JUL-2001.
XX
XX PF 26-DEC-2000; 2000WO-US034263.
XX
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX
XX DR WPI; 2001-442253/47.
XX DR N-PSDB; AAI60204.
XX
XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX PS Example 2; SEQ ID NO 5979; 10078pp; English.
XX
XX CC The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AA038642-AA042213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
XX SQ Sequence 1149 AA;

Query Match 100.0%; Score 43; DB 4; Length 1149;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KLFYAKLV 9

Db 86 KLFYAKLV 96
|||||||
RESULT 15
ABU05242
ID ABU05242 standard; protein; 1149 AA.
XX
XX
XX
AC ABU05242;
XX
XX
DT 29-JAN-2003 (first entry)
XX
XX
DE Human expressed protein tag (EPT) #1908.
XX
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS
XX PN Homo sapiens.
XX
XX PD WO200278524-A2.
XX
XX PF 10-OCT-2002.
XX
XX PR 26-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX PA (ZYCO-) ZYCO INC.
XX
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
XX DR WPI; 2003-040607/03.
XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX PS Example 2; SEQ ID NO 1908; 134pp; English.
XX
XX CC The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, or protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1149 AA;

Query Match 100.0%; Score 43; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KLFYAKLV 9

Db 88 KLFPAKLNV 96

RESULT 16
ADR39747
ID ADR39747 standard; protein; 1192 AA.
XX
XX ADR39747;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human kinase and phosphatase KPP-20 protein SEQ ID NO:20.

XX human; kinase and phosphatase protein; KPP; enzyme; cytosolic;
XX antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
XX cerebroprotective; anti-HIV; anti-allergic; anti-inflammatory;
XX thyromimetic; gene therapy; cell proliferative disorder; cancer;
XX atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
XX stroke; immune disorder; inflammatory disorder; AIDS; allergy;
XX developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX KPP-20.
XX
XX Homo sapiens.
XX OS
XX PN WO2004074453-A2.
XX PD 02-SEP-2004.
XX PF 20-FEB-2004; 2004WO-US005092.
XX PR 20-FEB-2003; 2003US-0449059P.
XX PR 19-MAR-2003; 2003US-0456932P.
XX PR 28-MAR-2003; 2003US-0458844P.
XX PR 09-APR-2003; 2003US-0461678P.
XX PR 17-APR-2003; 2003US-0463937P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Ramkumar J, Margulis JP, Swarnakar A, Chawla NK, Tran UK;
XX Becha SD, Lee SY, Hafalla AJA, Richardson TW, Khare R, Jhang X;
XX Jackson AA, Yang J, Gorvad AE;
XX
XX WPI: 2004-635568/61.
XX DR N-PSDB; ADR39793.
XX
XX New human kinases and phosphatases (KPP) for diagnosing, treating and
XX preventing diseases or conditions associated with aberrant KPP expression
XX e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.
XX
XX Claim 1; SEQ ID NO 20; 299pp; English.

XX The present sequence represents the human kinase and phosphatase protein
XX (KPP), designated KPP-20. The human KPP sequences from the present
XX invention have cytosolic, antiarteriosclerotic, anticonvulsant,
XX neurotropic, neuroprotective, cerebroprotective, anti-HIV, anti-allergic,
XX anti-inflammatory and thyromimetic activities, and can be used in gene
XX therapy. The human KPP proteins and polynucleotides can be used in
XX diagnosing, treating and preventing diseases or conditions associated
XX with the decreased expression or overexpression of KPP, such as cell
XX proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
XX epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
XX allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
XX disorders, or infections. They can also be used in assessing the effects
XX of exogenous compounds on the expression of nucleic acid and amino acid
XX sequences of KPP. The KPP or its fragments are useful in screening
XX compounds for effectiveness as agonist or antagonist of the polypeptides,
XX or in altering the expression of the target polynucleotide and compounds
XX that specifically bind to or modulate the activity of the polypeptide.
XX
XX Sequence 1192 AA;

Query Match 100.0%; Score 43; DB 8; Length 1192;

Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFPAKLNV 9
Db 132 KLFPAKLNV 140

RESULT 17
ADQ39378
ID ADQ39378 standard; protein; 1219 AA.
XX
XX ADQ39378;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human myocardial infarction-associated gene derived protein, SEQ ID 1041.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiant; gene therapy; human.
XX
XX Homo sapiens.
XX OS
XX PN WO2004058052-A2.
XX PD 15-UTL-2004.
XX PF 22-DEC-2003; 2003WO-US040978.
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504935P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JT, Iakubova O;
XX
XX WPI: 2004-533949/51.
XX DR N-PSDB; ADQ38550.
XX
XX Identifying an individual who has an altered risk for developing
XX myocardial infarction by detecting a single nucleotide polymorphism in
XX the individual's nucleic acids.
XX
XX Claim 10; SEQ ID NO 1041; 145pp; English.

XX The invention relates to a novel method for identifying an individual who
XX has an altered risk for developing myocardial infarction. The method
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX the nucleotide sequences given in the specification in the individual's
XX nucleic acids, where the presence of the SNP is correlated with an
XX altered risk for myocardial infarction in the individual. The invention
XX further comprises: an isolated nucleic acid molecule comprising at least
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX the specification or its complement and encoding any one of the amino
XX acid sequences given in the specification; an isolated polypeptide
XX comprising an amino acid sequence given in the specification; an antibody
XX that specifically binds to the polypeptide or its antigen-binding
XX fragment; an amplified polynucleotide containing an SNP given in the
XX specification and which is between about 16 and 1000 nucleotides in
XX length; a kit for detecting an SNP in a nucleic acid, comprising the
XX polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX method for identifying an agent useful in treating or preventing
XX myocardial infarction. The novel detection method has cardiant activity.
XX The nucleic acids of the invention may be used in gene therapy. The
XX method is useful in identifying an individual who has an increased or
XX decreased risk for developing myocardial infarction and for preparing a
XX composition for treating or preventing myocardial infarction. This
XX sequence represents the protein of a human myocardial infarction-
XX associated gene containing one or more SNPs of the invention. Note: This
XX sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 1219 AA;

XX Query Match 100.0%; Score 43; DB 8; Length 1219;

XX Best Local Similarity 100.0%; Pred. No. 4.9;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLF7AKLV 9

DB 159 KLF7AKLV 167

RESULT 18

ADM67187

ID ADM67187 standard; protein; 1256 AA.

XX ADM67187;

DT 03-JUN-2004 (first entry)

DE Human adipocyte specific PTPase receptor type C protein SegID 541.

XX human; adipocyte specific; adipose tissue; anti-obesity;

KM high mobility group I-C protein; HMG1-C; obesity; leptin; ob; diabetes;

KM adipogenesis; hypertension; cardiovascular disease; anorectic;

KM antidiabetic; hypotensive; PTPase receptor type C.

XX Homo sapiens.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

XX 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

XX (HMG1-C) HMG1-C INC.

XX Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66908.

PT Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.

XX Disclosure; SEQ ID NO 541; 91pp; English.

XX This invention relates to a novel method for identifying genes that are
XX over-expressed in adipose tissue and as such it provides targets for anti-
XX -obesity pharmaceutical compositions. Specifically, it refers to a high
XX mobility group I-C protein (HMG1-C) that is associated with obesity and
XX is epistatic to leptin, furthermore, it refers to the ob gene where an
XX autosomal recessive trait is linked to obesity and diabetes. The present
XX invention describes performing differential gene expression analysis
XX between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
XX of any two different mice selected from a group consisting of wild-type,
XX HMG1-C -/-, ob/ob, or HMG1-C -/- ob/ob genotype mice. Accordingly, using
XX this method novel nucleotides and the encoded proteins thereof were
XX identified that are adipocyte specific, and as such can be used for
XX preventing adipogenesis, diagnosing and treating diabetes, obesity,
XX hypertension and cardiovascular disease, as well as screening for
XX compounds that can modulate or prevent adipogenesis and treat diabetes or
XX obesity. These compositions exhibit anorectic, antidiabetic and
XX hypotensive activities. This polypeptide sequence is a human homologue of
XX a murine adipocyte specific protein sequence of the invention.

XX Sequence 1256 AA;

QY Query Match 100.0%; Score 43; DB 8; Length 1256;

XX Best Local Similarity 100.0%; Pred. No. 5.1;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLF7AKLV 9

DB 196 KLF7AKLV 204

RESULT 19

ADP12966

ID ADP12966 standard; protein; 1256 AA.

XX ADP12966;

DT 12-AUG-2004 (first entry)

DE Protein encoding reference mRNA sequence #51.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;

KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

XX Homo sapiens.

PN WO2004042346-A2.

PD 21-MAY-2004.

PF 24-APR-2003; 2003WO-US012946.

XX 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

PI Rosenberg S;

DR WPI; 2004-400724/37.

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.

XX Claim 65; SEQ ID NO 2975; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprises detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX protein encoded by an mRNA sequence of the invention which show altered
XX expression in renal transplantation and expression.

XX Sequence 1256 AA;

QY Query Match 100.0%; Score 43; DB 8; Length 1256;

XX Best Local Similarity 100.0%; Pred. No. 5.1;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLF7AKLV 9

DB 196 KLF7AKLV 204

RESULT 20
ADQ39376
ID ADQ39376 standard; protein; 1258 AA.
XX AC ADQ39376;
XX DT 18-NOV-2004 (first entry)
XX DT 18-NOV-2004 (first entry)
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1039.
XX KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiact; gene therapy; human.
XX OS Homo sapiens.
XX PN WO2004058052-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US040978.
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX PA (APPL-) APPLERA CORP.
XX PI Cargill M, Devlin JJ, Iakubova O;
XX DR N-PDB; ADQ38548.
XX DR N-PDB; ADQ38548.
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX PS Claim 10; SEQ ID NO 1039; 145bp; English.
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiact activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC sequence represents the protein of a human myocardial infarction-
XX CC associated gene containing one or more SNPs of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.
SQ Sequence 1258 AA;
Query Match 100.0%; Score 43; DB 8; Length 1258;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLFTRAKLV 9
Db |||||
198 KLFTRAKLV 206
RESULT 21
ADQ39379
ID ADQ39379 standard; protein; 1267 AA.
XX AC ADQ39379;
XX DT 18-NOV-2004 (first entry)
XX DT 18-NOV-2004 (first entry)
XX DE Human myocardial infarction-associated gene derived protein, SEQ ID 1042.
XX KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiact; gene therapy; human.
XX OS Homo sapiens.
XX PN WO2004058052-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US040978.
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX PA (APPL-) APPLERA CORP.
XX PI Cargill M, Devlin JJ, Iakubova O;
XX DR N-PDB; ADQ38551.
XX DR N-PDB; ADQ38551.
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX PS Claim 10; SEQ ID NO 1042; 145bp; English.
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiact activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC sequence represents the protein of a human myocardial infarction-
XX CC associated gene containing one or more SNPs of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.

```
SQ Sequence 1267 AA;
Query Match          100.0%; Score 43; DB 8; Length 1267;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLFIAKLNV 9
   |||||
   |||||
   |||||
Db 207 KLFIAKLNV 215

RESULT 22
ABU05243
ID ABU05243 standard; protein; 1304 AA.
XX
AC ABU05243;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1909.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1909; 134pp; English.
XX
XX
The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a
mammal an immunogenic response directed against any of the purified
polypeptide. The purified polypeptide, or the antibody that binds to this
polypeptide, is useful for treating cancer. The polypeptide is also
useful for identifying compounds that binds to a naturally processed
class I or class II MHC-binding polypeptide. The polypeptides and
polynucleotides are particularly useful for treating or preventing
myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
lymphoma or leukaemia. These are also useful for screening agents for
treating the above mentioned diseases. This sequence represents an
expressed protein tag (EPT) isolated from human tissue for translational
profiling. Note: This sequence does not appear in the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
```

```
SQ Sequence 1304 AA;
Query Match          100.0%; Score 43; DB 6; Length 1304;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLFIAKLNV 9
   |||||
   |||||
   |||||
Db 244 KLFIAKLNV 252

RESULT 23
ABU05241
ID ABU05241 standard; protein; 1304 AA.
XX
AC ABU05241;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1907.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOs INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1907; 134pp; English.
XX
XX
The invention describes a purified polypeptide, which comprises a
fragment of a kinase, phosphatase, protease, protease inhibitor,
transporter, cytoskeletal protein, receptor or transcription factor. The
polypeptide is useful as an immunogenic composition for eliciting in a
mammal an immunogenic response directed against any of the purified
polypeptide. The purified polypeptide, or the antibody that binds to this
polypeptide, is useful for treating cancer. The polypeptide is also
useful for identifying compounds that binds to a naturally processed
class I or class II MHC-binding polypeptide. The polypeptides and
polynucleotides are particularly useful for treating or preventing
myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
lymphoma or leukaemia. These are also useful for screening agents for
treating the above mentioned diseases. This sequence represents an
expressed protein tag (EPT) isolated from human tissue for translational
profiling. Note: This sequence does not appear in the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
```

SQ Sequence 1304 AA;
 Query Match 100.0%; Score 43; DB 6; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLFYAKLVN 9
 DB 244 KLFYAKLVN 252
 RESULT 24
 ABU05244
 ID ABU05244 standard; protein; 1304 AA.
 AC ABU05244;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1910.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCO INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 DR WPI; 2003-040607/03.
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1910; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 1304 AA;
 Query Match 100.0%; Score 43; DB 6; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLFYAKLVN 9
 DB 244 KLFYAKLVN 252
 RESULT 25
 ADL16230
 ID ADL16230 standard; protein; 1304 AA.
 AC ADL16230;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human protein tyrosine phosphatase #26.
 XX
 KW cyostatic; immunosuppressive; antiallergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signalling pathway; cell proliferation; cancer;
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003068984-A2.
 PD 21-AUG-2003.
 PF 13-FEB-2003; 2003WO-EP001446.
 XX
 XX 13-FEB-2002; 2002US-0356810P.
 PR 12-FEB-2003; 2003US-00365547.
 PR 13-FEB-2002; 2002US-0356810P.
 PR 12-FEB-2003; 2003US-00365547.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA (CEPT-) CEPT INC.
 XX
 PI Tonks NK, Tzu-Ching M, Cool DE;
 DR WPI; 2003-712572/67.
 DR N-PSDB; ADL16229.
 PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
 PT screening for specific modulators, potential agents for treating e.g.
 PT cancer or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 79; 238pp; English.
 XX
 CC The invention relates to a method for identifying a protein tyrosine
 CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
 CC subjecting a sample, including a cell that contains at least one PTP, to
 CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
 CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
 CC irreversibly modifies the thiol group of an invariant Cys in the active
 CC site of PTP; and (iii) determining, under reducing conditions, the level
 CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host disease; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.
 CC
 CC Sequence 1304 AA;
 XX

Query Match 100.0%; Score 43; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYKLVN 9
 244 KLFYKLVN 252

RESULT 26

ADP65158
 ID ADP65158 standard; protein; 1304 AA.

AC ADP65158;
 XX

DT 12-AUG-2004 (first entry)
 XX

DE Human protein tyrosine phosphatase, receptor type, C, isoform 1.
 XX

XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antineumatic;
 KW antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX

OS Homo sapiens.
 XX

PN WO2003072827-A1.
 XX

PD 04-SEP-2003.
 XX

PF 31-OCT-2002; 2002WO-US035433.
 XX

PR 31-OCT-2001; 2001US-0336220P.
 XX

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX

PI Hirsch R, Thorton SL;
 XX

DR WPI; 2003-712740/67.
 XX

DR GENBANK; NP_002829.
 XX

PT Diagnosing and analyzing autoimmune disease using gene expression
 profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX

PS Disclosure; Page; 56pp; English.
 XX

XX The invention relates to a novel method for diagnosing and analyzing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analyzing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes comprises with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment

CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIFO.
 CC

XX SQ Sequence 1304 AA;
 XX

Query Match 100.0%; Score 43; DB 7; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLFYKLVN 9
 244 KLFYKLVN 252

RESULT 27

ADM67209
 ID ADM67209 standard; protein; 1304 AA.

AC ADM67209;
 XX

DT 03-JUN-2004 (first entry)
 XX

DE Human adipocyte specific leukocyte common antigen protein SeqID 563.
 XX

XX human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; leukocyte common antigen.
 XX

OS Homo sapiens.
 XX

PN WO2004011618-A2.
 XX

PD 05-FEB-2004.
 XX

PF 29-JUL-2003; 2003WO-US023684.
 XX

PR 29-JUL-2002; 2002US-0398785P.
 XX

PR 12-JUN-2003; 2003US-0478206P.
 XX

PA (HMGE-) HMGCE INC.
 XX

PI Chada K, Chouinard R, Ashar H, Sayed AMD;
 XX

DR WPI; 2004-143846/14.
 XX

DR N-PSDB; ADM66930.
 XX

PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX

PS Disclosure; SEQ ID NO 563; 91pp; English.
 XX

XX This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.

XX Sequence 1304 AA;
 SQ Query Match 100.0%; Score 43; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLFYAKLV 9
 DB 244 KLFYAKLV 252

RESULT 28
 ABO84455
 ID ABO84455 standard; protein; 1304 AA.
 AC ABO84455;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human cancer-associated protein HP13-011.2.
 KW Human; cancer-associated protein; cytosstatic; cancer; leukaemia;
 XX lymphoma; CAP.
 OS Homo sapiens.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-0038838-
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 PI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABD32626.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS claim 18; seqid 147; 310pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual), a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above

CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 1304 AA;
 SQ Query Match 100.0%; Score 43; DB 8; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLFYAKLV 9
 DB 244 KLFYAKLV 252

RESULT 29
 ADQ39380
 ID ADQ39380 standard; protein; 1304 AA.
 AC ADQ39380;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1043.
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 XX cardiac; gene therapy; human.
 OS Homo sapiens.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin JT, Iakoubova O;
 XX
 DR WPI; 2004-533949/51.
 DR N-PSDB; ADQ38552.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS claim 10; SEQ ID NO 1043; 145pp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide

comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

CC Sequence 1304 AA;

CC Query Match 100.0%; Score 43; DB 8; Length 1304;
CC Best Local Similarity 100.0%; Pred. NO. 5.3;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 KLFYKXNV 9
CC |||||
CC 244 KLFYKXNV 252

CC RESULT 30
CC ADO39375
CC ID ADO39375 standard; protein; 1306 AA.

CC ADQ39375;
CC 18-NOV-2004 (first entry)

CC Human myocardial infarction-associated gene derived protein, SEQ ID 1038.
CC Myocardial infarction; detection; single nucleotide polymorphism; SNP;
CC cardiant; gene therapy; human.

CC Homo sapiens.

CC WO2004058052-A2.

CC 15-JUL-2004.

CC 22-DEC-2003; 2003WO-US040978.

CC 20-DEC-2002; 2002US-0434778P.

CC 10-MAR-2003; 2003US-0453135P.

CC 30-APR-2003; 2003US-0466412P.

CC 23-SEP-2003; 2003US-0504955P.

CC (APPL-) APPLERA CORP.

CC Cargill M, Devlin JJ, Iakubova O;

CC WPI; 2004-533949/51.

CC N-PSDB; ADQ38547.

CC Identifying an individual who has an altered risk for developing

CC myocardial infarction by detecting a single nucleotide polymorphism in

CC the individual's nucleic acids.

CC Claim 10; SEQ ID NO 1038; 145pp; English.

CC The invention relates to a novel method for identifying an individual who

CC has an altered risk for developing myocardial infarction. The method

CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's

CC nucleic acids, where the presence of the SNP is correlated with an

CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

CC Sequence 1306 AA;

CC Query Match 100.0%; Score 43; DB 8; Length 1306;
CC Best Local Similarity 100.0%; Pred. NO. 5.3;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 KLFYKXNV 9
CC |||||
CC 246 KLFYKXNV 254

CC Search completed: May 3, 2005, 07:35:21
CC Job time : 67.6757 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2005, 05:49:25 ; Search time 31.1351 Seconds

(Without alignments)
148.023 Million cell updates/sec

Title: US-10-003-983C-2

Perfect score: 40

Sequence: 1 ALIAFLAFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	100.0	433	2	Q8MJQ3	Q8MJQ3 aotus vocif
2	40	100.0	451	2	Q7MXN3	Q7MXN3 porphyromon
3	40	100.0	756	2	Q6PJK7	Q6PJK7 homo sapien
4	40	100.0	1290	2	Q6ED60	Q6ED60 aotus vocif
5	40	100.0	1303	2	Q6ED61	Q6ED61 aotus nancy
6	40	100.0	1303	2	Q6ED62	Q6ED62 aotus nigril
7	40	100.0	1304	1	CD45 HUMAN	P08575 homo sapien
8	36	90.0	444	2	Q9XW10	Q9XW10 staphylococ
9	36	90.0	444	2	Q7A1V2	Q7A1V2 staphylococ
10	36	90.0	444	2	Q7A1S0	Q7A1S0 staphylococ
11	36	90.0	444	2	Q6GCI6	Q6GCI6 staphylococ
12	36	90.0	444	2	Q6GCI6	Q6GCI6 staphylococ
13	35	87.5	254	2	Q825Z3	Q825Z3 streptomyce
14	35	87.5	254	2	Q9RCX8	Q9RCX8 streptomyce
15	35	87.5	707	2	Q649H3	Q649H3 uncultured
16	35	87.5	1127	2	F87638	F87638 dengue viru
17	35	87.5	1291	2	Q9XV10	Q9XV10 caenorhabdi
18	34	85.0	114	2	Q67420	Q67420 dengue viru
19	34	85.0	114	2	Q76R51	Q76R51 dengue viru
20	34	85.0	114	2	Q89715	Q89715 dengue viru
21	34	85.0	122	2	Q9YX70	Q9YX70 dengue viru
22	34	85.0	125	2	Q747M4	Q747M4 geobacter s
23	34	85.0	125	2	Q9YX69	Q9YX69 dengue viru
24	34	85.0	133	2	Q719K5	Q719K5 dengue viru
25	34	85.0	133	2	Q719K6	Q719K6 dengue viru
26	34	85.0	133	2	Q719K7	Q719K7 dengue viru
27	34	85.0	133	2	Q719K8	Q719K8 dengue viru
28	34	85.0	133	2	Q719K9	Q719K9 dengue viru
29	34	85.0	133	2	Q719L0	Q719L0 dengue viru
30	34	85.0	133	2	Q719L1	Q719L1 dengue viru
31	34	85.0	133	2	Q719L2	Q719L2 dengue viru

32	34	85.0	133	2	Q719L3	Q719L3 dengue viru
33	34	85.0	133	2	Q719L4	Q719L4 dengue viru
34	34	85.0	133	2	Q719L5	Q719L5 dengue viru
35	34	85.0	134	2	Q91755	Q91755 dengue viru
36	34	85.0	134	2	Q9WLM3	Q9WLM3 dengue viru
37	34	85.0	135	2	Q91754	Q91754 dengue viru
38	34	85.0	135	2	Q91756	Q91756 dengue viru
39	34	85.0	135	2	Q9YX66	Q9YX66 dengue viru
40	34	85.0	135	2	Q9YX67	Q9YX67 dengue viru
41	34	85.0	135	2	Q9YX68	Q9YX68 dengue viru
42	34	85.0	139	2	Q96N74	Q96N74 homo sapien
43	34	85.0	151	2	Q9QF33	Q9QF33 dengue viru
44	34	85.0	151	2	Q64FN0	Q64FN0 dengue viru
45	34	85.0	151	2	Q64FN1	Q64FN1 dengue viru

ALIGNMENTS

RESULT 1
Q8MJQ3 PRELIMINARY, PRT, 433 AA.
ID Q8MJQ3
AC Q8MJQ3
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE CD45 phosphatase (Fragment).
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_Taxid=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Montoya G.E., Vernot J.P., Patarroyo M.E.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF364095; AAM48511.1; -
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00102; Y_PTYRPHPTASE.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT NON_TER
FT NON_TER
SQ SEQUENCE 433 AA; 50151 MW; BBAB00C4F008E8D0 CRC64;
Query Match 100.0%; Score 40; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
DB 114 ALIAFLAFL 122
RESULT 2
ID Q7MXN3 PRELIMINARY, PRT, 451 AA.
AC Q7MXN3
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Membrane-bound lytic murein transglycosylase D, putative.
 GN OrderedLocNames=RC0139;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteri; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 RA DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 Dewhirst F.E., Fraser C.M.;
 RA "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83."
 RT J. Bacteriol. 185:5591-5601(2003).
 DR EMBL: AE017172; AAQ65380.1; -.
 DR TIGR: PG0139; -.
 DR GO: GO:0016998; P:cell wall catabolism; IEA.
 DR InterPro: IPR002482; LysM.
 DR InterPro: IPR008258; SLT.
 DR InterPro: IPR000189; Transglyc_AS.
 DR Pfam: PF01476; LysM; 1.
 DR Pfam: PF01464; SLT; 1.
 DR PROSITE: PS00922; TRANSGLYCOSYLASE; UNKNOWN 1.
 KW Complete proteome.
 SQ SEQUENCE 451 AA; 50888 MW; C33F1475064384C CRC64;

Query Match 100.0%; Score 40; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAPL 9
 Db 11 ALIAFLAPL 19

RESULT 3
 ID 06PUK7 PRELIMINARY; PRT; 756 AA.
 AC 06PUK7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE PTPRC protein (Fragment).
 GN Name=PTPRC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haib H.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Miliaty S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Vallalou D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Heitton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywninski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maria M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014239; AAH14239.1; -.
 DR HSSP: P18031; IAA.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR00242; Tyr_PP.
 DR Pfam: PF00041; fn3; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00194; PTPc; 1.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 FT NON TER 756 756
 SQ SEQUENCE 756 AA; 85430 MW; 8A9A863827BD69E6 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 756;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAPL 9
 Db 528 ALIAFLAPL 536

RESULT 4
 ID 06ED60 PRELIMINARY; PRT; 1290 AA.
 AC 06ED60;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CD45.
 OS Aotus vociferans (Spix's owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15245371;
 RA Montoya G.E., Vernot J.P., Patatroyo M.E.;
 RT "Comparative analysis of CD45 protein in primate context: owl monkeys
 RT vs. human."
 RL Tissue Antigens 64:165-172(2004).
 DR EMBL: AY445818; AAS06903.1; -.
 DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003595; PTPC motif.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPHPTASE.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00194; PTPc; 2.
 DR SMART: SM00404; PTPC motif; 2.
 DR PROSITE: PS50853; FN3; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_PTP; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

KW Hydrolase. 1290 AA; 145616 MW; 99E810C75D932824 CRC64;
SQ SEQUENCE

Query Match 100.0%; Score 40; DB 2; Length 1290;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAPL 9
|||||
Db 562 ALIAFLAPL 570

RESULT 5

Q6ED61 PRELIMINARY; PRT; 1303 AA.

AC Q6ED61; 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE CD45.

OC Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;

RN [1]
RP SEQUENCE FROM N.A.

RX PubMed=15245371;

RA Montoya G.E., Vernot J.P., Patarroyo M.E.;

RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human.";

RL Tissue Antigens 64:165-172(2004).

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR008957; FN_III-like.

DR InterPro: IPR003595; PTPC_motif.

DR InterPro: IPR000242; TYR_PP.

DR Pfam: PF00041; fn3_2.

DR PRINTS: PR00700; PRTYPHPTASE.

DR SMART; SM00060; FN3; 2.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS50853; FN3_2.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

KW Hydrolase. 1303 AA; 146929 MW; D0EB0C640D1D17E8 CRC64;
SQ SEQUENCE

Query Match 100.0%; Score 40; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 71;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAPL 9
|||||
Db 575 ALIAFLAPL 583

RESULT 6

Q6ED62 PRELIMINARY; PRT; 1303 AA.

AC Q6ED62; 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DE CD45.

OC Aotus nigriceps (Black-headed owl monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=57175;

RN [1]
RP SEQUENCE FROM N.A.

RX PubMed=15245371;

RA Montoya G.E., Vernot J.P., Patarroyo M.E.;

RT "Comparative analysis of CD45 protein in primate context: owl monkeys
vs. human.";

RL Tissue Antigens 64:165-172(2004).

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR008957; FN_III-like.

DR InterPro: IPR003595; PTPC_motif.

DR InterPro: IPR000242; TYR_PP.

DR Pfam: PF00041; fn3_2.

DR PRINTS: PR00700; PRTYPHPTASE.

DR SMART; SM00060; FN3; 2.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS50853; FN3_2.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.

DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.

KW Hydrolase. 1303 AA; 146586 MW; 9BB023EBF4BC1165 CRC64;
SQ SEQUENCE

Query Match 100.0%; Score 40; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 71;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAFLAPL 9
|||||
Db 575 ALIAFLAPL 583

RESULT 7

CD45 HUMAN STANDARD; PRT; 1304 AA.

AC P08575; Q16614; Q9H0Y6;

DT 01-AUG-1988 (Rel. 08, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Leukocyte common precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)
(T200).

GN Name=PTPRC; Synonyms=CD45;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING.

RC TISSUE=Lymphocytes;

RX MEDLINE=8601067; PubMed=2824653;

RA Streuli M., Hall L.R., Suga Y., Schloeman S.F., Saito H.;

RT "Differential usage of three exons generates at least five different
mRNAs encoding human-leukocyte common antigens.";

RL J. Exp. Med. 166:1548-1566(1987).

RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING.

RX MEDLINE=87275816; PubMed=2956090;

RA Ralph S.J., Thomas M.L., Morton C.C., Trowbridge I.S.;

RT "Structural variants of human T200 glycoprotein (leukocyte-common
antigen).";

RL EMBO J. 6:1251-1257(1987).

RN [3]
RP SEQUENCE OF 191-1304 FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=89009812; PubMed=2971730;

RA Hall L.R., Streuli M., Schloeman S.F., Saito H.;

RT "Complete exon-intron organization of the human leukocyte common
antigen (CD45) gene.";

RL J. Immunol. 141:2781-2787 (1988).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=89017162; PubMed=2845400;
 RA Chabouneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
 RT "The leukocyte common antigen (CD45): a putative receptor-linked
 protein tyrosine phosphatase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186 (1988).
 RN [5]
 RP MUTAGENESIS.
 RX MEDLINE=90316093; PubMed=1695146;
 RA Striell M., Krueger N.X., Thai T., Tang M., Salto H.;
 RT "Distinct functional roles of the two intracellular phosphatase like
 domains of the receptor-linked protein tyrosine phosphatases LCA and
 LAR.";
 RL EMBL J. 9:2399-2407 (1990).
 CC -1- FUNCTION: Required for T-cell activation through the antigen
 receptor. The first PTase domain has enzymatic activity, while
 the second one seems to affect the substrate specificity of the
 first one.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 tyrosine + phosphate.
 CC -1- SUBUNIT: Binds GANAB and PRKCSH (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=At least 8 isoforms are produced;
 CC Name=1;
 CC IsoId=P08575-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P08575-2; Sequence=VSP_007780;
 CC -1- PTM: Heavily N- and O-glycosylated.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 1/6 subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD45 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; Y00638; CA68669.1; -;
 DR EMBL; Y00662; CA68669.1; -;
 DR EMBL; M23492; AAD15273.2; -;
 DR EMBL; M23496; AAD15273.2; JOINED.
 DR EMBL; M23466; AAD15273.2; JOINED.
 DR EMBL; M23467; AAD15273.2; JOINED.
 DR EMBL; M23468; AAD15273.2; JOINED.
 DR EMBL; M23469; AAD15273.2; JOINED.
 DR EMBL; M23470; AAD15273.2; JOINED.
 DR EMBL; M23471; AAD15273.2; JOINED.
 DR EMBL; M23472; AAD15273.2; JOINED.
 DR EMBL; M23473; AAD15273.2; JOINED.
 DR EMBL; M23474; AAD15273.2; JOINED.
 DR EMBL; M23475; AAD15273.2; JOINED.
 DR EMBL; M23476; AAD15273.2; JOINED.
 DR EMBL; M23477; AAD15273.2; JOINED.
 DR EMBL; M23478; AAD15273.2; JOINED.
 DR EMBL; M23479; AAD15273.2; JOINED.
 DR EMBL; M23480; AAD15273.2; JOINED.
 DR EMBL; M23481; AAD15273.2; JOINED.
 DR EMBL; M23482; AAD15273.2; JOINED.
 DR EMBL; M23483; AAD15273.2; JOINED.
 DR EMBL; M23484; AAD15273.2; JOINED.
 DR EMBL; M23485; AAD15273.2; JOINED.
 DR EMBL; M23486; AAD15273.2; JOINED.
 DR EMBL; M23487; AAD15273.2; JOINED.

DR EMBL; M23488; AAD15273.2; JOINED.
 DR EMBL; M23489; AAD15273.2; JOINED.
 DR EMBL; M23490; AAD15273.2; JOINED.
 DR EMBL; M23491; AAD15273.2; JOINED.
 DR PIR; A46546; A46546.
 DR HSSP; P18031; 1C88.
 DR IntAct; P08575; -;
 DR GlycoSiteDB; P08575; -;
 DR GeneW; HGNC:9666; PTPRC.
 DR MIM; 151460; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0005001; F: transmembrane receptor protein tyrosine pho. . .; TAS.
 DR GO; GO:0007166; P: cell surface receptor linked signal transdu. . .; TAS.
 DR InterPro; IPR003951; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00700; PTPPHPTASE.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR KW Alternative splicing; Antigen; Glycoprotein; Hydrolase;
 KW Phosphorylation; Protein phosphatase; Repeat; Signal; T-cell;
 KW Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 1304
 FT DOMAIN 24 575
 FT TRANSMEM 576 597
 FT DOMAIN 598 1304
 FT DOMAIN 390 478
 FT DOMAIN 482 570
 FT DOMAIN 670 919
 FT DOMAIN 961 1235
 FT ACT_SITE 851 851
 FT ACT_SITE 1167 1167
 FT CARBOHYD 78 78
 FT CARBOHYD 90 90
 FT CARBOHYD 95 95
 FT CARBOHYD 184 184
 FT CARBOHYD 190 190
 FT CARBOHYD 197 197
 FT CARBOHYD 222 232
 FT CARBOHYD 260 260
 FT CARBOHYD 270 270
 FT CARBOHYD 276 276
 FT CARBOHYD 335 335
 FT CARBOHYD 378 378
 FT CARBOHYD 419 419
 FT CARBOHYD 468 468
 FT CARBOHYD 488 488
 FT CARBOHYD 529 529
 FT VARSPLYC 32 192
 FT MUTAGEN 851 851
 FT CONFLICT 650 650
 FT CONFLICT 1207 1207
 SQ SEQUENCE 1304 AA; 147253 MW; A08FC22D069BAF7 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 1304;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALIAPLAPL 9
 Db 576 ALIAPLAPL 584

RESULT 8
 Q99WU0

ID 099WU0 PRELIMINARY; PRT; 444 AA.
AC 099WU0;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SAV0286;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chi L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani U.-I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003358; BAB56448.1; -;
DR PIR; H89792; H89792.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 444 AA; 52024 MW; FACCPE3353DE1F77 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LIAFLAFL 9
DB 241 LIAFLAFL 248

RESULT 9
ID 07A1V2 PRELIMINARY; PRT; 444 AA.
AC 07A1V2;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein MW0262.
GN OrderedLocustNames=MM0262;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Chi L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004823; BAB94127.1; -;
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 444 AA; 52024 MW; FACCPE3353DE1F77 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LIAFLAFL 9
DB 241 LIAFLAFL 248

RESULT 10

O7A7S0
ID 07A7S0 PRELIMINARY; PRT; 444 AA.
AC 07A7S0;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein SA0275.
GN OrderedLocustNames=SA0275;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chi L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani U.-I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003130; BAB41499.1; -;
KM Complete proteome.
SQ SEQUENCE 444 AA; 52024 MW; FACCPE3353DE1F77 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LIAFLAFL 9
DB 241 LIAFLAFL 248

RESULT 11
ID 06GCI6 PRELIMINARY; PRT; 444 AA.
AC 06GCI6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Putative membrane protein.
GN OrderedLocustNames=SA50262;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Foster T.J., Moore C.E., Hurst L., Ackin R., Barron A.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Ackin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsis K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG42033.1; -;
KM Complete proteome.
SQ SEQUENCE 444 AA; 52024 MW; FACCPE3353DE1F77 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LIAFLAFL 9

Db 241 LIAFLAFL 248

RESULT 12

OG6K25 PRELIMINARY; PRT; 444 AA.

AC 06GK25
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative membrane protein.
 GN OrderedLocustNames=SAV7300;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282458;
 RN [1]

SEQUENCE FROM N.A.

RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Knight M.C., Foster T.U., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Baason N., Bentley S.D., Chillingworth T., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571856; CAG39310.1; -
 KW Complete proteome.
 SQ SEQUENCE 444 AA; 52039 MW; 3D3DF9721F093AFD CRC64;

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 444;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LIAFLAFL 9
 Db 241 LIAFLAFL 248

RESULT 13

OG25Z3 PRELIMINARY; PRT; 254 AA.

AC 0825Z3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Putative integral membrane protein.
 GN OrderedLocustNames=SAV7300;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=33903;
 RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]

RN SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,

RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005050; BAC75011.1; -
 KW Complete proteome.
 SQ SEQUENCE 254 AA; 27937 MW; E236371BEF6216E CRC64;

Query Match

Best Local Similarity 87.5%; Score 35; DB 2; Length 254;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIAFLAFL 9
 Db 218 LIAFLAFL 226

RESULT 14

OG9CX8 PRELIMINARY; PRT; 254 AA.

AC 09RCX8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Putative integral membrane protein.
 GN ORFNames=SCM10.20;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]

SEQUENCE FROM N.A.

RX STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J.R., Barrett B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939107; CAB63181.1; -
 KW Complete proteome.
 SQ SEQUENCE 254 AA; 27737 MW; 350FD1F25C288155 CRC64;

Query Match

Best Local Similarity 87.5%; Score 35; DB 2; Length 254;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIAFLAFL 9
 Db 218 LIAFLAFL 226

RESULT 15

OG49H3 PRELIMINARY; PRT; 707 AA.

AC 0649H3;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Sterol-regulatory element-binding protein intramembrane protease.
 GN ORFNames=GZ35A2.29;
 OS Uncultured archaeon GZf0835A2.
 OC Archaea; environmental samples.
 OX NCBI_TaxID=285357;
 RN [1]

RN SEQUENCE FROM N.A.

RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Deter J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics.";
RL Science 305:1457-1462(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Deter J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY714863; AAU83954.1; -.
KW Protease.
SQ SEQUENCE 707 AA; 77979 MW; EE0581020FC9E469 CRC64;
Query Match 87.5%; Score 35; DB 2; Length 707;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALIAFLAFL 9
Db 227 ALIAFLFL 235

Search completed: May 3, 2005, 05:58:30
Job time : 40.1351 secs

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